

144326

From: Riggins, Patrick S.
Sent: Monday, February 07, 2005 8:35 AM
To: STIC-Biotech/ChemLib
Subject: seq search

This is in regard to case #10006265

Please search SEQ ID NOs, 2, 4, and 17(protein) against the commercial nucleotide databases in both a standard search and a standard oligomer search. The following information may be helpful in the search. I previously requested an alignment of these sequences. The results were as follows: SEQ ID NOs 2 and 17 are identical from 1-642. SEQ ID NO 2 and 17 are identical with SEQ ID NO 4 from 1-238. If this is in any way unclear, please call and I'll be happy to clarify.

The claims of interest are appended below. If you identify any other necessary searches based on these claims I would appreciate they be performed also. I'm fairly confident I have requested all that is necessary though. Incidentally, SEQ ID NOs 1, 3, and 16 encode SEQ ID NOs 2, 4, and 17, respectively.

1. An isolated nucleic acid of any one of (a) to (d) below:

(a) a nucleic acid encoding a protein comprising the amino acid sequence of any one of SEQ ID NOs:2, 4 or 17,

(b) a nucleic acid comprising a coding region in the nucleotide sequence of any one of SEQ ID NOs:1, 3 or 16,

(c) a nucleic acid encoding a protein that comprises the amino acid sequence of any one of SEQ ID NOs:2, 4 or 17, in which one or more amino acids are replaced, deleted, inserted and/or added and that is functionally equivalent to the protein comprising the amino acid sequence of any one of SEQ ID NOs:2, 4 or 17, and

(d) a nucleic acid that hybridizes under stringent conditions with the nucleic acid comprising the nucleotide sequence of any one of SEQ ID NOs:1, 3 or 16, and that encodes a protein functionally equivalent to the protein comprising the amino acid sequence of any one of SEQ ID NOs:2, 4 or 17.

2. An isolated nucleic acid encoding the amino acid sequence of any one of SEQ ID NOs:2, 4 or 17 or a fragment thereof.

Thank you,
Pat Riggins

Patrick Riggins
Examiner
Art Unit 1636
REM 3A64
571-272-6102

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FEB - 7 2005
STIC

STAFF USE ONLY

Searcher: _____
Searcher Phone: 2- _____
Date Searcher Picked up: _____
Date Completed: 2-7-05
Searcher Prep/Rev. Time: _____
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Type of Search

NA Sequence: # _____
AA Sequence: # _____
Structure: # _____
Bibliographic: _____
Litigation: _____
Patent Family: _____
Other: _____

Vendors and cost where applicable

STN: _____
DIALOG: _____
QUESTEL/ORBIT: _____
LEXIS/NEXIS: _____
SEQUENCE SYSTEM: _____
WWW/Internet: _____
Other(Specify): _____

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OM protein - nucleic search, using frame_plus_p2n model

Run on: February 23, 2005, 07:24:37 ; Search time 8242.85 Seconds

(without alignments)
3832.754 Million cell updates/sec

Title: US-10-006-265-2

Perfect score: 3484

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Searched: 4708233 seqs, 24227607955 residues

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Post-processing: Minimum Match 0%
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Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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ALIGNMENTS

RESULT 1	LOCUS	DEFINITION	ACCESSION	VERSION	KEYWORDS	SOURCE	ORGANISM	REFERENCE	TITLE	AUTHORS	JOURNAL	COMMENT
BD091864	Novel hemopoietin receptor protein, NR10.	BD091864	BD091864.1	GI:22637475	WO 0075314-A/1.	Homo sapiens (human)	Homo sapiens	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.	Maeda,M. and Yaguchi,N.	Novel hemopoietin receptor protein, NR10	Patent: WO 0075314-A 14-DEC-2000;	CHUGAI RESEARCH INSTITUTE FOR MOLECULAR MEDICINE INC, MASATSUGU
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BD091864	Novel hemopoietin receptor protein, NR10.	BD091864	BD091864.1	GI:22637475	WO 0075314-A/1.	Homo sapiens (human)	Homo sapiens	Eukaryota; Metazoa; Chordata; Crani				

FEATURES

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ORIGIN

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DB:	6	Gaps:	0

US-10-006-265-2 (1-652) x BD091864 (1-2969)

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 QY 261 ArgLeuLeuTrpLysLysAlaArgGlyAlaProValLeuGluLysThrLeuGlyTyTrpAsn 280
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RESULT 2
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LOCUS Novel hemopoietin receptor protein, NR10.
DEFINITION BD091877
ACCESSION BD091877.1 GI:22637488
VERSION WO 0075314-A/14.
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
REFERENCE 1 (bases 1 to 2119)
AUTHORS Maeda,M. and Yaguchi,N.
TITLE Novel hemopoietin receptor protein, NR10
JOURNAL Patent: WO 0075314-A 14 14-DEC-2000;
CHUGAI RESEARCH INSTITUTE FOR MOLECULAR MEDICINE INC, MASATSUGU
MADA, NORIKO YAGUCHI
COMMENT OS Homo sapiens (human)
PN WO 0075314-A/14
PD 14-DEC-2000
PF 01-JUN-2000 WO 2000JP003556
PR 02-JUN-1999 JP 99P 155797,30-JUL-1999 JP 99P 217797 PI
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PC C12N15/12,C12N5/10,C07K14/715,C07K16/28,C12P21/02,G01N33/53,
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FH Key Location/Qualifiers
FT CDS (11)..(1996).
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Qy 441 LysValGluAsnLLeGlyValLysThrValThrLLeThrTrpLysGluLLeProLysSer 460
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Qy 461 GluArgLysGlyLLeLLeCysAsnTyrThrLLePheTyrGlnAlaGluGlyLysGly 480
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RESULT 3
AX365201 LOCUS AX365201 2903 bp DNA linear PAT 15-FEB-2002
DEFINITION Sequence 53 from Patent WO0200721.
ACCESSION AX365201
VERSION AX365201.1 GI:18696955
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 Sprecher, C.A., Presnell, S.R., Gao, Z., Whitmore, T.E., Kuiper, J.L.
AUTHORS and Maurer, M.F.
TITLE Cytokine receptor zcytor17
JOURNAL Patent: WO 0200721-A 53 03-JAN-2002;
Zymogenetics, Inc. (US)
FEATURES
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Alignment Scores:
Pred. No.: 3,226-300 Length: 2903
Score: 3451.00 Matches: 650
Percent Similarity: 99.85% Conservative: 1
Best Local Similarity: 99.69% Mismatches: 1
Query Match: 99.05% Indels: 1
DB: 6 Gaps: 0

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Qy	621	LeuValValAsnPheGlyAsnValLeuGlnGluIlePheThrAspGluAlaArgThrCly	640
Db	2357	TTGGTGGGAACCTTTGGGAATGTTCTTGAAGAAATTTTCAAGATGAAGAACGAAACGGGT	2416
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Db	2417	CAGCA-AAAACATTTTGAAGGGGAAAAAATGGGAC 2451	

LOCUS	AY499342	2903 bp	mRNA	linear	PRI 10-JUL-2004
DEFINITION	Homo sapiens interleukin 31RA splice variant x4 (IL31RA) mRNA,				
ACCESSION	AY499342	complete cds, alternatively spliced.			
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ORGANISM	Homo sapiens				
REFERENCE	Mukaiyoti, A.; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.				
AUTHORS	1 (bases 1 to 2903)				
TITLE	Dillon,S.R., Sprecher,C., Hammond,A., Bilborough,J.,				
JOURNAL	Rosenthal-Franklin,M., Pressnell,S.R., Haugen,H.S., Maurer,M.,				
PUBMED	Harder,B., Johnston,J., Bort,S., Mudri,S., Kullper,J.L.,				
REFERENCE	Bukowski,T., Shea,P., Dong,D.L., Dasovich,M., Grant,F.J.,				
AUTHORS	Lockwood,L., Levin,S.D., LeCiel,C., Maggie,K., Day,H., Topouzis,S.,				
	Kramer,J., Kuestner,R., Chen,Z., Foster,D., Parrish-Novak,J. and				
	Gross,J.A.				
	Interleukin 31, a cytokine produced by activated T cells, induces				
	dermatitis in mice				
	Nat. Immunol. 5 (7), 752-760 (2004)				
	15184896				
	2 (bases 1 to 2903)				
	Dillon,S.R., Sprecher,C., Hammond,A., Rosenthal-Franklin,M.,				
	Pressnell,S.R., Haugen,H., Bilborough,J., Maurer,M., Harder,B.,				
	Johnston,J., Bort,S., Mudri,S., Kullper,J., Bukowski,T., Shea,P.,				
	Dong,D., Dasovich,M., Lockwood,L., Levin,S., LeCiel,C., Maggie,K.,				
	Kramer,J., Kuestner,R., Chen,Z., Foster,D., Parrish-Novak,J. and				
	Gross,J.A.				
	Direct Submission				
	Submitted (10-DEC-2003) Bioinformatics, ZymoGenetics, Inc., 1201				
	Eastlake Avenue East, Seattle, WA 98102, USA				
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 REFERENCE
 1 Sprecher, C.A., Presnell, S.R., Gao, Z., Whitmore, T.E., Kuiper, J.L.
 and Maurer, M.F.

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DEFINITION complete cde, alternatively spliced.
ACCESSION AY499339 GI:46276456
VERSION AY499339.1
KEYWORDS
SOURCE Homo sapiens (human)
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 2529)
AUTHORS Dillon,S.R., Sprecher,C., Hammond,A., Bilborough,J.,
Rosenfeld-Franklin,M., Presnell,S.R., Haugen,H.S., Maurer,M.,
Harder,B., Johnston,J., Bort,S., Mudri,S., Kuijper,J.L.,
Bukowski,T., Shea,P., Dong,D.L., Dasovich,M., Grant,F.J.,
Lockwood,L., Levin,S.D., Leciel,C., Maggite,K., Day,H., Topouzis,S.,
Kramer,J., Kuestner,R., Chen,Z., Foster,D., Parrish-Novak,J. and
Gross,J.A.
TITLE Interleukin 31, a cytokine produced by activated T cells, induces
dermatitis in mice
JOURNAL Nat. Immunol. 5 (7), 752-760 (2004)
PUBMED 15184896
REFERENCE 2 (bases 1 to 2529)
AUTHORS Dillon,S.R., Sprecher,C., Hammond,A., Rosenfeld-Franklin,M.,
Presnell,S.R., Haugen,H., Bilborough,J., Maurer,M., Harder,B.,
Johnston,J., Bort,S., Mudri,S., Kuijper,J., Bukowski,T., Shea,P.,
Dong,D., Dasovich,M., Lockwood,L., Levin,S., Leciel,C., Maggite,K.,
Kramer,J., Kuestner,R., Chen,Z., Foster,D., Parrish-Novak,J. and
Gross,J.A.
TITLE Direct Submission
JOURNAL Submitted (10-DEC-2003) Bioinformatics, ZymoGenetics, Inc., 1201
Eastlake Avenue East, Seattle, WA 98102, USA
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 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 REFERENCE 1 (bases 1 to 4315)
 AUTHORS Maeda, M., Yaguchi, N. and Hasegawa, M.
 TITLE NR10 splicing variants
 JOURNAL Patent: WO 02077230-A 1 03-OCT-2002;
 CHUGAI PHARMACEUTICAL CO LTD, MASATSUGU MAEDA, NORIKO YAGUCHI,
 MASAKAZU HASEGAWA
 OS Homo sapiens (human)
 PN WO 02077230-A/1
 PD 03-OCT-2002
 PF 22-MAR-2002 WO 2002JP002769
 PR 26-MAR-2001 JP 01P 087298
 PI MASATSUGU MAEDA, NORIKO YAGUCHI, MASAKAZU HASEGAWA PC
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 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 REFERENCE 1
 AUTHOR Cosman, D.J., Mosley, B.A., Bird, T.A., Dubose, R.F. and Wiley, S.R.
 TITLE Hematopoietic receptors hprt1 and hprt2
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 ImmuneX Corporation (US)
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Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
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Bukowski,T., Shea,P., Dong,D.L., Dasovich,M., Grant,F.J.,
Lockwood,L., Levin,S.D., Leckel,C., Waggle,K., Day,H., Topouzis,S.,
Kramer,J., Kuestner,R., Chen,Z., Foster,D., Parrish-Novak,J. and
Gross,J.A.
Interleukin 31, a cytokine produced by activated T cells, induces
dermatitis in mice
Nat. Immunol. 5 (7), 752-760 (2004)
15184896
2 (bases 1 to 2393)
Dillon,S.R., Sprecher,C., Hammond,A., Rosenfeld-Franklin,M.,
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Johnston,J., Bort,S., Mudri,S., Kuljper,J., Bukowski,T., Shea,P.,
Dong,D., Dasovich,M., Lockwood,L., Levin,S., Leckel,C., Waggle,K.,
Kramer,J., Kuestner,R., Chen,Z., Foster,D., Parrish-Novak,J. and
Gross,J.A.
Direct Submission
Submitted (10-DEC-2003) Bioinformatics, ZymoGenetics, Inc., 1201
Eastlake Avenue East, Seattle, WA 98102, USA
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Alignment Scores:
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Score: 3435.00 Matches: 647
Percent Similarity: 99.85% Conservative: 1
Best Local Similarity: 99.69% Mismatches: 1
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LOCUS AX365149
DEFINITION Sequence 1 from Patent WO0200721.
ACCESSION AX365149
VERSION AX365149.1 GI:18696908
KEYWORDS
SOURCE
ORGANISM Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE
1 Sprechet,C.A., Presnell,S.R., Gao,Z., Whitmore,T.E., Kuiper,J.L.
AUTHORS and Maurer,M.F.
TITLE Cyokine receptor zcytor17
JOURNAL Patent: WO 0200721-A 1 03-JAN-2002;
ZymoGenetics, Inc. (US)
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ORIGIN
Alignment Scores:
Pred. No.: 6,84e-299 Length: 2402
Score: 3435.00 Matches: 647
Percent Similarity: 99.85% Conservative: 1
Best Local Similarity: 99.69% Mismatches: 1
Query Match: 98.59% Indels: 1
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 DEFINITION Sequence 3 from Patent WO0229060.
 ACCESSION AX467333
 VERSION AX467333.1 GI:21900584
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 ORGANISM Homo sapiens
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 Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
 REFERENCE
 AUTHORS Cosman, D.J., Mosley, B.A., Bird, T.A., Dubose, R.F. and Wiley, S.R.
 TITLE Hematopoietic receptors hprt1 and hprt2
 JOURNAL Patent: WO 0229060-A 3 11-Apr-2002;
 Immunex Corporation (US)
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RESULT 12
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 ACCESSION BD178872
 VERSION BD178872.1 GI:30016139
 KEYWORDS WO 02077230-A/3
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
 1 (bases 1 to 2952)
 REFERENCES
 AUTHORS Maeda, M., Yaguchi, N. and Hasegawa, M.
 TITLE NR10 splicing variants
 JOURNAL CHUGAI PHARMACEUTICAL CO LTD, MASATSUGU MAEDA, NORIKO YAGUCHI,
 MASAKAZU HASEGAWA
 OS Homo sapiens (human)
 PN WO 02077230-A/3
 PD 03-OCT-2002
 PF 22-MAR-2002 WO 2002JP002769
 PR 26-MAR-2001 JP 01P 087298
 PI MASATSUGU MAEDA, NORIKO YAGUCHI, MASAKAZU HASEGAWA PC
 C12N15/12, C07K14/715, C07K16/28, C12N1/15, C12N1/19, C12N1/21, PC
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Alignment Scores:

Pred. No.: 9,08e-299 Length: 2952
 Score: 3435.00 Matches: 647
 Percent Similarity: 99.85% Conservative: 1
 Best Local Similarity: 98.69% Mismatches: 1
 Query Match: 98.59% Indels: 1
 DB: 6 Gaps: 0

US-10-006-265-2 (1-652) x BD178872 (1-2952)

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 QY 403 ProPheTrpCysTYrAsnIleSerValTYrProMetLeuHisAspIysValGlyGluPro 422
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 QY 443 GluAsnIleGlyValIysThrValThrIleThrTrpIysGluIleProIysSerGluArg 462
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 QY 463 IysGlyIleIleCysAsnTYrThrIlePheTYrGlnAlaGluIleGlyIysGlyPheSer 482
 DB 1450 AAGGATATCATCTGCAATCACACATCTTTTCAAGCTGAAAGGTGAAAAAGATTTCTCC 1509
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 DB 1510 AAGACAGTAAATTCAGCATCTTGCAGTACGAGCTGAGATCCCTGAAGAAAGACCTT 1569
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RESULT 13
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 LOCUS BD178871
 DEFINITION NR10 splicing variants.
 ACCESSION BD178871

VERSION BDI78871.1 GI:30016138
KEYWORDS MO 02077230-A/2.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Mammalia; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Eumetazoa; Eutheria; Primates; Catarrhini; Homidae; Homo.
REFERENCE 1 (bases 1 to 5271)
AUTHORS Maeda, M., Yaguchi, N. and Hasegawa, M.
TITLE NR10 splicing variants
JOURNAL Patent: WO 02077230-A 2 03-OCT-2002;
CHUGAI PHARMACEUTICAL CO LTD, MASATSU MAEDA, NORIKO YAGUCHI,
MASAKAZU HASEGAWA
COMMENT OS Homo sapiens (human)
PN MO 02077230-A/2
PD 03-OCT-2002
PF 22-MAR-2002 WO 2002JP002769
PI 26-MAR-2001 JP 01P 087298
PI MASATSU MAEDA, NORIKO YAGUCHI, MASAKAZU HASEGAWA PC
C12N15/12, C07K14/715, C07K16/28, C12N1/15, C12N1/19, C12N1/21, PC
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Query Match: 99.59% Indels: 1
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QY 23 LeuProSerLeuCybLysPheSerLeuAlaAlaLeuProAlaLysProGlnAsnLysSer 42
DB CTCCCTCCTCAGCTGCAAAATTCAGCTGGCAGCTTCGACGTAAGCTGAGAACATTTCC 189
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ACCESSION AF486620
VERSION AF486620.1 GI:20563276

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KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
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AUTHORS Ghilardi, N., Li, J., Hongo, J. A., Yi, S., Gurney, A. and de
Savage, F. J.
TITLE A novel type I cytokine receptor is expressed on monocytes, signals
proliferation, and activates STAT-3 and STAT-5
JOURNAL J. Biol. Chem. 277 (19), 16831-16836 (2002)
MEDLINE 21988187
PUBMED 11877449
REFERENCE 2 (bases 1 to 2199)
AUTHORS Ghilardi, N., Li, J., Hongo, J. A., Yi, S., Gurney, A. and de
Savage, F. J.
TITLE Direct Submission
SUBMITTED (21-FEB-2002) Molecular Oncology, Genentech, 1 DNA Way,
South San Francisco, CA 94080, USA
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GenCore version 5.1.6
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Listing first 45 summaries

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-DB=N Geneseq_16Dec04 -QMT=fastcap -SUFFIX=ring -MINMATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blomsum62 -TRANS=human40.cdi
-LIST=45 -DOCALLIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15
-MODE=LOCAL -OUTPRNT=pco -NOR=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US10006265 @CGN_1_1_1098 @runat_18022005_094657_22172 -MCPU=6 -ICPU=3
-NO MMAP -LARGEOQUERY -NEG SCORES=0 -WAIT -DSPLOCK=100 -LONGLOG
-DEV TIMEOUT=130 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : N_Geneseq_16Dec04:*

1: Geneseqn1980s:*\n2: Geneseqn1990s:*\n3: Geneseqn2000s:*\n4: Geneseqn2001as:*\n5: Geneseqn2001bs:*\n6: Geneseqn2002as:*\n7: Geneseqn2002bs:*\n8: Geneseqn2003as:*\n9: Geneseqn2003bs:*\n10: Geneseqn2003cs:*\n11: Geneseqn2003ds:*\n12: Geneseqn2004as:*\n13: Geneseqn2004bs:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	3484	100.0	2969	4 AAC92337	Aac92337 Human hae
2	3451	99.1	2119	4 AAC92350	Aac92350 Human hae
3	3451	99.1	2903	6 ABA93808	Ab93808 Human zcy
4	3451	99.1	2903	10 ADD68146	Add68146 Human zcy
5	3451	99.1	2903	11 ADL26569	Adl26569 Human cyt

6	3441	98.8	2529	6 ABA93803	Ab93803 Human zcy
7	3441	98.8	2529	11 ADL26671	Adl26671 Human cyt
8	3441	98.8	4315	8 ABO83363	Ab83363 Human NR1
9	3435	98.6	2386	6 ABA93767	Ab93767 Human zcy
10	3435	98.6	2402	11 ADL26673	Adl26673 Human cyt
11	3435	98.6	2480	6 AAD38772	Aad38772 Human hae
12	3435	98.6	2481	10 ACF36434	Acf36434 Human typ
13	3435	98.6	2952	8 ABO83365	Ab83365 Human NR1
14	3435	98.6	5271	8 ABO83364	Ab83364 Human NR1
15	3405	97.7	3072	8 ABO83366	Ab83366 Human NR1
16	3245.5	93.2	2858	8 ABO83368	Ab83368 Human NR1
17	3232.5	92.8	2870	8 ABO83367	Ab83367 Human NR1
18	3065.5	88.0	2776	8 ABO83369	Ab83369 Human NR1
19	3049	87.5	2108	10 ADI21969	Adi21969 Novel hum
20	2850	81.8	2295	6 ABA93821	Ab93821 Human zcy
21	2850	81.8	2295	10 ADD68179	Add68179 Human zcy
22	2850	81.8	2295	11 ADL26602	Adl26602 Human zcy
23	2810	80.7	1986	6 ABA93809	Ab93809 Human zcy
24	2810	80.7	1986	11 ADL26685	Adl26685 Human cyt
25	2779	79.8	1557	10 ADD68201	Add68201 Human zcy
26	2779	79.8	1557	11 ADL26633	Adl26633 Human cyt
27	2758	79.2	1947	6 ABA93804	Ab93804 Human zcy
28	2758	79.2	1947	11 ADL26684	Adl26684 Human cyt
29	2758	79.2	2196	6 ABA93768	Ab93768 Human zcy
30	2758	79.2	2196	11 ADL26683	Adl26683 Human cyt
31	2606	74.8	2445	6 ABL83581	AbL83581 Human PRO
32	2606	74.8	2445	6 ABL88257	AbL88257 Human PRO
33	2606	74.8	2445	6 ABL95746	AbL95746 Human ang
34	2606	74.8	2445	6 ACA68542	Ac68542 Novel hum
35	2606	74.8	2445	9 ABL44271	AbL44271 Human PRO
36	2606	74.8	2445	9 ABL44554	AbL44554 Human PRO
37	2606	74.8	2445	9 ACD82221	AcD82221 Human sec
38	2606	74.8	2445	9 ABL43927	AbL43927 Human mem
39	2606	74.8	2445	9 ADB83581	AdB83581 Novel hum
40	2606	74.8	2445	9 ADB80687	AdB80687 Novel hum
41	2606	74.8	2445	9 ADB73228	AdB73228 Novel hum
42	2606	74.8	2445	9 ADB78310	AdB78310 Novel hum
43	2606	74.8	2445	10 ADB84958	AdB84958 Human PRO
44	2606	74.8	2445	10 ADB78064	AdB78064 Novel hum
45	2606	74.8	2445	10 ADB87130	AdB87130 Human PRO

ALIGNMENTS

RESULT 1
AAC92337
ID AAC92337 standard; cDNA; 2969 BP.
XX
AC AAC92337;
XX
DT 26-MAR-2001 (first entry)
XX
DE Human haemopoietin receptor protein NR10.1 encoding cDNA SEQ ID NO:1.
XX
KW Human; haemopoietin receptor; NR10.1; NR10.2; NR10.3; NR10;
KW immunoregulation; haematopoietic cell regulation; transmembrane;
KW immune disorder; haematopoietic disorder; autoimmune disease; allergy;
KW metal allergy; pollen allergy; ss.
XX
OS Homo sapiens.
XX
PM WO200075314-A1.
XX
PD 14-DEC-2000.
XX
PF 01-JUN-2000; 2000WO-JP003556.
XX
PR 02-JUN-1999; 99JP-00155797.
XX
PR 30-JUL-1999; 99JP-00217797.
PA (CHUG-) CHUGAI RES INST MOLECULAR MEDICINE INC.
XX
XX Maeda M, Yaguchi N.
PI

XX MPI; 2001-061720/07.
DR P-PSDB; AAB51242.
XX Hematopoietin receptor protein NR10 for screening potential ligands for
PT treatment of immune and hematopoietic disorders such as autoimmune
PT diseases and allergies.
XX
XX Claim 1; Fig 3-5; 127bp; Japanese.
XX
CC The present sequence encodes a human haemopoietin receptor protein
CC (NR10), specifically designated NR10.1. NR10 occurs as a transmembrane
CC protein and a soluble protein. NR10 is a haemopoietin receptor molecule
CC which participates in immunoregulation and haematopoietic cell regulation
CC in vivo, and is useful in searching for haematopoietic factors capable of
CC binding to the receptor. NR10 can be used for the identification of
CC substances for the treatment and prevention of immune and haematopoietic
CC disorders including autoimmune diseases and allergies such as metal and
CC pollen allergy
CC
SQ Sequence 2969 BP; 939 A; 618 C; 662 G; 750 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 0 Length: 2969
Score: 3484.00 Matches: 652
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 4 Gaps: 0

US-10-006-265-2 (1-652) x AAC92337 (1-2969)
QY 1 MetLysLeuSerProGlnProSerCysValAsnLeuGlyWceMetTrpThrTrpAlaLeu 20
Db 523 ATAAAGCTCTCTCCCAAGCCTTCACTGTTTAACTGGGAGTATGTGGAACCTGGCACTG 582
QY 21 TrpMetLeuProSerLeuCysLysPheSerLeuAlaAlaLeuProAlaLysProGlnAsn 40
Db 583 TGGATGCTCCCTCAGCTGCAATTCAGCCTGGAGCTTGCAGCTAAAGCTGAGAAC 642
QY 41 IleSerCysValIleTyrTyrArgIleAsnLeuThrCysThrTrpSerProGlyLysGlu 60
Db 643 ATTTCCTGTGTCTACACTATAGAAAATTTAACTGCATCTGGAGTCCAGAAAAGGAA 702
QY 61 ThrSerTyrThrGlnTyrThrValLysArgThrTyrAlaPheGlyGluLysIleAspAsn 80
Db 703 ACCAGTTATACCCAGTACACAGTAAAGAACTTACGCTTCCGAGAAAACATGATAT 762
QY 81 CysThrThraAsnSerSerThrSerGluAsnArgAlaSerCysSerPhePheLeuProArg 100
Db 763 TGTACAAACCAATAGTTCTACAGTGAATAATCGTTCGTTCCTTTTCTTCCAAAG 822
QY 101 IleThrIleProAspAsnTyrThrIleGluValGluAlaGluAsnGlyAspGlyValIle 120
Db 823 ATTAACATCCCAATATATATACCATTTGAGTGAAGCTGAAAATGAGATGCTGTAAT 882
QY 121 LysSerHisMetThrTyrTrpArgLeuGluAsnIleAlaLysThrGluProProLysIle 140
Db 883 AAATTCATATGCAATCTGAGATTAAGAAACATACCAAACTGAAACCACTTAAGATT 942
QY 141 PheArgValLysProValLeuGlyIleLysArgMetIleGlnIleGluTrpIleLysPro 160
Db 943 TTCGATGTGAACCAAGTTTGGGCATCAACGAATGATTCAAATTTGATGAATGAAGCT 1002
QY 161 GluLeuAlaProValSerSerAspLeuLysTyrThrLeuArgPheArgThrValAsnSer 180
Db 1003 GAGTGGCGGCTTTTCATCTGATTTAAATACACACTTCGATTCAGGACAGTCACAGT 1062
QY 181 ThrSerTrpMetGluValaAsnPheAlaLysAsnArgLysAspLysAsnGlnIleThrTyrAsn 200
Db 1063 ACCAGCTGGAGTGAAGTCAACTTCGCTAACACCGTAAAGATTAACCAAGCTTCAAC 1122
QY 201 LeuThrGlyLeuGlnProPheThrGluTyrValIleAlaLeuArgCysAlaValLysGlu 220

Db 1123 CTCACGGGGCTCAGCCTTTTACAGAAATATGTCAATAGCTCTCGATGTCCGGTCAAGAG 1182
QY 221 SerLysPheTrpSerAspTrpSerGlnGluLysMetGlyWceThrGluGluGluAlaPro 240
Db 1183 TCAAACTTGTGAAGTACTGGAGCCAGAAATAAGGAATATACCTGAGAAAGAGCTTCCA 1242
QY 241 CysGlyLeuGluLeuTrpArgValLeuLysProAlaGluAlaAspGlyArgArgProVal 260
Db 1243 TGTGGCTTGAACCTGTGAGAGATCTCGAAAACAGCTGAGCGCGATGAGAAAGGCCAGTG 1302
QY 261 ArgLeuLeuTrpLysLysAlaArgGlyAlaProValLeuGluLysThrLeuGlyTyrAsn 280
Db 1303 CGGTGTTATGAGAGAGGCAAGAGAGCCCAAGTCTTAAGAAAAACCTTGGCTTACAAC 1362
QY 281 IleTrpTyrTyrProGluSerAsnThrAsnLeuThrGluThrMetAsnThrThrAsnGln 300
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QY 301 GlnLeuGluLeuHisLeuGlyLysGlySerPheTrpValSerMetIleSerTyrAsnSer 320
Db 1423 CAGCTTGAACCTGCATCTGGAGGCGAGAGCTTTGGGTCTATGATTTCTTATATATCT 1482
QY 321 LeuGlyLysSerProValAlaThrLeuArgIleProAlaIleGlnGluLysSerPheGln 340
Db 1483 CTTGGGAAGTCTCCAGTGGCCACCCTGAGGATTCACAGCTATTCAGAAAAATCATTTCAG 1542
QY 341 CysIleGluValMetGlnAlaCysValAlaGluAspGlnLeuValLysTrpGlnSer 360
Db 1543 TGCATTGAGTCAATGAGGCGCTGCTGCTGAGAACCAAGTATGTGTAAGTGGCAAGC 1602
QY 361 SerAlaLeuAspValAsnThrTrpMetIleGluTrpPheProAspValAspSerGluPro 380
Db 1603 TCTGCTCTGAGTGAACCTTGGAGATTAATGATTTCCGAGTGGACCTCAGAGCCC 1662
QY 381 ThrThrLeuSerTrpGluSerValSerGlnAlaThrAsnTrpThrIleGlnGluAspLys 400
Db 1663 ACCACCTTTCCTGGGAATCTGTCTCAGGCGACAGACATGACAGATCCAGCAAGATTA 1722
QY 401 LeuLysProPheTrpCysTrpThrAsnIleSerValTyrProMetLeuHisAspLysVal 420
Db 1723 TTAAACCTTTCTGGGCTATACATCTGTGTATCAATGTTTCATACAAAGTTGGC 1782
QY 421 GluProTyrSerIleGlnAlaTyrAlaLysGluGlyValProSerGluGlyProGluThr 440
Db 1783 GAGCATATTCATCCAGCTTATGCAAAAGAGGCTTCCATCAGAAAGTCTCAGAGCC 1842
QY 441 LysValGluAsnIleGlyValLysThrValThrIleThrTrpLysGluIleProLysSer 460
Db 1843 AAGGTGAGAAACATTTGGCTGAAGACGTCACGATCACATGAAAGAGATTCACAGAGT 1902
QY 461 GluArgLysGlyIleIleCysAsnTyrThrIlePheTyrGlnAlaGluGlyLysGly 480
Db 1903 GAGAGAAAGGATATCTGTCAACTACACATCTTTTACCAAGCTGAAAGTGAAGAAAG 1962
QY 481 PheSerLysThrValaAsnSerSerIleLeuGlnTyrGlyLeuGluSerLeuLysArgLys 500
Db 1963 TTCTCCAAACAGTCAATTCAGACANTTGCAGTACGCTGGAAGTCCCTGAAACGAAAG 2022
QY 501 ThrSerTyrIleValGlnValMetAlaAsnThrSerAlaGlyGlyThrAsnGlyThrSer 520
Db 2023 ACCTCTTACATTTGTCAGTCAATGACCAACACAGGCTGGGGGAAACCAACGGACAC 2082
QY 521 IleAsnPheLysThrLeuSerPheSerValIlePheGluIleIleLeuIleThrSerLeu 540
Db 2083 ATTAATTTAAGACATTTGCATTCAGTGTCTTGAATTAATCTCTAATCTTCTGATT 2142
QY 541 GlyGlyGlyLeuLeuIleLeuIleIleLeuThrValAlaTyrGlyLeuLysLysProAsn 560
Db 2143 GGTGGAGGCTTCTTATTTCTATTAATCTGACAGTGCATATAGTGTCAAAAAACCAAC 2202
QY 561 LysLeuThrHisLeuCysTrpProThrValProAsnProAlaGluSerSerIleAlaThr 580

Accession	Gene	Protein	Length	Score	Percent Similarity
DB 2203	AAATGACTCACTCTGTGTTGGCCACC	CGTCCCAACCTCGTGGAAAGTAATACCA	2262		
QY 561	TRPHISG1YA8PASPPhelysAp1yLeuAenLeuLySG1uSerAspAspSerValAen	600			
DB 2263	TGGCATGTGAGATGATTTCAAGATTAAGCTTAACCTGAAGAGATCTGATGACTCTGAA	2322			
QY 601	Thrg1uAPAPArg11leuLeuLyPrcYsSerThrProSerAspLyLeuVal11leuLyys	620			
DB 2333	ACAGAAAGACAGGATCTTTAAACCAATGTTCCACCCACAGACAGATGGTGTGTAACAAG	2382			
QY 621	LeuVal1ValAenPheG1yAenValLeuG1ng1u1lePheThrAspG1u1AArgThrG1y	640			
DB 2383	TTGGTGGTGGAAGTCTTTGGCAATCTTCTGCAGAAATTTTTCACAGATGAAGCCAGACGG	2442			
QY 641	G1ng1uLySG1nPhearGArgG1yLySG1uTTPAap	652			
DB 2443	CAGGAAAAACATTTTAGAGGGGGAAGAAAGATGGAGC	2478			
RESULT 2					
AAC92350					
ID AAC92350	standard; CDNA, 2119 BP.				
XX AC	AAC92350;				
XX DT	26-MAR-2001 (first entry)				
XX DE	Human haemopoietin receptor protein NR10.3 encoding cDNA SEQ ID NO.16.				
XX KW	Human; haemopoietin receptor; NR10.1; NR10.2; NR10.3; NR10;				
XX KW	immunoregulation; haematopoietic cell regulation; transmembrane;				
XX KW	immune disorder; haematopoietic disorder; autoimmune disease; allergy;				
XX KW	metal allergy; pollen allergy; ss.				
XX OS	Homo sapiens.				
XX PN	WO200075314-A1.				
XX PD	14-DEC-2000.				
XX PF	01-JUN-2000; 2000MO-JP003556.				
XX PR	02-JUN-1999; 99JP-00155797.				
XX PR	30-JUL-1999; 99JP-00217797.				
XX PA	(CHUG-1) CHUGAI RES INST MOLECULAR MEDICINE INC.				
XX PI	Maeda M, Yaguchi N;				
XX DR	WPI; 2001-061720/07.				
XX DR	P-PsDB; AAB51244.				
XX PT	Hemopoietin receptor protein NR10 for screening potential ligands for				
XX PT	treatment of immune and hematopoietic disorders such as autoimmune				
XX PT	diseases and allergies.				
XX PS	Claim 1; Fig 13-14; 127bp; Japanese.				
XX CC	The present sequence encodes a human haemopoietin receptor protein				
XX CC	(NR10), specifically designated NR10.3. NR10 occurs as a transmembrane				
XX CC	protein and a soluble protein. NR10 is a haemopoietin receptor molecule				
XX CC	which participates in immunoregulation and haematopoietic cell regulation				
XX CC	in vivo, and is useful in searching for haematopoietic factors capable of				
XX CC	binding to the receptor. NR10 can be used for the identification of				
XX CC	substances for the treatment and prevention of immune and hematopoietic				
XX CC	disorders including autoimmune diseases and allergies such as metal and				
XX CC	pollen allergy				
XX SQ	Sequence 2119 BP; 643 A; 459 C; 504 G; 513 T; 0 U; 0 Other;				
Alignment Scores:					
Pred. No.:	4,33e-316	Length:	2119		
Score:	3451.00	Matches:	650		
Percent Similarity:	99.85%	Conservative:	1		

Best Local Similarity:	99.69%	Mismatches:	1
Query Match:	99.05%	Indels:	1
DB:	4	Gaps:	0
US-10-006-265-2 (1-652) x AAC92350 (1-2119)			
QY	1 MetLysLeuSerProGlnProSerCysValAsnLeuGlyMetMetTrpThrTrpAlaLeu	20	
DB	11 ATGAAGCTCTCTCCACCTTCAAGTGTAACTCGGGAGATGTGACCTGGGCACCTG	70	
QY	21 TrpMetLeuProSerLeuCysLeysPheSerLeuAlaAlaLeuProAlaLysProGluAsn	40	
DB	71 TGGAGTCTCCCTCACTCTGCAAAATTACGCTGGAGCTCTCCAGCTAAAGCTAGAAC	130	
QY	41 IleSerCysValTyTrpTyTrpArgLysAsnLeuThrCysTrpTrpSerProGlyLysGlu	60	
DB	131 ATTCTCTGTGCTACTACTATATAGAAAATTAACTTACCTGCACCTTGGAGTCCAGAAAGAA	190	
QY	61 ThrSerTyTrpGlnTyTrpValLysArgThrTyAlaPheGlyGluLysPheHisAspPhe	80	
DB	191 ACCAGCTTATACCCAGTACACAGTTAAGAACTTACGCTTTGGAGAAAACATATATAT	250	
QY	81 CysTrpTrpAsnSerSerTherSerGluAsnArgAlaSerCysSerPhePheLeuProArg	100	
DB	251 TGTACACCAATAGTTCTTCAAGATGAAATCGTCTGTGCTCTTTTCTCTTCCACAG	310	
QY	101 IleThrIleProAspAsnTyTrpIleGluValGluAlaGluAsnGlyAspGlyValIle	120	
DB	311 ATTAAGATCCCGAATATTAATTAACCTTAGGTGGAGAGCTGAATAATGGATGTATAT	370	
QY	121 LysSerHisMetThrTyTrpArgLeuGluAsnIleAlaLysTrpGluProLysIle	140	
DB	371 AAATCTCATATGACATACCTGAGATTAAGAAACATAGCAAAACCTGAACCACTTAAGATT	430	
QY	141 PheArgValLysProValLeuGlyLysLysArgMetIleGlnIleGluTrpIleLysPro	160	
DB	431 TTCCTGTGAACCAAGTTTGGGACATCAACGAATGATTCATTAATGAATGATTAAGCT	490	
QY	161 GluLeuAlaProValSerSerAspLeuLysTyTrpThrLeuArgPheArgThrValAsnSer	180	
DB	491 GAGTTGGGGCGCTGTTTCATCTGATTTTAAATATACACACTTCGATTGAGACAGTCAACGT	550	
QY	181 ThrSerTrpMetGluValAsnPheAlaLysAsnArgLysAspLysAsnGlnThrTrpAsn	200	
DB	551 ACCAGCTGATGGAAGTCAACTCCCTTAAGAACCTTAAGATTAATAAACCAACCTTAACAC	610	
QY	201 LeuThrArgLysLeuGlnProPheThrGluTyTrpValIleAlaLeuArgCysAlaValLysGlu	220	
DB	611 CTCAGGGGGCGTCCAGCCCTTTTACAGAAATATGTCAATGCTTCGCGATGGCGGTCAAGAG	670	
QY	221 SerLysPheTrpSerAspTrpSerGlnGlyLysMetGlyMetThrGluGluGluAlaPro	240	
DB	671 TCMAAGTCTCGAGTGAATCGAGCCMAAATAATGGAAATGACCTGAGAGAAAGACTCCA	730	
QY	241 CysGlyLeuGluLeuTrpArgValLeuLysProAlaGluAlaAspGlyArgArgProVal	260	
DB	731 TGTGGCTCGAATCTGTGAGAGTCTCTGAACCAAGCTGAGCGGATGGAAGAGGCAAGTGTG	790	
QY	261 ArgLeuLeuTrpLysLysAlaArgGlyAlaProValLeuGlnLysTrpLeuGlyTyTrpAsn	280	
DB	791 CGGTGTATATGGAAGAAAGCAAGAGAGCCCAAGCTTAAGAGAAACCTGGCTTAACAC	850	
QY	281 IleTrpTyTrpProGluSerAsnThrAsnLeuThrGluTrpMetAsnThrThrAsnGln	300	
DB	851 ATATGATCTATCCAGAAAGCAACCTAACTCACAGAAACATATGACACTAACTAACAG	910	
QY	301 GlnLeuGluLeuHisLeuGlyLysArgPheTrpValSerMetIleSerTyTrpAsnSer	320	
DB	911 CAGCTGAACTGCATCTGGAGGCGAGAGCTTTTGGGTGTCTATGATTTCTTAATATCT	970	
QY	321 LeuGlyLysSerProValAlaThrLeuArgLysProAlaIleGlnGlnLysSerPheGln	340	
DB	971 CTGGGAAGTGTCCAGTGGCCACCTGAGATTCACGATATTTCAAGAAAAATCATTTTACG	1030	

[illegible]

DE	Human zcytor17 cDNA sequence SEQ ID NO:53.	
XX		
KM	zcytor17, chromosome 5, 5q11; cytokine receptor; immunomodulatory;	
KM	antihypertensive; antiviral; antineuritic; antidiabetic; cytosolic;	
KM	muscular; lymphoid; immune; inflammatory; splenic; blood; bone;	
KM	infection; immunosuppression; cytotoxicity; leukopenia; Crohn's disease;	
KM	autoimmune disease; rheumatoid arthritis; multiple sclerosis; cancer;	
KM	inflammatory disease; pancreatitis; inflammatory bowel disease; ss.	
XX		
OS	Homo sapiens.	
XX		
PN	WO200200721-A2.	
XX		
PD	03-JAN-2002.	
XX		
PF	26-JUN-2001; 2001WO-US020484.	
XX		
PR	26-JUN-2000; 2000US-0214282P.	
PR	29-JUN-2000; 2000US-0214955P.	
PR	08-FEB-2001; 2001US-0267963P.	
XX		
PA	(ZYMO) ZYMOGENETICS INC.	
XX		
PI	Speicher CA, Presnell SR, Gao Z, Whitmore TE, Kuijper JL;	
PI	Maurer ME;	
XX		
DR	WPI; 2002-090519/12.	
XX	P-PSDB; ABB05741.	
PT	Isolated polynucleotide encoding a cytokine receptor zcytor17 which is	
PT	useful for treating and diagnosing lymphoid, immune, inflammatory,	
PT	splenic, blood or bone disorders.	
XX		
PS	Example 1; Page 199-203; 235pp; English.	
XX		
CC	The present invention describes a cytokine receptor designated zcytor17.	
CC	zcytor17 has immunomodulatory, antiinflammatory, antiviral, cytosolic,	
CC	antineuritic, antidiabetic and muscular activities. The zcytor17	
CC	proteins are useful for treating and diagnosing lymphoid, immune,	
CC	inflammatory, splenic, blood or bone disorders. Agonists or anti-	
CC	zcytor17 antibodies are useful in stimulating cell-mediated immunity and	
CC	for stimulating lymphocyte proliferation, such as in the treatment of	
CC	infections involving immunosuppression, including certain viral	
CC	infections. They are also useful for inducing cytotoxicity and for	
CC	treating leukopenias. Antagonist of zcytor17 polypeptides are useful for	
CC	treating autoimmune diseases (e.g. rheumatoid arthritis and multiple	
CC	sclerosis), inflammatory diseases (e.g. Crohn's disease), cancer,	
CC	pancreatitis, and inflammatory bowel disease. Zcytor17 was mapped to	
CC	chromosome 5, specifically to the 5q11 chromosomal region. ABA93767 to	
CC	ABA93943 and ABB05730 to ABB05745 represent sequences used in the	
CC	exemplification of the present invention	
XX		
SQ	Sequence 2903 BP; 862 A; 620 C; 664 G; 757 T; 0 U; 0 Other;	
	Alignment Scores:	
	Pred. No.: 6,92e-316 Length: 2903	
	Score: 3451.00 Matches: 650	
	Percent Similarity: 99.85% Conservative: 1	
	Best Local Similarity: 99.69% Mismatches: 1	
	Query Match: 99.05% Indels: 1	
	DB: 6 Gaps: 0	
	US-10-006-265-2 (1-652) x ABA93808 (1-2903)	
QY	1 MetLysLeuSerProGlnProSerGlyValaIleuGlyMetMetTrpTrtTAlaLeu 20	
DB	497 ATAAAGCTCTCTCCAGGCTTCAGTGTATTAACCTGGGGAAGATGTGACCTGGCACTG 556	
QY	21 TrpMetLeuProSerSerLeuGlyLysPheSerLeuAlaIleuProAlaLysProGluAsn 40	
DB	557 TGAATGCTCCCTTCACTCTGCAAATTACAGCTCGAGCTCTGCACGCTAAGCTGAAAC 616	
QY	41 IleSerCysValIleTyTrtArgLysaIleuThrCysTrhTrpSerProGlyLysGlu 60	

```

Db      617 ATTTCCTGCTACTACTATAGAGAAAATTAACTGCAGCTTGGAGTCCAGGAAGAA 676
Qy      61  ThrSerTyrThrGlnTyrThyValIlysaGthrTyrAlaPheGlyGluLeuHisAspAsn 80
Db      677 ACCAGTTATACCACAGTACACAGTTAAGAACTTACGCTTTGGAGAAAACATGATATAT 736
Qy      81  CysThrThrAsnSerSerThrSerGluAsnArgAlaSerCysSerPheLeuProArg 100
Db      737 TGTACACCAATAGTCTACAGAGTGAATAATGCTGCTGCTCTTTTCTTCCACAGA 796
Qy      101  IleThrIleProAspAsnTyrThrIleGluValGluAlaGluAsnGlyAspGlyValIle 120
Db      797 ATAAAGATCCAGATTAATTATACATTGAGGTGGAAGCTGAAGAAAGAGTGTATAT 856
Qy      121  LysSerHisMetThrTyrTrpArgLeuGluAsnIleAlaIlyGthrGluProProlysIle 140
Db      857 AAATCTCATATGACATACCTGAGATTAGAGAACATAGCGAAAACCTAAGCAT 916
Qy      141  PheArgValIlyProValIleGluIlyIleYsaRgmMetIleGlnIleGluTrpIleLeuPro 160
Db      917 TTCGTTGGAACCAAGTTTGGGCATCAACGAATGATTCAAATTTGAATGAATAAAGCCT 976
Qy      161  GluLeuAlaProValSerSerAspLeuIlySerTyrThrLeuArgPheArgThrValAsnSer 180
Db      977 GAGTTGGCGCTGTTTCATCTGATTTAAATACACACTTCGATTCAGAGACAGTCAACAGT 1036
Qy      181  ThrSerTrpMetGluValAsnPheAlaIlysaAsnArgIlysaAspIlysaAsnGlnThrTyrAsn 200
Db      1037 ACCAGCTGAGTGAAGTCAACTCCCTTAAGAAACCTTAAGAGATTAAGAAACCAACGTAAC 1096
Qy      201  LeuThrGlyLeuGlnProPheThrGluTyrValIleAlaLeuArgCysAlaValIleGlu 220
Db      1097 CTCACGGGGCTGCAGCCTTTTACAGAAATATGTCATAGCTCTGCGATGGCGCTCAAGAG 1156
Qy      221  SerIlyPheTrpSerAspTrpSerGlnGluIlysaMetGlyMetThrGluGluValPro 240
Db      1157 TCAAAGTTCTGAGAGTGAAGTGAAGCCAAAGAAAATGAGAAATGACGAGAGAAAGACTCA 1216
Qy      241  CysGlyLeuGluLeuTrpArgValIleuIlysaProAlaGluAlaAspGlyArgArgProVal 260
Db      1217 TGTGGCCTGGAACGTGGAGAGTCTCTGAACCAAGTGAAGCGAGTGAAGAAAGGCAAGTG 1276
Qy      261  ArgLeuLeuTrpIlysaIlysaAlaArgIlyAlaProValIleuGluIlysaThrLeuGlyTyrAsn 280
Db      1277 CGGTGTTATGAGAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1336
Qy      281  IleTrpTyrTyrProGluSerAsnThrAsnLeuThrGluTrpMetAsnThrThrAsnGln 300
Db      1337 ATATGTAATCTATCCAGAAAGCAACATCACTCACAGAAACAAATGACATCACTAACAG 1396
Qy      301  GlnLeuGluLeuHisIleuGlyGlyLeuSerPheTrpValSerMetIleSerTyrAsnSer 320
Db      1397 CAGCTTGAACGTGATCTGGAGGCGAGAGCTTTTGGGTGTCTATGATTTCTTATATATCT 1456
Qy      321  LeuGlyIlysaSerProValAlaThrLeuArgIleProAlaIleGlnGluIlysaSerPheGln 340
Db      1457 CTTGGGAAGTCTCAAGTGGCAACCTTGAGATTCAGAGTATTCAGAGAAAATCAATTCAG 1516
Qy      341  CysIleGluValIleMetGlnAlaCysValAlaIleGluAspGlnLeuValIlysaTrpGlnSer 360
Db      1517 TGCATTAGATCATGACAGGCTGCGCTTCTGAGACCGACTAGTGTGTAAATGGCAAGC 1576
Qy      361  SerAlaLeuAspValAsnThrTrpMetIleGluTrpPheProAspValAspSerGluPro 380
Db      1577 TCTGCTCTAGACGTAACATCTTGATGATGATGATTCGAGATGTGAGACTCAGAGGCC 1636
Qy      381  ThrThrLeuSerTrpGluSerValSerGlnAlaThrAsnTrpThrIleGlnGlnAspIlysa 400
Db      1637 ACCACCCCTTCTGGAATCTGTCTCAGGCGCAAGAGTGAAGATCAGCAAGATTA 1696
Qy      401  LeuIlysaProPheTrpCysTyrAsnIleSerValTyrProMetLeuHisAspIlysaValGly 420

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Db      1697 TTAACCTTCTGAGTCTATATACATCTCTGTATCCAAATGTTGATGACAAAGTTGGC 1756
Qy      421  GluProTyrSerIleGlnAlaTyrAlaIlysaGluIlysaProSerGluGlyProGluThr 440
Db      1757 GAGCATATTTCCATCCAGGCTTATATGCAAAAGAGCGCTTCATAGAAAGTCTGAGACC 1816
Qy      441  LysValGluAsnIleGlyValIlysaThrValThrIleThrTrpIlysaGluIleProLysSer 460
Db      1817 AAGGTGAGAACATTTGGCGTGAACAGGTCCAGTCACTACATGAAAGAGATTTCCAAAGCT 1876
Qy      461  GluArgIlysaGlyIleIleCysAsnTyrThrIlePheTyrGlnAlaGluIlysaGly 480
Db      1877 GAGAGAAAGGGTATCATCTGCACTTCAACCATTTTACCAAGCTGAAGGTGGAAGAAAGGA 1936
Qy      481  PheSerIlysaThrValAsnSerSerIleLeuGlnTyrGlyLeuGluSerLeuIlysaArgIlysa 500
Db      1937 TTCCTCAAGACAGCAATTCAGCATCTTGAGATCGGCGTGAAGTCTCTGAAGCGAAG 1996
Qy      501  ThrSerTyrIleValIleGlnValMetAlaAsnThrSerAlaGlyIlysaAsnGlyThrSer 520
Db      1997 ACCTCTTACATTTGTTCAAGTATAGCCAGCACAGCTGCGGGAGAACCAAGGAGCACAGC 2056
Qy      521  IleAsnPheIlysaThrLeuSerPheSerValPheGluIleIleLeuIleThrSerLeuIle 540
Db      2057 ATAAATTTCAAGACATTTGTATTCAGTGTCTTTGAGATTAATCCATTAATCTTCTGATT 2116
Qy      541  GlyGlyGlyLeuLeuIleLeuIleIleLeuThrValAlaTyrGlyLeuIlysaIlysaProAsn 560
Db      2117 GGTGAGGCTCTTCTTATTCATATCTGACAGTGGCATATGTGTCTCAAAAACCCAAAC 2176
Qy      561  LysLeuThrHisLeuCysTrpProThrValProAsnProAlaGluSerSerIleAlaThr 580
Db      2177 AAATTAATCATCTGTTGTTGGCCCAAGCTTCCAAACCTGCTGAAGAGTATGATGCCACA 2236
Qy      581  TrpHisGlyAspAspPheIlysaAspIlysaLeuAsnLeuIlysaGluSerAspAspSerValAsn 600
Db      2237 TGGCATGGAAGTATTTCAAGATTAACCTTAACAGAGAGTGTGATGATCTGTGATAC 2296
Qy      601  ThrGluAspArgIleLeuIlysaProCysSerThrProSerAspIlysaLeuValIleAspIlysa 620
Db      2297 ACAGAAAGACGAGATCTTAACCAATGTTCCACACCCCGAGTGCACAAAGTGTGATGACAAAG 2356
Qy      621  LeuValIleAsnPheGlysaAsnValIleuGlnIlysaPheThrAspGluAlaArgThrGly 640
Db      2357 TTGGTGTGAACCTTGGGAATGTTCTTCAGAGAAATTTTCACAGATGAGACCAAGACGGGT 2416
Qy      641  GlnGluIlysaGlnPheArgArgGlyIlysaGluTrpAsp 652
Db      2417 CAGGA-AAACATTTTGAAGGGGAAAAGATGGGAC 2451

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RESULT 4
ADD68146
ID ADD68146 standard; cDNA; 2903 BP.
AC ADD68146;
DT 15-JAN-2004 (first entry)
XX Human zcytor17 cDNA SEQ ID NO:4.
XX ss; gene; human; zcytor17; antiinflammatory; dermatological;
XX immunosuppressive; antimicrobial; vaccine; inflammatory disease;
XX inflammatory bowel disease; ulcerative colitis; Crohn's disease;
XX atopic dermatitis; eczema; psoriasis; endotoxaemia; septicemia;
XX toxic shock syndrome; infectious disease.
OS Homo sapiens.
XX Key Location/Qualifiers
FH 497..2485
FT CDS /*CDS= a
FT /product= "zcytor17"
XX

PN W02003060090-A2.
 XX 24-JUL-2003.
 XX
 PF 21-JAN-2003; 2003WO-US001984.
 XX 18-JAN-2002; 2002US-0350325P.
 PR 25-APR-2002; 2002US-0375323P.
 PR 19-DEC-2002; 2002US-0435315P.
 XX
 PA (ZYMO) ZYMOGENETICS INC.
 XX
 PI Sprecher CA, Kuiper JL, Dasovich MM, Grant FJ, Hammond AK;
 PI Novak JE, Gross JA, Dillon SR;
 XX
 DR WPI: 2003-618179/58.
 DR P-PsDB; ADB68147.
 XX
 PT New zcytor17 ligand polypeptides, useful for treating inflammatory
 PT diseases, such as inflammatory bowel disease, ulcerative colitis, Crohn's
 PT disease, atopic dermatitis, eczema, psoriasis, endotoxemia, septicemia.
 XX
 PS Example 3; SEQ ID NO 4; 372bp; English.
 XX
 CC The invention relates to a novel isolated zcytor17 ligand polypeptide. A
 CC polypeptide of the invention has antiinflammatory, dermatological,
 CC immunosuppressive, and antimicrobial activity, and may have a use in a
 CC vaccine. The polypeptide is useful for treating inflammatory diseases,
 CC such as inflammatory bowel disease, ulcerative colitis, Crohn's disease,
 CC atopic dermatitis, eczema, psoriasis, endotoxemia, septicemia, toxic
 CC shock syndrome or infectious diseases. The present sequence is used in
 CC the exemplification of the invention.
 XX
 SQ Sequence 2903 BP; 862 A; 620 C; 664 G; 757 T; 0 U; 0 Other;

Alignment Scores:
 Pred. No.: 6,92e-316 Length: 2903
 Score: 3451.00 Matches: 650
 Percent Similarity: 99.85% Conservative: 1
 Best Local Similarity: 99.69% Mismatches: 1
 Query Match: 99.05% Indels: 1
 DB: 10 Gaps: 0

US-10-006-265-2 (1-652) x ADB68146 (1-2903)

QY 1 MetIleuSerProGlnProSerCysValAsnLeuGlyMetMetTrpThrTPAAlaLeu 20
 DB 497 ATGAAGCTCTCTCCCAAGCCTTCATGTGTTAACCTGGGAGTGAATGGAGCTGGCACTG 556
 QY 21 TrpMetLeuProSerLeuCysLysPheSerLeuAlaAlaLeuProAlaLysProGluAsn 40
 DB 557 TGGATGTCCTCCCTCACTCTGCAGAAATTCAGCTGGAGCTCTGCAGAGTAACTGGAGAAC 616
 QY 41 IleSerCysValIleTyrrTyraGlyAsnLeuThrCysThrTrpSerProGlyLysGlu 60
 DB 617 ATTTCTGTGTCTACTACTATAGAAAATTTTAACTGGCACTGGAGTCCAGAAAAGGAA 676
 QY 61 ThrSerTyThrGlnIleTyrrValLysArgThrTyrrAlaPheGlyGluLysHisAspAsn 80
 DB 677 ACCAGTTTAAACCCAGTACACAGTTTAAAGAACTTACGCTTTGAGAAAAAATGATTAAT 736
 QY 81 CysThrThrAsnSerSerThrSerGluAsnArgAlaSerCysSerPhePheLeuProArg 100
 DB 737 TGTACAAACCAATAGTCTTACAAAGTGAATAATCGCTTCCTGCTCTTTTCCCTTCCAAAG 796
 QY 101 IleThrIleProAspAsnTyrrThrIleGluValGluAlaGluAsnGlyAspGlyValIle 120
 DB 797 ATAACATCCCAATATATATACATTGAGGTGAAGCTGAATAATGAGATGTGTAAT 856
 QY 121 LysSerHisMetThrTyrrTPAArgLeuGluAsnIleAlaLysThrGluProProlysIle 140
 DB 857 AAATTCATATGACATATCTGAGATTATAGAAACATAGCGAAAATCTGAACCACTTAAGATT 916

QY 141 PheArgValIleProValIleuGlyIleLysArgMetIleGlnIleGluTrpIleLysPro 160
 DB 917 TTCGGTGTGAACCAAGTTTGGGATCAAAACGAATGATTCAAATTGAATGATTAAGCCCT 976
 QY 161 GluLeuAlaProValIleSerSerAspLeuLysTyrrThrLeuArgPheArgThrValAsnSer 180
 DB 977 GAGTTGGCGCCTGTTTCATCTGATTTAAATACACTTCGATTCAGGACAGTCAACAT 1036
 QY 181 ThrSerTrpMetGluValAsnPheAlaLysAsnArgLysAspLysAsnGlnThrTyrrAsn 200
 DB 1037 ACCAGCTGATGAGAACTCAACTTCCTGAAGAACCGTGAAGATTAATAACCAACGTTCAAC 1096
 QY 201 LeuThrGlyLeuGlnProPheThrGlnTyrrValIleAlaLeuArgCysAlaValLysGlu 220
 DB 1097 CTCACGGGCTCAGACCTTTTACAGAAATGTGTCATAGCTCTCGATGTGCGGTCAAGGAG 1156
 QY 221 SerLysPheTrpSerAspTrpSerGlnGlyLysMetGlyMetThrGluGluGluAlaPro 240
 DB 1157 TCAAAATTCTGAGAGTACCTGAGGCCAAGAAAAATGGGAATGACTGAGAGAAAGCTCCA 1216
 QY 241 CysGlyLeuGluLeuTrpArgValIleuLysProAlaGluAlaAspGlyArgArgProVal 260
 DB 1217 TGTGGCTTGAACCTGTGAGAGTCTTGAAACCACTGAGGCCGAGTGAAGAAAGCCAGTG 1276
 QY 261 ArgLeuLeuTrpLysLysAlaArgGlyAlaProValIleuGlyLysThrLeuGlyTyrrAsn 280
 DB 1277 CGGTGTTATGGAAGAAGCAAGAGAGCCCAAGTCTTGAAGAAAACATTGGCTTCAAC 1336
 QY 281 IleTrpTyrrTyrrProGluSerAsnThrAsnLeuThrGluThrMetAsnThrThrAsnGln 300
 DB 1337 AATGTGTACTATCCAGAAAGCAACTAACCTTCACAGAAACATGAACTCACTAACCCAG 1396
 QY 301 GlnLeuGluLeuHisLeuGlyLysGlyLysSerPheTrpValSerMetIleSerTyrrAsnSer 320
 DB 1397 CAGCTTGAACCTGCATCTGGAGGCCAGAGACTTTTGGGTCTATGATTTCTTAATTAATCT 1456
 QY 321 LeuGlyLysSerProValAlaThrLeuArgIleProAlaIleGlnGlyLysSerPheGln 340
 DB 1457 CTTGGGAATCTTCCAGTGGCCACCCGAGAGATTCCAGTATTCAAGAAAATCATTTTCAG 1516
 QY 341 CysIleGluValIleMetGlnAlaCysValAlaGluAspGlnLeuValValIleTrpGlnSer 360
 DB 1517 TGCATTGAGGTATGAGAGCCCTGCTGCTGAGAACCACTAGTGTGTAAGTGGCAAAAC 1576
 QY 361 SerAlaLeuAspValAsnThrTrpMetIleGluTrpPheProAspValAspSerGluPro 380
 DB 1577 TCTGCTTACAGCTGAACCTTGGATGATTGAATGTTTCCGAGTGTGAATCTCAAGGCC 1636
 QY 381 ThrThrLeuSerTrpGluSerValSerGlnAlaThrAsnTrpThrIleGlnGlnAspLys 400
 DB 1637 ACCACCTTTCTCGGAATCTGTGTCTCAGGCCAGCACTGAGACATCCAGCAAGATTAAT 1696
 QY 401 LeuLysProPheTrpCysTyrrAsnIleSerValIleTyrrProMetLeuHisAspLysValGly 420
 DB 1697 TTAAAACCTTTCTGTGGCTATTAACATCTGTGTATCCAAATGTGATCAAAAGTTGGC 1756
 QY 421 GluProTyrrSerIleGlnAlaTyrrAlaLysGlyValIleProSerGluGlyProGluThr 440
 DB 1757 GAGCCATATTCATCCAGGCTTATGCCAAGAAAGGCGTTCATCCAGAGCTCTGAGACC 1816
 QY 441 LysValGluAsnIleGlyValLysThrValThrIleThrTrpLysGluIleProLysSer 460
 DB 1817 AAGGTGGAAGAACTTGGCGTGAAGACGGTCAAGATCACTGAAAGAGATTCCCAAGACT 1876
 QY 461 GluArgLysGlyIleIleCysAsnTyrrThrIlePheTyrrGlnAlaGluGlyGlyLysGly 480
 DB 1877 GAGAGAAAGGATATCATCTGCAACTACACACATCTTTTACCAAGCTGAGAGTGAAGAA 1936
 QY 481 PheSerLeuThrValAsnSerSerIleLeuGlnTyrrGlyLeuGlnSerLeuLysArgLys 500
 DB 1937 TTCTCCAAACAGTCAATTCAGCAATCTTGCAATAGGCGCTGAGAGTCCCTGAAACCAAAAG 1996
 QY 501 ThrSerTyrrIleValGlnValMetAlaAsnThrSerAlaGlyGlyTyrrAsnGlyThrSer 520


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Db      1997  ACCCTTACATTTGTCAGTCAATGCCACGACCAAGTCTGGGGGAAACCAAGGACCGACG 2056
Qy      521  ILeaenPhelyrThrLeuSerPheSerValPheGluIleIleLeuIleThrSerLeuIle 540
Db      2057  ATTAATTCAGACACTTCTCATTCAGTCTTTGAGATTATTCCTCATTAATCTCTCATTT 2116
Qy      541  GLyGlyGlyLeuLeuIleIleIleIleThrValAlaIleTyrGlyLeuIleLysProAsn 560
Db      2117  GGTGAGGCGCTTCTTATTCATTATCCTGACAGTGGCATGTGCTCAAAAAACCCCAAC 2176
Qy      561  LysLeuThrHisLeuCyseTyrProThrValProAsnProAlaGluSerSerIleAlaThr 580
Db      2177  AAATTGACTCATCTGTGTGGCCCAACCTTCCCAACCTCTGTAAGAGTATGATCCCA 2236
Qy      581  TrpHisGlyAspAspPheLysAspIleuAsnLeuLysGluSerAspAspSerValAsn 600
Db      2237  TGGCATGGAGATGATTTCAAGGATTAACCTGAAGAGTGTGATGACTCTGTGAAC 2296
Qy      601  ThrGluAspArgIleLeuLysProCyseSerThrProSerAspIleValIleAspLys 620
Db      2297  ACAGAAAGCAGATCTTAAACCATGTCCACCCCAAGTACAAAGTTGTGATTCACAAAG 2356
Qy      621  LeuValValaenPheGlyAsnValLeuGlnGluIlePheThrAspGluAlaArgThrGly 640
Db      2357  TTGGTGTGGAATCTTGGGAATCTTCTGCAGAAATTTTTCACAGATGAAGCCAGAACGGGT 2416
Qy      641  GlnGluLysGlnPheArgArgGlyLysGluTyrAsp 652
Db      2417  CAGGA-AAACAATTAGGAGGGAAGAAAGATGGGAC 2451

RESULT 5
ADL26569
ID      ADL26569 standard; cDNA; 2903 BP.
AC      ADL26569;
XX      20-MAY-2004 (first entry)
DT      Human cytokine receptor zcytor17 DNA seqid 4.
XX      KW antiinflammatory; antitumor; dermatological; antiallergic; antipsoriatic;
KW antibacterial; immunosuppressive; cell proliferation inhibitor;
KW immune response inhibitor; inflammatory response inhibitor;
KW multimeric cytokine receptor; heterodimeric cytokine receptor; cancer;
KW cytokine-binding domain; class I cytokine receptor; hematopoietic cell;
KW zcytor17lig-induced proliferation; zcytor17lig-induced differentiation;
KW hematopoietic progenitor cell; zcytor17lig-induced inflammation;
KW inflammatory disease; inflammatory bowel disease; ulcerative colitis;
KW Crohn's disease; atopic dermatitis; eczema; psoriasis; endotoxaemia;
KW septicemia; toxic shock syndrome; zcytor17; human; gene; ss.
XX      OS Homo sapiens.
XX      PN US2003215638-A1.
XX      PD 20-NOV-2003.
XX      PF 21-JAN-2003; 2003US-00351157.
XX      PR 18-JAN-2002; 2002US-0350325P.
XX      PR 14-JUN-2002; 2002US-0389108P.
XX      PR 19-DEC-2002; 2002US-0435361P.
XX      PA (SPRE/) SPRECHER C A.
XX      PA (GAOZ/) GAO Z.
XX      PA (KUIJ/) KUIJPER J L.
XX      PA (DASO/) DASOVICH M M.
XX      PA (GRAN/) GRANT F J.
XX      PA (PRES/) PRESNEL S R.
XX      PA (WHIT/) WHITMORE T E.
XX      PA (HAMM/) HAMMOND A K.
XX      PA (NOVA/) NOVAK J E.

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PA      (GROS/) GROSS J A.
PA      (DILL/) DILLON S R.
XX      PI Sprecher CA, Gao Z, Kuijper JL, Dasovich MM, Grant FJ,
XX      PI Presnell SR, Whitmore TE, Hammond AK, Novak JE, Gross JA, Dillon SR,
XX      PI WPI: 2003-876545/81.
DR      P-PSDB: ADL26570.
XX      PT Novel multimeric or heterodimeric cytokine receptors useful for treating
XX      PT chronic inflammatory disease such as inflammatory bowel disease,
XX      PT ulcerative colitis, acute inflammatory disease such as endotoxaemia,
XX      PT septicemia.
XX      PS Example 3: SEQ ID NO 4; 205pp; English.
XX      CC The invention describes an isolated multimeric or heterodimeric cytokine
XX      CC receptor (I) having at least one polypeptide having 90 percent sequence
XX      CC identity with a 732 (S1) or 649 (S2) amino acid sequence given in
XX      CC specification, and where (I) binds a ligand comprising a 164 (S3) amino
XX      CC acid sequence, given in specification, or at least one polypeptide
XX      CC comprising residue 20-227 of (S1). (I) is useful for killing cancer cells
XX      CC and producing an antibody to (I) and a cytokine-binding domain of a class
XX      CC I cytokine receptor. A composition (C1) comprising (I) and a cytokine-
XX      CC binding domain of a class I cytokine receptor and a vehicle is useful
XX      CC for: reducing hematopoietic cells and hematopoietic progenitor cells in
XX      CC a mammal; inhibiting zcytor17lig-induced proliferation or differentiation
XX      CC of hematopoietic cells and hematopoietic progenitor cells; reducing
XX      CC zcytor17lig-induced inflammation; treating a mammal afflicted with an
XX      CC inflammatory disease in which zcytor17lig plays a role. The disease is a
XX      CC chronic inflammatory disease such as inflammatory bowel disease,
XX      CC ulcerative colitis, Crohn's disease, atopic dermatitis, eczema and
XX      CC psoriasis. The disease is acute inflammatory disease such as
XX      CC endotoxaemia, septicemia, toxic shock syndrome and infectious disease.
XX      CC An immune response inhibiting composition is useful for inhibiting an
XX      CC immune response in a mammal exposed to an antigen or pathogen. An
XX      CC inflammatory response inhibiting composition is useful for suppressing an
XX      CC inflammatory response in a mammal with inflammation. An antibody that
XX      CC specifically binds to (I) is useful for detecting the presence of a
XX      CC multimeric or heterodimeric cytokine receptor in a biological sample.
XX      CC This sequence encodes a human zcytor17 cytokine receptor.
XX      SQ Sequence 2903 BP; 862 A; 620 C; 664 G; 757 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 6,92e-316 Length: 2903
Score: 3451.00 Matches: 650
Percent Similarity: 99.85% Conservative: 1
Best Local Similarity: 99.69% Mismatches: 1
Query Match: 99.05% Indels: 1
DB: 11 Gaps: 0

US-10-006-265-2 (1-652) x ADL26569 (1-2903)
Qy      1  MetLysLeuSerProGlnProSerCysValAsnLeuGlyMetTyrThrTrpAlaLeu 20
Db      497  ATGAAGCTCTCTCCCGCCCTTCATGTGTAACTGGGAGATGATGAACTGGGACCTG 556
Qy      21  TrpMetLeuProSerLeuCyLysPheSerLeuAlaIleuProAlaLysProGluAsn 40
Db      557  TGGATGCTCCCTTACCTGCAAAATTCAGCCTGGCACTCTGCCAGATTAGCCGAGAAC 616
Qy      41  ILeSerCysValTyrTyrTyrArgLysAsnLeuThrCysThrTrpSerProGlyLysGlu 60
Db      617  ATTTCTGTGTCTACTACTATAGAAAAATTAACTGCACCTTGAGATCCAGGAAAGAA 676
Qy      61  ThrSerTyrThrGlnTyrThrValLysArgThrTyrAlaPheGlyGlyLysAspAsn 80
Db      677  ACCAGTTATACCCAGTACAGATTAAAGAACTTATGGAGAAAAACATGATTAAT 736
Qy      81  CysThrThrAsnSerSerThrSerGluAsnArgAlaSerCysSerPhePheLeuProArg 100
Db      737  TGTACACCAATAGTTTATACAGATGAAGAAATCGTGGCTTCTTTCTTTCTTCCAAAG 796

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QY 101 ILeThrIleProAspAsnTyrThrIleGluValGluAlaGluAsnGlyAspGlyValIle 120
 DB 797 ATPACATATCCAGATATATTTACCATTTGAGGTGAAAGCTGAAAATGGAGATGTTGAATT 856
 QY 121 LysSerHisMetThrTyrTrpArgGluAsnIleAlaLysThrGluProProlYsIle 140
 DB 857 AAATCTCATATGACATCTAGAGATTAAGAAACATGCGMAAACGAAACCACTTAAGATT 916
 QY 141 PheArgValLysProValIleuGlyIleLysArgMetIleGlnIleGluTrpIleLysPro 160
 DB 917 TTCGGGTGAAACCAATTTGGGCATCAACGAATATTCMAATGGAATGAAGAAAGCCCT 976
 QY 161 GluLeuAlaProValSerSerAspLeuLysTyrThrLeuArgPheArgThrValAsnSer 180
 DB 977 GAGTTGGCCCTCTTCACTGATTTAAATACACACTTCGATTCAAGACAGCAACAGT 1036
 QY 181 ThrSerTrpMetGluValAsnPheAlaLysAsnArgLysAspLysAsnGlnThrTyrAsn 200
 DB 1037 ACCAGCTGATGAGATCAAACTTCGCTAAGAACCGTAAGGATMAAAACGTAACAAC 1096
 QY 201 LeuThrGlyLeuGlnProPheThrGluTyrValIleAlaLeuArgCysAlaValLysGlu 220
 DB 1097 CTCACGGGGCTGACGCTTTTACGAATATGTCATAGCTCTGGGATGTGGGTCAAGAG 1156
 QY 221 SerLysPheTrpSerAspTrpSerGlnGluLysMetGlyMetThrGluGluGluAlaPro 240
 DB 1157 TCMAATTTCTGAGATGACCTGAGACCAAGAAAATGGGAATGACTGAGAGAAAGCTCCA 1216
 QY 241 CysGlyLeuGluLeuTrpArgValLeuLysProAlaGluAlaAspGlyArgArgProVal 260
 DB 1217 TGTGGCTGGAACCTGAGAGAGTCTGMAACAGCTGAGGCGGATGGAAGAAAGCCAGTG 1276
 QY 261 ArgLeuLeuTrpLysAlaArgGlyAlaProValLeuGluLysThrLeuGlyTyrAsn 280
 DB 1277 CGGTTTGTAGAAAGAGCAAGAGAGGCCCACTGCTAGAGAAAACACTGTGCTCAAC 1336
 QY 281 IleTrpTyrTyrProGluSerAsnThrAsnLeuThrGluThrMetAsnThrTranGln 300
 DB 1337 ATRTGTACTATCAAGAAACCACTAACCTCACAGAAACATGAACTAACTAACCAAG 1396
 QY 301 GlnLeuGluLeuHisLeuGlyGlyGluSerPheTrpValSerMetIleSerTyrAsnSer 320
 DB 1397 CAGCTTGAACCTGATCGGAGGCGAGAGCTTTGGGTGTCTATGATTTCTTAATTTCT 1456
 QY 321 LeuGlyLysSerProValAlaThrLeuArgIleProAlaIleGlnGluLysSerPheGln 340
 DB 1457 CTYGGAGAAGCTCCAGTGGCCACCTGAGGATTCCAGCTAATCAAGAAAATCATTTCA 1516
 QY 341 CysIleGluValMetGlnAlaCysValAlaGluAspGlnLeuValValLysTrpGlnSer 360
 DB 1517 TGCATTTGAGGTATGACAGGCTCGTGTCTGAGAGACCACTATGTTGAAAGTGGCAAGC 1576
 QY 361 SerAlaLeuAspValAsnThrTrpMetIleGluTrpPheProAspValAspSerGluPro 380
 DB 1577 TCTGCTCTAGACGTGAACACTTGATGATGATGATTTCCGATGTGAGCTCAGAGCCC 1636
 QY 381 ThrThrLeuSerTrpGluSerValSerGlnAlaThrAsnTrpThrIleGlnGlnAspLys 400
 DB 1637 ACCACCCCTTCCGGGAATCTGTCTCAGGCCACCAACGACGATCCAGCAAGATMAA 1696
 QY 401 LeuLysProPheTrpCysTyrAsnIleSerValTyrProMetLeuHisAspLysValGly 420
 DB 1697 TTBAACCTTTCTGGTGTCTTAACATCTCTGTGTATCCAAATTTGATGACAAAGTTGGC 1756
 QY 421 GluProTyrSerIleGlnAlaTyrAlaLysGluGlyValProSerGluGlyProGluTrp 440
 DB 1757 GAGCCATATTCATCCAGGCTTATGCAAAAGAGGGTTCATCAGAGAGTCTCGAGACC 1816
 QY 441 LysValGluAsnIleGlyValLysThrValThrIleThrTrpLysGluIleProlYsSer 460
 DB 1817 AAGGTGAGAAACATTGGCGTGAAGACGCTCAGATCAATGAGAAAGATTTCCCAAGAGT 1876

QY 461 GluArgLysGlyIleIleCysAsnTyrThrIlePheTyrGlnAlaGluGlyLysGly 480
 DB 1877 GAGAGAAAGGATATCATCTGCAACATACCACTTTTACCAAGCTGGAAGTGGAAAAGGA 1936
 QY 481 PheSerLysThrValAsnSerSerIleLeuGlnTyrGlyLeuGluSerLeuLysArgLys 500
 DB 1937 TTCTCCAAAGACAGTCAATTCAGCATCTTGACGTACGGCTCGAAGTCCCTGAAAAG 1996
 QY 501 ThrSerTrpIleValGluValMetAlaAsnThrSerAlaGlyGlyThrAsnGlyThrSer 520
 DB 1997 ACCCTTACATTTGTCAGTCAAGGACACAGCTGGGGGAAACCAAGGACCAAGC 2056
 QY 521 IleAsnPheLysThrLeuSerPheSerValPheGluIleIleLeuIleThrSerLeuIle 540
 DB 2057 ATPAATTTCAAGACATTTGTCATTCAGTGTCTTGAGATTATCTCATTAATCTTCGATT 2116
 QY 541 GlyGlyGlyLeuLeuIleLeuIleIleLeuThrValAlaTyrGlyLeuLysLysProAsn 560
 DB 2117 GGTGGAGGCTCTTATCTCATTTCTGACACAGTGGCATATGTGCTCAAAAACCCAAAC 2176
 QY 561 LysLeuThrHisLeuCysTrpProThrValProAsnProAlaGluSerSerIleAlaThr 580
 DB 2177 AATTTGACTCATCTGTGTGTGGCCACCGTTCCCAACCTGCTGAAGTATGTAAGCCACA 2236
 QY 581 TrpHisGlyAspAspPheLysAspLysLeuAsnLeuLysGluSerAspAspSerValAsn 600
 DB 2237 TGGCATGAGATGATTTTCAAGATTAAGCTAAACCTGAAGAGATCTGATCACTGTGAAC 2296
 QY 601 ThrGluAspArgIleLeuLysProCysSerThrProSerAspLysLeuValIleAspLys 620
 DB 2297 ACAGAAAGACAGATCTTAAACCATGTTCCACCCACAGGACAAAGTGTGATTGCAAG 2356
 QY 621 LeuValAlaAsnPheGlyAsnValLeuGlnGluIlePheThrAspGluAlaArgThrGly 640
 DB 2357 TGTGTGTGTAACCTTTGGGATGTTCTGCAGAAATTTTCACAGATGAAACCAAGCGGT 2416
 QY 641 GlnGluLysGlnPheArgArgGlyLysGluTrpAsp 652
 DB 2417 CAGGA-AAACATTTTGAAGGGGAAAAGATGGAC 2451

RESULT 6
 ABA93803
 ID ABA93803 standard; cDNA; 2529 BP.
 XX
 AC ABA93803;
 XX
 DT 01-MAY-2002 (first entry)
 XX
 DE Human zcytor17 cDNA sequence SEQ ID NO:45.
 XX
 KW Zcytor17; chromosome 5; 5q11; cytokine receptor; immunomodulatory;
 KW anti-inflammatory; antiviral; antineumatic; antiarthritic; cyostatic;
 KW muscular; lymphoid; immune; inflammatory; splenic; blood; bone;
 KW infection; immunosuppression; cytotoxicity; leukopenia; Crohn's disease;
 KW autoimmune disease; rheumatoid arthritis; multiple sclerosis; cancer;
 KW inflammatory disease; pancreatitis; inflammatory bowel disease; ss.
 XX
 OS Homo sapiens.
 XX
 PN W0200200721-A2.
 XX
 PD 03-JAN-2002.
 XX
 PF 26-JUN-2001; 2001WO-US020484.
 XX
 PR 26-JUN-2000; 2000US-0214282P.
 PR 29-JUN-2000; 2000US-0214955P.
 PR 08-FEB-2001; 2001US-0267963P.
 XX
 PA (ZYMO) ZYMOGENETICS INC.
 XX
 PI Sprecher CA, Prensell SR, Gao Z, Whitmore TE, Kuiper JL,
 Maurer MF;

XX MPI: 2002-090519/12.
 DR P-PSDB: ABB05738.
 XX Isolated polynucleotide encoding a cytokine receptor zcytor17 which is
 PT useful for treating and diagnosing lymphoid, immune, inflammatory,
 PT splenic, blood or bone disorders.
 XX
 PS Claim 2; Page 190-194; 235pp; English.
 XX
 CC The present invention describes a cytokine receptor designated zcytor17.
 CC Zcytor17 has immunomodulatory, antiinflammatory, antiviral, cytostatic,
 CC antineumatic, antiarthritic and muscular activities. The zcytor17
 CC proteins are useful for treating and diagnosing lymphoid, immune,
 CC inflammatory, splenic, blood or bone disorders. Agonists or anti-
 CC zcytor17 antibodies are useful in stimulating cell-mediated immunity and
 CC for stimulating lymphocyte proliferation, such as in the treatment of
 CC infections involving immunosuppression, including certain viral
 CC infections. They are also useful for inducing cytotoxicity and for
 CC treating leukopenias. Antagonist of zcytor17 polypeptides are useful for
 CC treating autoimmune diseases (e.g. rheumatoid arthritis and multiple
 CC sclerosis), inflammatory diseases (e.g. Crohn's disease), cancer,
 CC pancreatitis, and inflammatory bowel disease. Zcytor17 was mapped to
 CC chromosome 5, specifically to the 5q11 chromosomal region. ABA93767 to
 CC ABA93843 and ABB05730 to ABB05745 represent sequences used in the
 CC exemplification of the present invention
 CC
 XX
 SQ Sequence 2529 BP, 764 A, 530 C, 576 G, 659 T, 0 U, 0 Other;
 Alignment Scores:
 Pred. No.: 4.93e-315 Length: 2529
 Score: 3441.00 Matches: 648
 Percent Similarity: 99.85% Conservative: 1
 Best Local Similarity: 99.69% Mismatches: 1
 Query Match: 98.77% Indels: 1
 DB: Gaps: 0
 US-10-006-265-2 (1-652) x ABA93803 (1-2529)

Db 609 GCGCGTGTTCATCGATTTAAATAACACCTCGATTGAGACAGTCACAGTACAGC 668
 Qy 183 TTPMETGIVAlaenPheAlaLysAsnArgLysAspLysAsnGlnThrTyrAsnLeuThr 202
 Db 669 TGGATGGAAAGCAACTTCGCTACAGAACCGTAAAGATTAACAAACCAACCTACACCTCAGC 728
 Qy 203 G1yleuGlnProPheThrGluTyrVal11leAlaLeuArgCysAlaVal11leGlySerLys 222
 Db 729 GGGCTGACGCTTTTACGAAATATGTCATAGCTCTGCAATGCGGTCAAGAGTCAAAG 788
 Qy 223 PheTTPSerAspTTPSerGlnGluLysMetGlyMetThrGlnGlnAlaProCysGly 242
 Db 789 TTTCTGAGTGACTGAGCAAGAAATAATGGGATGACTGAGAAAGCTCCATGTGGC 848
 Qy 243 LeuGluLeuThrPArgVal11leuLysProAlaGluAlaAspGlyValArgArgProValArgLeu 262
 Db 849 CTGAACCTGTGGAAGCTCTGAAACACGCTGAGCGATGGAAGAGCCAGTCGGTGG 908
 Qy 263 LeuThrLysLysAlaArgGlyAlaProValLeuGlnLysThrLeuGlyTyrAsn11eTTP 282
 Db 909 TTAATGAGAAAGGACAGAGAGCCCTCAGTCTTAAGAAACACTTGGCTACACATATAG 968
 Qy 283 TyrTyrProGlnSerAsnThrAsnLeuThrGluThrMetAsnThrThrAsnGlnLeu 302
 Db 969 TACTATCCAGAAACCAACACTTAACCTACAGAAACAAATGAACACTTACACAGAGCTT 1028
 Qy 303 GluLeuHiLsLeuGlyGlyLysSerPheTTPValSerMet11SerTyrAsnSerLeuGly 322
 Db 1029 GACCTGATCTGGAGAGCGAGAGCTTTGGGTGTCATGATTTCTTAATCTCTTGGG 1088
 Qy 323 LysSerProValAlaThrLeuArg11eProAla11leGlnGluLysSerPheGlnCys11e 342
 Db 1089 AAGTCTCCAGTGGCCACCTCGAGATTCACACTTACAGAAATACTTTCACTGATTT 1148
 Qy 343 GluValMetGlnAlaCysValAlaGluAspGlnLeuValVal11eTTPGlnSerSerAla 362
 Db 1149 GAGGTCAATGACAGGCTCGGTGTGAGAGACACGATGAGTGAAGTGGCAAAAGCTCTGCT 1208
 Qy 363 LeuAspValAsnThrTTPMet11eGluTTPPheProAspValAspSerGluProThrThr 382
 Db 1209 CTAGACGTGAACACTTGAATGATGAATGATTTCCGATGTGAGCTCAGACCCACACACC 1268
 Qy 383 LeuSerTTPGlnSerValSerGlnAlaThrAsnTTPThr11leGlnGlnAspLysLeuLys 402
 Db 1269 CTTTCTGGGAATTTGTTCTCAGGCCACAGACGATCCAGACAGATTAATTAATAA 1328
 Qy 403 ProPheTTPCysTyrAsn11eSerValTyrProMetLeuHiLsAspLysVal11eGluPro 422
 Db 1329 CTTTCTGGTGTCTAATCATCTCTGTATCATATGTTGATGACAAAGTTGGGAGCCA 1388
 Qy 423 TyrSer11eGlnAlaTyrAlaLysGluGlyValProSerGluGlyProGluThrLysVal 442
 Db 1389 TATTCATCCACGCTTATGCCAAAGAGGCTTCATCAGAAAGTCTCGAGACCAAGGTG 1448
 Qy 443 GluAsn11eGlyValLysThrValThr11eThrTTPLysGlu11eLeuPheSerGluArg 462
 Db 1449 GAGAAACATTTGGCGTGAAGAGCGTACACATCACTGAAGAGATTTCCACAGAGGAGA 1508
 Qy 463 LysGly11e11eCysAsnTyrThr11ePheTyrGlnAlaGluGlyGlyLysGlyPheSer 482
 Db 1509 AAGGATTCATCTGCACTACACATCTTTTACCAACTGAAGTGAAGAAAGATTTCTCC 1568
 Qy 483 LysThrValAsnSerSer11eLeuGlnTyrGlyLeuGlnSerLeuLysArgLysThrSer 502
 Db 1569 AAGACAGTCAATTCACACATCTTGACATAGGCGCTGAGAGTCCCGAAGACCAACCTCT 1628
 Qy 503 Tyr11eValGlnValMetAlaAsnThrSerAlaGly11eLysThrAsnGlnThrSer11eAsn 522
 Db 1629 TACTTTGTCAAGGATGAGCCAGCAACGATGCTGGGGGAACCAAGGGACCAAGCATTAAT 1688
 Qy 523 PheLysThrLeuSerPheSerValPheGlu11e11eLeu11eThrSerLeu11eGly11e 542
 Db 1689 TTCAAGACATTTGATTCATTCAGTCTTGAAGTTATCTCATTAACCTTCTCGATTGGTGA 1748

QY 543 GAlYLeuLeuLeuLeuLeuLeuLeuValAlaTyrgLYLeuLysLysProAsnLysLeu 562
 DB 1749 GGGCTTCTATTCTCTATTCTCGAAGAGTGGCATATGCTCAAAAAACCAACCAATTG 1808
 QY 563 ThHleLeuCYsTrpProThrValProAsnProAlGlySerSerIlealThrPHis 582
 DB 1809 ACTCATCTGTGTGGCCCAACCGTTCCCAACCTGTGAAAGTAGTATAGCCATGGCAT 1868
 QY 583 GYAAspAspPheYAspLysLeuAsnLeuLysGlySerAspAspSerValAsnThrGlu 602
 DB 1869 GGAGATGATTTCAGAGATTAAGCTAAACCTGAAGAGTCTGATACCTGTGAACACAGAA 1928
 QY 603 AspArgIleLeuLysProCYsSerThrProSerAspLysLeuValIleAspLysLeuVal 622
 DB 1929 GACAGATCTTAAACCACTGTTCCACCCGAGACAGAACTGTGATGACAACTGGTG 1988
 QY 623 ValAsnPheGlyAsnValLeuGlnGluIlePheThrAspGluAlaArgThrGlnGlu 642
 DB 1989 GTGACCTTGGGAATGTTCTGCAAGAAATTTTCACAGATGACCAAGACGGTCAAGA- 2047
 QY 643 LysGlnPheArgArgGlyLysGlyLysLysLysLysLysLysLysLysLysLysLys 652
 DB 2048 AAACAATTGAAGAGGGGAAAGATGGAC 2077

RESULT 7

ADL26671 standard; cDNA; 2529 BP.

ADL26671;

20-MAY-2004 (first entry)

Human cytokine receptor zcytor17 DNA seqid 108.

antiinflammatory; antitumor; dermatological; antiallergic; antipsoriatic;
 anti-bacterial; immunosuppressive; cell proliferation inhibitor;
 immune response inhibitor; inflammatory response inhibitor;
 multimeric cytokine receptor; heterodimeric cytokine receptor; cancer;
 cytokine-binding domain; class I cytokine receptor; haematopoietic cell;
 zcytor17lg-induced proliferation; zcytor17lg-induced differentiation;
 hematopoietic progenitor cell; zcytor17lg-induced inflammation;
 inflammatory disease; inflammatory bowel disease; ulcerative colitis;
 Crohn's disease; atopic dermatitis; eczema; psoriasis; endotoxaemia;
 septicemia; toxic shock syndrome; zcytor17; human; gene; ss.

Homo sapiens.

US2003215838-A1.

20-NOV-2003.

21-JAN-2003; 2003US-00351157.

18-JAN-2002; 2002US-0350325P.

14-JUN-2002; 2002US-0389108P.

19-DEC-2002; 2002US-0435361P.

(SPRE/) SPRECHER C A.

(GAOZ/) GAO Z.

(KUIP/) KUIJPER J L.

(DASO/) DASOVICH M M.

(GRAN/) GRANT F J.

(PRES/) PRESNELL S R.

(WHIT/) WHITMORE T E.

(HAMM/) HAMMOND A K.

(NOVA/) NOVAK J E.

(GROS/) GROSS J A.

(DILL/) DILLON S R.

Sprecher CA, Gao Z, Kuijper JL, Dasovich MM, Grant FJ,
 Presnell SR, Whitmore TE, Hammond AK, Novak JE, Gross JA, Dillon SR;

DR WPI; 2003-876545/81.
 DR P-PSDB; ADL26672.

PT Novel multimeric or heterodimeric cytokine receptors useful for treating
 PT chronic inflammatory disease such as inflammatory bowel disease,
 PT ulcerative colitis, acute inflammatory disease such as endotoxaemia,
 PT septicemia.

PS Disclosure; SEQ ID NO 108; 205pp; English.

CC The invention describes an isolated multimeric or heterodimeric cytokine
 CC receptor (I) having at least one polypeptide having 90 percent sequence
 CC identity with a 732 (S1) or 649 (S2) amino acid sequence given in
 CC specification, and where (I) binds a ligand comprising a 164 (S3) amino
 CC acid sequence, given in specification, or at least one polypeptide
 CC comprising residue 20-227 of (S1). (I) is useful for killing cancer cells
 CC and producing an antibody to (I) and a cytokine-binding domain of a class
 CC I cytokine receptor. A composition (CI) comprising (I) and a cytokine-
 CC binding domain of a class I cytokine receptor and a vehicle is useful
 CC for: reducing haematopoietic cells and hematopoietic progenitor cells in
 CC a mammal; inhibiting zcytor17lg-induced proliferation or differentiation
 CC of hematopoietic cells and hematopoietic progenitor cells; reducing
 CC zcytor17lg-induced inflammation; creating a mammal afflicted with an
 CC inflammatory disease in which zcytor17lg plays a role. The disease is a
 CC chronic inflammatory disease such as inflammatory bowel disease,
 CC ulcerative colitis, Crohn's disease, atopic dermatitis, eczema and
 CC endotoxaemia, septicemia, toxic shock syndrome and infectious disease.
 CC An immune response inhibiting composition is useful for inhibiting an
 CC immune response in a mammal exposed to an antigen or pathogen. An
 CC inflammatory response inhibiting composition is useful for suppressing an
 CC inflammatory response in a mammal with inflammation. An antibody that
 CC specifically binds to (I) is useful for detecting the presence of a
 CC multimeric or heterodimeric cytokine receptor in a biological sample.
 CC This sequence encodes a human zcytor17 cytokine receptor that can be used
 CC in a comparison with other zcytor17 receptors.

SQ Sequence 2529 BP; 764 A; 530 C; 576 G; 659 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.: 4,93e-315 Length: 2529
 Score: 3441.00 Matches: 648
 Percent Similarity: 99.85% Conservative: 1
 Best Local Similarity: 99.69% Mismatches: 1
 Query Match: 98.77% Indels: 1
 DB: 11 Gaps: 0

US-10-006-265-2 (1-652) x ADL26671 (1-2529)

QY 3 LeuSerProGlnProSerCyValAsnLeuGlyMetMetTrpThrTrpAlaLeuTrpMet 22
 DB 129 CTCTCTCCCAACGCTTCAATGTTAACTGGGAGATATGACCTGGGCACTGTGGAG 188
 QY 23 LeuProSerLeuCYsLysPheSerLeuAlaLeuProAlaLysProGluAsnIleSer 42
 DB 189 CTCCTCTCACTGCAAAATTCAGCTGCGACCTGCTCCAGCTAAGCTGAGAACTTCC 248
 QY 43 CyValTyrrTyrrTyrrArgLysAsnLeuThrCySerTrpTrpSerProGlyLysGluThrSer 62
 DB 249 TGTGTCTACTACTATAGAAAATTTAACTGCTCAGCTGAGTCCAGAGAAAGAAACCACT 308
 QY 63 TyrThrGlnTyrThrValLysArgThrTyrAlaPheGlyGlyLysHisAspAsnCyThr 82
 DB 309 TATACCACTATACAGCTTAAGAACTTACGCTTTTGGAGAAAACATATATATGTACA 368
 QY 83 ThrAsnSerSerThrSerGluAsnArgAlaSerCySerPhePheLeuProArgIleThr 102
 DB 369 ACCAATAGTTTACAAGTGAATCGTGTCTGCTCTTTTCTCTTCCCAAGAAATTAAG 428
 QY 103 IleProAspAsnTyrThrIleGlyValGlyLysGlyLysGlyLysGlyLysGlyLys 122
 DB 429 ATCCCAATTAATTAATCACTTGAAGTGAAGCTGAAAATGAGATGTATTAATTAATCT 488

QY 123 HIsMeTThrTYrTPArgLeuGluuSniIeAlaTySrhGluProProlySilePheArg 142
 Db 489 CATATGACATCTGAGATTTAGAGAAACATAGCGAAACCTGAAACCACTTAAGTTTTCCT 548
 QY 143 ValIysProValLeuGlyIleIySArgMeCileGlnIleGluTrpIleIySProGluLeu 162
 Db 549 GTGAACCAAGTTTGGGATCAACCAATGATTCAATTAAGATTAAGCTTCAAGTTG 608
 QY 163 AlaProValSerSerAspLeuIySrhTYrThIleuArgPheArgThValAsnSerThSer 182
 Db 609 GCGCTGTTTCACTTGATTTAAATAACACTTCATTCAGGACGTCAACGTGACAGC 668
 QY 183 TrpMeCgluValAsnPheAlaIySAsnArgIySAspIySAsnGlnThrTYrAsnLeuThr 202
 Db 669 TGGATGAAAGTCACTTCCTTAAGAACCTTAAGATTAATAAACCAACGTAACCTCAG 728
 QY 203 GlyLeuGlnProPheThrGluTYrValIleAlaIySArgCySAlaValIleGluSerIyS 222
 Db 729 GGGCTGACCCCTTTTACAGAAATATGTCAATAGCTCGCATGTGCGGTCAAGAGTCAAG 788
 QY 223 PheTrpSerAspTrpSerGlnGluIySMeCglyMeCThrGluGluAlaProCySgly 242
 Db 789 TTCTGAGTGACTGGAGCCAGAAATAATGGAAATGACTGAGAGAAAGCTTCATGTGAC 848
 QY 243 LeuGluLeuTrpArgValIleuIySProAlaGluAlaAspGlyArgArgProValArgLeu 262
 Db 849 CTGGAACGTGGAGAGTCTTGAAACCACTGAGGGGATGAAAGAGCCAGTGGGTG 908
 QY 263 LeuTrpIySAlaArgGlyAlaProValLeuGluIySrhLeuGlyTYrAsnIleTrp 282
 Db 909 TTATGAGAGAGGCAAGAGAGCCCACTGCTAGAGAAACCTTGCGTCAACATATAGG 968
 QY 283 TYrTYrProGluSerAsnThrAsnLeuThrGluThrMeCAsnThrThAsnGlnIleu 302
 Db 969 TACTATCCAGAAAGCAACACTCACTCAAGAAACATGAAACACTCAACAGCAGCTT 1028
 QY 303 GluIeuHisIeuGlyGlyIySrhPheTrpValSerMeCileSerTYrAsnSerLeuGly 322
 Db 1029 GAACGTGATCTGGAGGCGAGAGCTTTTGGGTCTTAAGATTTCTTAATAATTCCTTTGG 1088
 QY 323 LysSerProValAlaThrLeuArgIleProAlaIleGlnGluIySrhPheGlnCySile 342
 Db 1089 AAGTCTCCAGTGGCCACCTGAGATTCAGCTATCAAGAAATAATCAATTCAGTGCATT 1148
 QY 343 GluValMeCgluAlaCySValAlaGluAspGlnLeuValIySrhGlnSerSerAla 362
 Db 1149 GAGGTCAAGCAGGCTGCTGCTGAGCAGCAGCTAGTGTGAAGTGTGCAAAAGCTCTCT 1208
 QY 363 LeuAspValAsnThrTrpMeCileGluTrpPheProAspValAspSerGluProThrThr 382
 Db 1209 CTTAGCGTGAACCTTGATGATGATGATTTCCGAGATGTGACTCAAGGCCACCCACC 1268
 QY 383 LeuSerTrpGluSerValSerGlnAlaThrAsnTrpThrIleGlnGlnAspIySLeuIyS 402
 Db 1269 CTTTCTCGGAATCTGTCTCAAGCCCAAGACTGAGATCCAGCAAGATTAATAA 1328
 QY 403 ProPheTrpCySrhTYrAsnIleSerValIySrhPheMeCLeuHisAspIySValIyGluPro 422
 Db 1329 CTTTCTGCTGTATTAACATCTGTGTATCCAAATGTGACAAAGTTGGCGAGCCA 1388
 QY 423 TYrSerIleGlnAlaTYrAlaIySgluIyValProSerGluIyProGluThrIySVal 442
 Db 1389 TATTCATCCAGGCTTATGCCAAAGAGCGTTCCATCAAGAGGCTCTGAGACCAAGGTG 1448
 QY 443 GluAsnIleGlyValIySrhValThrIleThrTrpIySgluIleProIySrhGluArg 462
 Db 1449 GAGAAACATGGCGTGAACCGTCAAGTCAATCAATGAAGAGATTCACCAAGGTGAGAGA 1508
 QY 463 LysGlyIleIleCySAsnTYrThrIlePheTYrGlnAlaGluIyGlyIySrhPheSer 482
 Db 1509 AAGGTATACATCTGCACTCAACCATCTTTTACCAAGCTGAAGGTGAAGAGATTCCTCC 1568
 QY 483 LysThrValAsnSerSerIleuGlnIySrhGlyLeuGluIySrhLeuIySArgIySrhSer 502

Db 1569 AAGACAGTCAATTCAGCATCTTGACAGTACGGCTGGAGTCCCTGAAACGAAAGACCTCT 1628
 QY 503 TYrIleValGlnValMeCAlaAsnThrSerAlaGlyIyThrAsnGlyThSerIleAsn 522
 Db 1629 TACATTTGTCAGGTGATGAGCAGCAGCTGTGGGGAAACCAACGGACGATTAAT 1688
 QY 523 PheIySrhLeuSerPheSerValPheGluIleIleIleuIleThrSerIleuIleGlyGly 542
 Db 1689 TTCAGACATTTGTCATTAAGTGTCTTTGAGATTATCTCATTAACCTTCTGTATGTGGA 1748
 QY 543 GlyLeuLeuIleIleuIleIleuThrValAlaTYrGlyLeuIySAlaProAsnIySLeu 562
 Db 1749 GGCCTTCTTATCTCATTAATCTGACAGTGCATATGTGTCCTCAAAAACCAACAAATTTG 1808
 QY 563 ThrHisLeuCySrhProThrValIleProAsnProAlaGluSerSerIleAlaThrTrpHis 582
 Db 1809 ACTCATCTGTGTGGCCACCGTTCCTCAACCTGTGAAAGTATAGCCACATGTGCAT 1868
 QY 583 GlyAspAspPheIySAspIySLeuAsnLeuIySrhIySAspAspSerValAsnThrGlu 602
 Db 1869 GAGATGATTTCAAGATTAACCTTAACGAGGTGATGACTGTGAAACAGAGA 1928
 QY 603 AspArgIleLeuIySProCySrhThrProSerAspIySLeuValIleAspIySLeuVal 622
 Db 1929 GACAGGATCTTAACCAACATGTTCCACCCCGACGTAACAGTTGGTATGACAAATTTG 1988
 QY 623 ValAsnPheGlyAsnValLeuGlnGluIlePheThrAspGluAlaArgThrGlyGlnGlu 642
 Db 1989 GTGAACCTTTGGGAAATGTTCTCAAGAAATTTTCAACATGAAGCAGAAACGGGTCAAGA - 2047
 QY 643 LysGlnPheArgArgGlyIySgluTrpAsp 652
 Db 2048 AAACATTTAGAGAGGAGAAAGATGGAC 2077
 RESULT 8
 AB083363
 ID AB083363 standard; cDNA: 4315 BP.
 AC AB083363;
 DT 20-JAN-2003 (first entry)
 XX
 DE Human NR10.3 splicing variant encoding cDNA SEQ ID NO:1.
 XX
 KW NR10; splicing variant; haematopoietin receptor; immunomodulator;
 KW haemostatic; haematopoietic factor; immunological disease;
 KW haematopoietic disease; haematopoietic cell regulation; gene; ss.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT CDS 7..2052
 FT /*tag= a
 FT /product= "NR10.3"
 XX
 EN WO200277230-A1.
 PD 03-OCT-2002.
 PE 22-MAR-2002; 2002WO-JP002769.
 PR 26-MAR-2001; 2001JP-00087298.
 PA (CHUS) CHUGAI SEIYAKU KK.
 PI Maeda M, Yaguchi N, Hasegawa M;
 XX
 DR WPI; 2003-018925/01.
 DR P-PSDB; ABP54363.
 XX
 PT NR10 splicing variants of haematopoietin receptor proteins and encoded
 genes, applicable in searching haematopoietic factors and developing

PT remedies for immunological and hematopoietic diseases.
XX
PS Example 2; Fig 1-2; 250pp; Japanese.
XX
CC The present invention describes hematopoietic receptor NR10 splicing
CC variants (1). (1) have immunomodulator and hemostatic activities. The
CC proteins and encoded genes are applicable in searching for novel
CC hematopoietic factors, and developing remedies for immunological and
CC hematopoietic diseases. The hematopoietic receptor genes participate in
CC in vivo immunomodulation and hematopoietic cell regulation, and in the
CC search for hematopoietic factors capable of functionally binding to the
CC receptors. The present sequence encodes the human NR10.3 protein from the
CC present invention
XX
SQ Sequence 4315 BP; 1187 A; 1008 C; 1061 G; 1059 T; 0 U; 0 Other;
Alignment Scores:
Pred. No.: 1,07e-314 Length: 4315
Score: 3441.00 Matches: 648
Percent Similarity: 99.85% Conservative: 1
Best Local Similarity: 99.69% Mismatches: 1
Query Match: 98.77% Indels: 1
DB: 8 Gaps: 0
US-10-006-265-2 (1-652) x AB083363 (1-4315)
QY 3 LeuSerProGlnProSerCysValAsnLeuGlyMetMetTrpThrTrpAlaLeuTpmet 22
DB CTCTCTCCCGAGCCTTCATGTGTAACTTGGGATGATGTGAGACTGGGCACTGTGGATG 129
QY 23 LeuProSerLeuCysIysPheSerLeuAlaAlaLeuProAlaIysProGluAsnIleSer 42
DB CTCGCCCTCACTCGAAATTCAGCCTGCGAGCTCTGCACTAAGCCTGAGAACATTTCC 189
QY 43 CysValIleTrpTrpIleArgIysAsnLeuThrCysThrTrpSerProGlyIleGluThrSer 62
DB TGTGTCTACTACTATGAGAAATTTAACTGCACTTGAGCTCAGGAAAGGAAACAGT 249
QY 63 TyrThrGlnIleThrValIleValArgTrpTrpAlaPheGlyGluIleIleAspAsnCysThr 82
DB TATTAACCACTGACAGTTAAGAACTTACGCTTTTGGAGAAACATGATTAATTGTACA 309
QY 83 ThrAsnSerSerThrSerGluAsnArgAlaSerCysSerPhePheLeuProArgIleThr 102
DB ACCAATAGTCTCAAGTGAATAATCGTCTGCGCTCTTTTCCCTTCCAGAAATPACG 369
QY 103 IleProAspAsnTrpThrIleGluValGluAlaGluAsnGlyAspGlyValIleIleYser 122
DB ATCCCGATTAATTAATACCATTTGAGGTGAGAGCTGAAATGAGATGCTGTAATTAATCT 429
QY 123 HisMetThrTyrTrpArgLeuGluAsnIleAlaIleThrGluProProIlePheArg 142
DB CATATGACATACCTGAGATTAAGAACATTAAGCAAACTGAAACCACTTAAGATTTCCGT 489
QY 143 ValIleProValIleuGlyIleIleValArgMetIleGlnIleGluTrpIleIleYserProGluLeu 162
DB GTGAAACCAAGTTTGGGCATCAAAACGATGATTCAATTGAATGAATAAAGCCGAGTTG 549
QY 163 AlaProValSerSerAspLeuIleIleValIleThrLeuArgPheArgThrValAsnSerThrSer 182
DB GGCCTGTTTTCATCTGATTTTAAATACACCTTCGATTGAGACAGCAACAGTACACAGC 609
QY 183 TrpMetGluValAsnPheAlaValAsnArgIleAspIleAsnGlnIleThrTrpAsnLeuThr 202
DB TGAATGAGATCAACTTCCTGCTAAGAACCGTAAGGATTAACCAACGATCAACCTCAGC 669
QY 203 GlyLeuGlnProPheThrGluTrpValIleAlaLeuArgCysAlaValIleGluSerIleYs 222
DB GGGCTGAGGCTTTTACAGAAATATGTATAGCTCTGCGATGTGCGGTCAAGAGTCAAG 729
QY 223 PheIleTrpSerAspTrpSerGlnGluIleYsMetGlyMetThrGluGluGluAlaProCysGly 242
DB TTCTGAGTGAAGTGAAGCAAAAGAAATGGAATGACTGAGGAGAAAGAAAGTCCATGTGCG 789

QY 243 LeuGluLeuTrpArgValIleuIysProAlaGluAlaAspGlyArgArgProValArgLeu 262
DB CTGGAACCTGTGAGAGCTCTGAAACCAAGCTGAGGCGGATGGAAGAAAGCCAGTGGCTTG 849
QY 263 LeuTrpIleValAlaArgGlyAlaProValIleuGluIleThrLeuGlyIleThrAsnIleTrp 282
DB TTAATGAAAGAGCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 909
QY 283 TyrTrpProGluSerAsnThrAsnLeuThrGluThrMetAsnThrThrAsnGlnIleu 302
DB TACTATCCGAAAGCAACCTTAACCTCACAGAAACATATACATTAACCAAGCAGCTT 969
QY 303 GluLeuHisLeuGlyIleGluSerPheTrpValIleSerMetIleSerTyrAsnSerLeuGly 322
DB GAACTGCATCTGGAGGCGAGAGCTTTTGGGTGATGATTTCTTAATATCTCTGGG 1029
QY 323 IysSerProValAlaThrLeuArgIleProAlaIleGlnGluIleYserPheGlnCysIle 342
DB AAGTCTCCAGTGGCCACCTCGAGAGATTCAGCTATTCAAGAAATCAATTCAGTCCATT 1089
QY 343 GluValMetGlnAlaCysValAlaGluAspGlnLeuValValIleTrpGlnSerSerAla 362
DB GAGGTGATGACAGGCTGCGTGTCTGAGACAGCTAAGTGAAGTGGCAAGCTGTGCT 1149
QY 363 LeuAspValAsnThrTrpMetIleGluTrpPheProAspValAspSerGluProThrThr 382
DB CTAGAGTGAACACTTGATGATTAATGATTTCCGAGATGTGAGCTCAAGCCACACAC 1209
QY 383 LeuSerTrpGluSerValSerGlnAlaThrAsnTrpThrIleGlnGlnAspIleuIleYs 402
DB CTTTCTGGGAAATCTGTGTCTCAGGCAAGAACTGACCATCAGCAAAATTAATTAATA 1269
QY 403 ProPheTrpCysThrAsnIleSerValIleTrpMetLeuHisAspIleValGlyGluPro 422
DB CTTTGTGATCAATTAACATCTGTGTATCCAAAGTTCAGAACAAAGTGGCGAGCA 1329
QY 423 TyrSerIleGlnAlaIleValIleYsGluGlyValProSerGluGlyProGluThrIleYsVal 442
DB TATTCATCAAGGCTTATTCGCAAGAGGCGTTCCATCAAGAGTCTCTAGACCAAGGTG 1389
QY 443 GluAsnIleGlyValIleYsThrValThrIleThrTrpIleGluIleProIleYserGluArg 462
DB GAGAACATTTGGCGTGAAGCGGTCAAGATCAATGAAAGAGTATCCCAAGGTGAGAA 1449
QY 463 IysGlyIleIleCysAsnTrpThrIlePheTrpGlnAlaGluGlyIleYsGlyPheSer 482
DB AAGGATATCATCTGCACTACACCATCTTTTACCAAGCTGAAGGTGAAGAGATTTCTCC 1509
QY 483 TyrThrValAsnSerSerIleLeuGlnIleYsGlyLeuGluSerLeuIysArgIleYsThrSer 502
DB AAGACAGTCAATTTCCAGCATCTTTGCAAGTACGGGCTGAGATCCCTGAAAGAAAGACTCT 1569
QY 503 TyrIleValGlnValMetAlaAsnThrSerAlaGlyIleThrAsnGlyThrSerIleAsn 522
DB TACATGTTCAAGTATGCGCACCAAGCTGCGGGGAAACCAACCGGACATCAATTAAT 1629
QY 523 PheIleThrLeuSerPheSerValPheGluIleIleLeuIleThrSerLeuIleGlyIle 542
DB TTCAGACATTTGATTCAGTGTCTTTGAGATTATCTATTAATCTCTGATGTGTGA 1689
QY 543 GlyLeuLeuIleLeuIleIleLeuThrValAlaTyrGlyIleuIleYsProAsnIleuIle 562
DB GGCCTTCTTATTTCTATTCTCTGACAGTGGCATATGTCTCAAAAAACCAACCAATTTG 1749
QY 563 ThrHisLeuCysTrpProThrValProAsnProAlaGluSerSerIleAlaThrTrpHis 582
DB ACTCATCTGTGTGGCCACCGTTCCCAACCTGCTGAAGATGATTAACCATGTCAT 1809
QY 583 GlyAspAspPheIleAspIleYsLeuAsnLeuIleGluSerAspAspSerValAsnThrGlu 602
DB GGAGATGATTTCAAGATTAAGCTTAACCTGAAGAGATGATGATCTGTGAACACAGAA 1869

QY 603 AsparagileuleuLyseProCySerThrProSerAspLyLeuValIleAspLyLeuVal 622
 DB 1870 GACAGGACTTTAAACCATGTTCCACCCCACTGACCACTGCTGATTCACAGTTGGTG 1929
 QY 623 ValaenpneGlyAsnValleuGlnGluIlePheThrAspGluAlaArgThrGlyGlnGlu 642
 DB 1930 GTGAACCTTGGGAATGTTCTTCGACAGAAATTTTACAGATGAAGCCAGAACGGGTCAAGA- 1988
 QY 643 LyseGlnPheArgArgGlyLyseGluTrpAsp 652
 DB 1989 AAACAAATTTAGAGGAGGAAAGAAATGGGAC 2018
 RESULT 9
 ABA93767
 ID ABA93767 standard: cDNA, 2386 BP.
 XX ABA93767;
 AC ABA93767;
 XX ABA93767;
 DT 01-MAY-2002 (first entry)
 XX
 DE Human zcytor17 cDNA sequence SEQ ID NO:1.
 XX
 KW Zcytor17; chromosome 5; 5q11; cytokine receptor; immunomodulatory;
 KW antiinflammatory; antiviral; antirheumatic; antiarthritis; cytostatic;
 KW muscular; lymphoid; immune; inflammatory; splenic; blood; bone;
 KW infection; immunosuppression; cytotoxicity; leukopenia; Crohn's disease;
 KW autoimmune disease; rheumatoid arthritis; multiple sclerosis; cancer;
 KW inflammatory disease; pancreatitis; inflammatory bowel disease; ss.
 XX
 OS Homo sapiens.
 XX
 PN MO200200721-A2.
 XX
 ED 03-JAN-2002.
 XX
 PF 26-JUN-2001; 2001MO-US020484.
 XX
 PR 26-JUN-2000; 2000US-0214282P.
 PR 29-JUN-2000; 2000US-0214955P.
 PR 08-FEB-2001; 2001US-0267963P.
 XX
 PA (ZYMO) ZYMOGENETICS INC.
 XX
 PI Sprecher CA, Presnell SR, Gao Z, Whitmore TE, Kuiper JL;
 PI Maurer MF;
 XX
 DR WP1; 2002-090519/12.
 DR P-PSDB; ABB05730.
 XX
 PT Isolated polynucleotide encoding a cytokine receptor zcytor17 which is
 PT useful for treating and diagnosing lymphoid, immune, inflammatory,
 PT splenic, blood or bone disorders.
 PS
 PS Claim 2; Page 161-166; 235pp; English.
 XX
 CC The present invention describes a cytokine receptor designated zcytor17.
 CC Zcytor17 has immunomodulatory, antiinflammatory, antiviral, cytostatic,
 CC antirheumatic, antiarthritis and muscular activities. The zcytor17
 CC proteins are useful for treating and diagnosing lymphoid, immune,
 CC inflammatory, splenic, blood or bone disorders. Agonists or anti-
 CC zcytor17 antibodies are useful in stimulating cell-mediated immunity and
 CC for stimulating lymphocyte proliferation, such as in the treatment of
 CC infections involving immunosuppression, including certain viral
 CC infections. They are also useful for inducing cytotoxicity and for
 CC treating leukopenias. Antagonist of zcytor17 polypeptides are useful for
 CC treating autoimmune diseases (e.g. rheumatoid arthritis and multiple
 CC sclerosis), inflammatory diseases (e.g. Crohn's disease), cancer,
 CC pancreatitis, and inflammatory bowel disease. Zcytor17 was mapped to
 CC chromosome 5, specifically to the 5q11 chromosomal region. ABA93767 to
 CC ABA93767; and ABB05730 to ABB05745 represent sequences used in the
 CC exemplification of the present invention
 XX
 SO Sequence 2386 BP; 711 A; 525 C; 575 G; 575 T; 0 U; 0 Other;

Alignment Scores:
 Pred. No.: 1,676-314 Length: 2386
 Score: 3435.00 Matches: 647
 Percent Similarity: 99.85% Conservative: 1
 Best Local Similarity: 99.69% Mismatches: 1
 Query Match: 98.59% Indels: 1
 DB: 6 Gaps: 0
 US-10-006-265-2 (1-652) x ABA93767 (1-2386)
 QY 3 LeuSerProGlnProSerCysValAsnLeuGlyMetCysTrpThrAlaLeuTrpMet 22
 DB CTCTCTCCCAAGCCTTCACTGCTTAACTGGGAGATGATGACTGGCACTGTGATG 197
 QY 23 LeuProSerLeuCysLysPheSerLeuAlaAlaLeuProAlaLysProGluAsnLysSer 42
 DB CTCCCTCAGCTCTGCAATTCAGCTGGCAGCTCTGCGCAGCTAAGCTGAGAACATTTCC 257
 QY 43 CysValTyrTyrTyrArgLysAsnLeuThrCysThrTrpSerProGlyLysGluThrSer 62
 DB TGTGCTACTACTATAGGAAATTTAACTGCACTTGAGTCCAGAGAAAGAAACAGT 317
 QY 63 TyrThrGlnTyrThrValLysArgThrTyrAlaPheGlyGlyLysHisAspAsnCysThr 82
 DB TATACCCAGTACACAGTTAAAGAACTTACCTTTGGAGAAACATGATATTTGATCA 377
 QY 83 ThrAsnSerSerThrSerGluAsnArgAlaSerCysSerPheLeuProArgLleThr 102
 DB ACCAATAGTCTTACAAGTGAATGCGTCTGAGTCTCTTTTCCCTTCAAGATAACG 437
 QY 103 IleProAspAsnTyrThrIleGluValGluAlaGluAsnGlyAspGlyValIleLysSer 122
 DB ATCCAGATTAATTTATACCATTTAGAGTGGAGTGAAGTGAATGAGATGGTAAATTAATCT 497
 QY 123 HisMetThrTyrTrpArgLeuGluAsnIleAlaLysThrGluProLysIlePheArg 142
 DB CATATGACATCTGAGATTTAGAGAACATGACGAAACCTGAAACCATTAATTTCCGT 557
 QY 143 ValLysProValLeuGlyLysArgMetIleGlnIleGluTrpLysAspProGluLeu 162
 DB GTGAACCAAGTTTGGGATCAAAAGCAATGATTAATTAATGATGATTAACCTGAGTTG 617
 QY 163 AlaProValSerSerAspLeuLysTyrThrLeuArgPheAlaGlnThrValAsnSerThrSer 182
 DB GCGCCTGTTTATCTGATTTAAATTAACACACTTGCATTCAGACAGTCAACAGTACCAAGC 677
 QY 183 TrpMetGluValAsnPheAlaLysAsnArgLysAspLysAsnGlnThrTyrAsnLeuThr 202
 DB TGGATGGAAGTCAACTTCGCTAAGAACCTGTAAGATTAATAACCAACGTAACCTCAAGC 737
 QY 203 GlyLeuGlnProPheThrGluTyrValIleAlaLeuArgCysAlaValLysGluSerLys 222
 DB GGGCTGAGCCTTTTACAGATATGTCATAGCTCTGCGAGTGTGGTCAAGAGTCAAG 797
 QY 223 PheTrpSerAspTrpSerGlnGluLysMetGlyMetThrGlnGluGluAlaProCysGly 242
 DB TTCGAGGTGACTGAGACCAAGAAATGGGAATGACTGAGGAAGACCTCATGTGGC 857
 QY 243 LeuGluLeuTrpArgValLleLysProAlaGluAlaAspGlyAspProValArgLeu 262
 DB CTGGAACGTGTGAAGATCCTGTAACCAAGCTGAGCGGATGAGAAAGCCAGTGGGTTG 917
 QY 263 LeuTrpLysLysAlaArgLysAlaProValLeuGluLysThrLeuGlyTyrAsnIleTrp 282
 DB TTATGGAAGAAAGCAAGGAGGCCCAAGTCTTACAGAAACATCTGCTCAACATATGG 977
 QY 283 TyrTyrProGluSerAsnThrAsnLeuThrGluThrMetAsnThrAsnGlnGluLeu 302
 DB TACTATCAGAAACCAACACTACCTCAAGAAACATGAACATTAACCAACCACTT 1037
 QY 303 GluLeuHisLeuGlyGlyLysSerPheTrpValSerMetLysSerTyrAsnSerLeuGly 322

Db	1038	GAACGCACTCGGAGGCGAAGACGCTTTGGGTGTCATGATATTTCTTAATATTCCTTGGG	1097
Qy	323	LysSerProValAlaThrLeuArgIleProAlaIleGlnIuLysSerPheGlnCysIle	342
Db	1098	AAAGTCACAGTGGCCACCCTGAGGATTCACGCTATTCCAGAAAATATCTTCAAGTCATT	1157
Qy	343	GluValMetGlnAlaCysValAlaGluAspGlnLeuValValIleTTPGlnSerSerAla	362
Db	1158	GAGGTGCATGCAAGGCGCTGCGTTCGAGGACCAAGCTAGTGAAGTGGCAAGGCTGCTGC	1217
Qy	363	LeuAspValAsnTrpTrpMetIleGluTrpPheProAspValAspSerGluProThrThr	382
Db	1218	CTAAGCGTGAAACACTTGGAATGATGAAATGGTTTCCGATGTGGACTCAGAGCCACCAACC	1277
Qy	383	LeuSerTrpGluSerValSerGlnAlaThrAsnTrpThrIleGlnGlnAspLysLeuLys	402
Db	1278	CTTTCCTGGGAATCGTGCTCCAGGCCCAAGATCGAGATCCAGCAAGATTAATTAATA	1337
Qy	403	ProHeterProCysIleTrpAsnIleSerValIleProMetLeuHisAspLysValGlyGluPro	422
Db	1338	CCCTTCGTCGCTTAACATCTCTGTGTATCCAATGTCATGACAAAGTTGGCGAGCA	1397
Qy	423	TyrSerIleGlnAlaIleTyrAlaLysGlnGluIleProSerGluGlyProGluThrLysVal	442
Db	1398	TATTCATCCAGGCTTATGCCAAGAAAGCGCTTCATAGAAAGGCTCTGAGACCAAGGTG	1457
Qy	443	GluAsnIleGlyValLysThrValThrIleThrTrpLysGluIleProLysSerGluArg	462
Db	1458	GAGAACATATGGCGTGAAGACGGTCACGATCAATGAAAGAGATTCCCAAGATGAGAGA	1517
Qy	463	LysGlyIleIleCysAsnTrpThrIlePheTyrGlnAlaGluGlyGlyLysGlyPheSer	482
Db	1518	AAAGGTATCACTCTCACTACACCATCTTTTACCAAGCTGAAGGTGAAAGGATTCCTCC	1577
Qy	483	LysThrValAsnSerSerIleLeuGlnTrpGlyLeuGlnSerLeuLysArgLysThrSer	502
Db	1578	AAAGACGTCAATTCAGCATCTTCGAGTACGAGCTGAGTCCCTGAAACGAAAGCCTCT	1637
Qy	503	TyrIleValGlnAlaMetAlaAsnThrSerAlaGlyIleTrpAsnGlyThrSerIleAsn	522
Db	1638	TACATGTGTCAGTCATATGGCCAGCACCGATCCTGGGGGCAACCAACGGGACCATTAAT	1697
Qy	523	PheLysThrLeuSerPheSerValPheGluIleIleLeuIleThrSerLeuIleGlyGly	542
Db	1698	TTCAAGACATGTCAATCAGTGTCTTGAAGATTATCCATTAACCTTCTGATTGTGGA	1757
Qy	543	GlyLeuLeuIleLeuIleIleLeuThrValAlaTyrGlyLeuLysLysProAsnLysLeu	562
Db	1758	GGCCTCTTATATTCATATATATCTGACATGCGCATATGGTCTCAAAAAACCAACAATTG	1817
Qy	563	ThrHisLeuCysTrpProThrValProAsnProAlaGluSerSerIleAlaThrTrpHis	582
Db	1818	ACTCATCTGTGTGGCCCAACCGTTCCCAACCTGCTGAAATAAGTATGCCACATGGCAT	1877
Qy	583	GlyAspAspPheLysAspLysLeuAsnLeuLysGlnSerAspAspSerValAsnThrGlu	602
Db	1878	GGAATGATTTTCAAGATTAACCTAAACCTGAAGAGTCTGATGACTCTGTGAACAACAGAA	1937
Qy	603	AspArgIleLeuLysProCysSerThrProSerAspLysLeuValIleAspLysLeuVal	622
Db	1938	GACGAGATCTTAANAACATGTTCACCCCAAGTACCAAGTTGGATTTGACCAAGTTGGTG	1997
Qy	623	ValAsnPheGlyAsnValLeuGlnGluIlePheThrAspGluAlaArgThrGlyGlnGlu	642
Db	1998	GTGAACCTTGGGAATGTTCTCGCAAGAAATTTTTCACAGTGAAGCCAGAACGGGTCAAGA-	2056
Qy	643	LysGlnPheArgArgGlyLysGluTrp	651
Db	2057	AAACATTTTGAAGAGGAAAAAGAAATGG	2083
RESULT 10			
ADL2673			
ID	ADL26673	standard; cDNA; 2402 BP.	

CC An immune response inhibiting composition is useful for inhibiting an
 CC immune response in a mammal exposed to an antigen or pathogen. An
 CC inflammatory response inhibiting composition is useful for suppressing an
 CC inflammatory response in a mammal with inflammation. An antibody that
 CC specifically binds to (1) is useful for detecting the presence of a
 CC multimeric or heterodimeric cytokine receptor in a biological sample.
 CC This sequence encodes a human zcytor17 cytokine receptor that can be used
 CC in a comparison with other zcytor17 receptors.

XX Sequence 2402 BP; 713 A; 532 C; 580 G; 577 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.:	1,696-314	Length:	2402
Score:	3435.00	Matches:	647
Percent Similarity:	99.85%	Conservative:	1
Best Local Similarity:	99.69%	Mismatches:	1
Query Match:	11	Indels:	1
DB:		Gaps:	0

US-10-006-265-2 (1-652) x ADL26673 (1-2402)

Qy	3	LeuSerProGlnProSerCysValAsnLeuGlyMetMetTrpThrTyrAlaLeuTrpMet	22
Db	138	CTCTCTCCCGACCTTCACTGTGTAACTGGGAGATGATGGACCTGGGCACTGTGGATG	197
Qy	23	LeuProSerLeuCysValPheSerLeuAlaLeuProAlaValProGlnAsnIleSer	42
Db	198	CTCCCTCACTCTGCAAAATTCAGCTGGAGCTCTGCGACGCTGAGAAACATTTCC	257
Qy	43	CysValTyrTyrTyrArgLysAsnLeuThrCysThrTrpSerProGlyLysGluThrSer	62
Db	258	TGTGTCTACTACTATAGAAAAATTTAACTGGCATTTGGAGTCCAGAAAGAAACCGT	317
Qy	63	TyrThrGlnTyrThrValLysArgThrTyrAlaPheGlyGluLysHisAspAsnCysThr	82
Db	318	TATACCCGATCACAGATTAGAGAACTTACGCTTTGGAGAAAAACATGATATTGTACA	377
Qy	83	ThrAsnSerSerThrSerGluAsnArgAlaSerCysSerPhePheLeuProArgIleThr	102
Db	378	ACCAATACCTTCAAGGAAATGCTGCTGCTCTTTTCTTCCCAAGATTAACG	437
Qy	103	IleProAspAsnTyrThrIleGluValGluAlaGluAsnGlyAspGlyValIleLysSer	122
Db	438	ATCCAGATATTTATACATTGAGGTGAGCTGAAATGAGATGCTGTAATTAATCT	497
Qy	123	HisMetThrTyrTrpArgLeuGluAsnIleAlaLysThrGluProProLysIlePheArg	142
Db	498	CATATGACATACGTGAGATTAGAGAACATAGCAAAACCTAAGATTTCCGT	557
Qy	143	ValLysProValLeuGlyIleLysArgMetIleGlnIleGluTrpIleLysProGluLeu	162
Db	558	GTAAGAACAGATTGGGATCAACAGAAATGATTCATTAATGATGATTAACCTGAGTTG	617
Qy	163	AlaProValSerSerAspLeuLysTyrThrLeuArgPheArgThrValAsnSerThrSer	182
Db	618	GCGCTGTTTCACTGATTTAAATACACACTTCGATTCAAGACAGTCAACAGTACCGC	677
Qy	183	TrpMetGluValAsnPheAlaLysAsnArgLysAspLysAsnGlnThrTyrAsnLeuThr	202
Db	678	TGGATGGAAGTCACTTCGCTAAGAACCGTAAGATTAACCAACGTAACAACCTGACG	737
Qy	203	GlyLeuGlnProPheThrGluTyrValIleAlaLeuArgCysAlaValLysGluSerLys	222
Db	738	GGGCTGAGCCTTTTACAGATATGTCATGCTCTGCATGTGGCTCAAGAGTCAAG	797
Qy	223	PheTrpSerAspTrpSerGlnGlyLysMetGlyMetThrGluGluGluAlaProCysGly	242
Db	798	TTCTGAGAGTGACTGAGGCAAGAAAAATGGGATGACTGAGAAAGAGCTCCATGTGGC	857
Qy	243	LeuGluLeuTrpArgValLeuLysProAlaGluAlaAspGlyArgArgProValArgLeu	262
Db	858	CTGGAACGTGGAGAGTCTGTAACACAGCTGAGCGGATGAGAAAGGCGAGTGGTGG	917

Qy	263	LeuTrpLysLysAlaArgGlyAlaProValLeuGluLysThrLeuGlyTyrAsnIleTrp	282
Db	918	TTATGAAAGAAAGGCAAGAGGAGCCCACTCTTACAGAAAAACCTTGGCTTACACATAGG	977
Qy	283	TyrTrpProGlnSerAsnThrAsnLeuThrGluThrMetAsnThrThrAsnGlnLeu	302
Db	978	TACTATCCAGAAAGCAACACTACCTCAAGAAAAATGAACTACTACACAGACAGCTT	1037
Qy	303	GluLeuHisLeuGlyGlyGluSerPheTrpValSerMetIleSerTyrAsnSerLeuGly	322
Db	1038	GAACGACATCTGGAGAGGAGGAGCTTTGGTGTCTTGAATTTCTTAAATCTCTTGGG	1097
Qy	323	LysSerProValAlaThrLeuArgIleProAlaIleGlnGluLysSerPheGlnCysIle	342
Db	1098	AAGTCTCCAGTGGCCACCTTAGAATTCACCTTTCAGAAAAATCTTTCAGTGCATT	1157
Qy	343	GluValMetGlnAlaCysValAlaGluAspGlnLeuValLysTrpGlnSerSerAla	362
Db	1158	GAGGTGATGAGGCTGGTGTGTGAGGACCAAGCTAGTGGAGTGGCAAAAGCTGTGCT	1217
Qy	363	LeuAspValAsnThrTrpMetIleGluTrpPheProAspValAspSerGluProThr	382
Db	1218	CTAGACGTGAACACTGGATGATGAAATGTTTCCGATGTGAGCTCAGACCCACCAACC	1277
Qy	383	LeuSerTrpGlnSerValSerGlnAlaThrAsnTrpThrIleGlnGluAspLysLeuLys	402
Db	1278	CTTTCCTGGAAATCTGTGTCTCAGGCCACGAACCTGACAGATCCAGCAAGATTAATAA	1337
Qy	403	ProPheTrpCysTyrAsnIleSerValTyrProMetLeuHisAspLysValGlyLysPro	422
Db	1338	CTTTCTGGTGTCTAATACATCTGTGTATCAATGTTGATGACAAAGTTGGGAGGCCA	1397
Qy	423	TyrlleGlnAlaTyrAlaLysGluGlyValProSerGluGlyProGluThrLysVal	442
Db	1398	TATTCATCCAGGCTTATGCAAGAAAGGCGTTCATCAGAGGCTCTGAAACCAAGGTG	1457
Qy	443	GluAsnIleGlyValLysThrValThrIleThrTrpLysGluIleProLysSerGluArg	462
Db	1458	GAGAACATTTGGCGTGAAGACGCTACACATCACTAGAAAGAGATTTCCAGAGTGAAGA	1517
Qy	463	LysGlyIleIleCysAsnTyrThrIlePheTyrGlnAlaGluGlyLysGlyPheSer	482
Db	1518	AAGGTATCATCTGCAACTACACATCTTTTACCAACGTGAGTGAAGAAAGATTTCTCC	1577
Qy	483	LysThrValAsnSerSerIleLeuGlnTyrGlyLeuGlnSerLeuLysArgLysThrSer	502
Db	1578	AAGACAGTCAATTCACACATCTTGCACTAGCGGCTGGAGTCCCTGAAACCAAAAGACCTCT	1637
Qy	503	TyrIleValGluValMetAlaAsnThrSerAlaGlyLysThrAsnGlyThrSerIleAsn	522
Db	1638	TACATGTTCAGTCAATGCGCAGCAAGTGTGGGGAAACCAACGGGACCAAGCATTAAT	1697
Qy	523	PheLysThrLeuSerPheSerValPheGluIleIleLeuIleThrSerLeuIleGlyLys	542
Db	1698	TTCAAGACATTTGTATTCAGATGCTTTGAGATTAATCTCTTAATCTTCTGATTTGGGA	1757
Qy	543	GlyLeuLeuIleLeuIleIleLeuThrValAlaTyrGlyLeuLysLysProAsnLysLeu	562
Db	1758	GGCCTTCTTATTCATTATCTGACAGTGGCATATGTCTCAAAAAAACCAAAATTTG	1817
Qy	563	ThrHisLeuCysTrpProThrValProAsnProAlaGluSerSerIleAlaThrTrpHis	582
Db	1818	ACTCATGTGTGGCCACCGTTCCCAACCTGCTGAAGATGATTAAGCACATGGCAT	1877
Qy	583	GlyAspAspPheLysAspLysLeuAsnLeuLysGlyLysAspAspSerValAsnThrGlu	602
Db	1878	GAGATGATTTTCAAGATTAAGCTTAACCTGAAGAAGTCTGATCTGTGAACACAGAA	1937
Qy	603	AspArgIleLeuLysProCysSerThrProSerAspLysLeuValIleAspLysLeuVal	622
Db	1938	GACAGATCTTAAACCATATGTCACCCCAAGTGAACAAAGTTGGATTTGCAAGTTGGTG	1997
Qy	623	ValAsnPheGlyAsnValLeuGlnGluIlePheThrAspGluAlaArgThrGlnGlu	642

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Db      1998  GTGAACCTTGAGGATGTTCTGCAAGAAATTTTCACAGATGAACGAGGAGGTCAAGAA- 2056
Qy      643  LysGlnPheArgArgGlyLysGluTTP 651
Db      2057  AACCAATTGAGGAGGGGAAAAAGAAATG 2083

RESULT 11
AAD38772
ID      AAD38772 standard; cDNA; 2480 BP.
AC      AAD38772;
XX      23-SEP-2002 (first entry)
DE      Human haematopoietin receptor 1 (HPR1) cDNA.
XX      Human, haematopoietin receptor; receptor; HPR1; HPR2; cell proliferation;
XX      pancytopenia; leukopenia; anaemia; thrombocytopenia; osteoporosis;
XX      neurodegenerative disorder; leukæmia; carcinoma; haematologic disorder;
XX      cancer; myelodysplastic syndrome; idiopathic thrombocytopenic purpura;
XX      ITP; sickle cell vasocclusive crisis; myelofibrosis; myeloid metaplasia;
XX      osteoclast disorder; peridontitis; acute polynuropathy; Bell's palsy;
XX      anorexia nervosa; chronic fatigue syndrome; Creutzfeld-Jacob disease;
XX      demyelinating neuropathy; Guillain-Barre syndrome; Gulf war syndrome;
XX      vertebral disc disease; myasthenia gravis; chronic neuronal degeneration;
XX      stroke; fatigue; tumour; sarcoma; osteoporosis; obesity; infertility;
XX      ischemic disease; gene; ss.
XX      Homo sapiens.
XX      Homo
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XX      FT      /note= "This region is specifically claimed as SEQ ID NO:
XX      FT      5 in claim 6 of the specification"
XX      FT      191..227
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XX      FT      /*tag= b
XX      FT      228..2366
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XX      FT      /*tag= d
XX      FT      variation
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XX      FT      /*tag= e
XX      FT      variation
XX      FT      replace(691, G)
XX      FT      /*tag= f
XX      FT      variation
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XX      FT      variation
XX      FT      replace(1216, G)
XX      FT      /*tag= h
XX      FT      variation
XX      FT      replace(1660, G)
XX      FT      /*tag= i
XX      FT      variation
XX      FT      replace(1680, G)
XX      FT      /*tag= j
XX      FT      variation
XX      FT      replace(2166, G)
XX      FT      /*tag= k
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XX      11-APR-2002.
XX      05-OCT-2001, 2001MO-US031634.
XX      06-OCT-2000, 2000US-0238706P.
XX      13-OCT-2000, 2000US-0240476P.
XX      20-FEB-2001, 2001US-0270282P.
XX      (IMMV ) IMMUNEX CORP.
XX      Cosman DJ, Mosley BA, Bird TA, Dubose RF, Wiley SR;

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XX      WPI; 2002-330172/36.
DR      P-PDB; AAE24024.
XX      Human and murine hematopoietin receptor polypeptides HPR1 and HPR2,
XX      useful for treating cell proliferation, metabolic, and reproductive
XX      hormone related conditions.
XX      Claim 6; Page 83-84; 136pp; English.
XX      The present invention relates to human and murine haematopoietin receptor
XX      polypeptides HPR1 and HPR2. Sequences of the invention are useful for
XX      treating cell proliferation conditions e.g., pancytopenia, leukopenia,
XX      anaemia, thrombocytopenia, neurodegenerative disorders and osteoporosis
XX      resulting from a lack of bone-forming cells. They are also useful for
XX      treating cell proliferation conditions such as leukaemia and tumour
XX      metastasis, osteoporosis resulting from an excess of bone-resorbing
XX      cells. HPR sequences are also useful for treating medical conditions and
XX      diseases such as cell proliferation, metabolic and reproductive hormone
XX      related conditions. They are useful for treating various haematologic and
XX      oncologic disorders e.g., Epstein-Barr virus-positive nasopharyngeal
XX      carcinoma, myelogenous leukemia, colon, stomach, prostate, renal cell,
XX      cervical and ovarian cancers, lung cancer (SCLC and NSCLC), including
XX      cancer-associated cachexia, fatigue, solid tumours (e.g., osteosarcoma,
XX      sarcoma), carcinoma (e.g., adenocarcinoma (for example, breast cancer),
XX      squamous cell carcinoma), haematologic disorders, anaemias (e.g., anaemia
XX      of chronic disease, aplastic anaemia, Fanconi's aplastic anaemia), myelo-
XX      dysplastic syndromes (including refractory anaemia, refractory anaemia
XX      with ringed sideroblasts or with excess blasts), idiopathic thrombocy-
XX      topenic purpura (ITP), sickle cell vasocclusive crisis, myelofibrosis/
XX      myeloid metaplasia, osteoclast disorders that lead to bone loss such as
XX      osteoporosis including post-menopausal osteoporosis, peridontitis
XX      resulting in tooth loosening or loss, prosthesis loosening after joint
XX      replacement, neurodegenerative conditions (e.g., acute polynuropathy,
XX      Bell's palsy, anorexia nervosa, chronic fatigue syndrome, transmissible
XX      dementia including Creutzfeld-Jacob disease, demyelinating neuropathy,
XX      Guillain-Barre syndrome, vertebral disc disease, Gulf war syndrome,
XX      myasthenia gravis, chronic neuronal degeneration, stroke including
XX      cerebral ischaemic diseases, HPR1 and HPR2 polypeptides are also useful
XX      for treating various other disorders such as osteoporosis, obesity,
XX      deficient mammary development and infertility. The present sequence is
XX      human HPR1 cDNA
XX      Sequence 2480 BP; 722 A; 558 C; 600 G; 600 T; 0 U; 0 Other;
XX      SQ
XX      Alignment Scores:
XX      Pred. No.:      1.77e-314      Length:      2480
XX      Score:      3435.00      Matches:      647
XX      Percent Similarity:      99.69%      Conservative:      2
XX      Best Local Similarity:      99.39%      Mismatches:      2
XX      Query Match:      98.59%      Indels:      1
XX      DB:      6      Gaps:      0
XX      US-10-006-265-2 (1-652) x AAD38772 (1-2480)
Qy      1  MetLysLeuSerProGlnProSerCysValAenLeuGlyMetMetTrpThrTrpAlaLeu 20
Db      132  ATGAACCTCTCTCCACGCTTCATGCTGTAACTCGGGATATGACCTGGGACCTG 191
Qy      21  TrpMetLeuProSerLeuCysLysPheSerLeuAlaLeuProAlaLeuProGluAan 40
Db      192  TGGATGCTCCCTTCACTCGCAAAATTCAGCTGGAGCTGCTCCAGCTTAAGCCTGAGAAC 251
Qy      41  IleSerCysValTyrTyrTyrArgLysAenLeuThrCysThrTrpSerProGlyLysGlu 60
Db      252  ATTTCTGTGTCTACTACTATAGAAAAATTTAACTGCACTTGAGCTCAGAGAAAGGAA 311
Qy      61  ThrSerTyrThrGlnTyrThrValLysArgTrpTyrAlaPheGlyGluIuYshIsaPaa 80
Db      312  ACCAGTTAACCAGACAGTAAAGAACTTACGCTTTGGAGAAAAAATCATGTAAAT 371
Qy      81  CysThrThrAanSerSerThrSerGluAenArgAlaSerCysSerPheLeuProArg 100

```

Db 372 TGACAAACCAATAGTCTTACAAAGTGAATACTGCTCGTCTTTTCTTCTTCCACAGA 431
 Qy 101 ILeThrIleProAspAsnTyrThrIleGluValIleGluValAsnGlyAspGlyValIle 120
 Db 432 ATAAGAAATCCAGATAATTAATACATGAGGTGAGAGCTGAATAAGATGGTGTAAATT 491
 Qy 121 LysSerHisMetThrTyrTrpArgLeuGluAsnIleAlaIleThrGluProProlysisIle 140
 Db 492 AAATTCATATGACACTACTGAGAGATTAGAGAACATACGGAACACTGAACCACTTAAGATT 551
 Qy 141 PheArgValIleProValIleuGlyIleIleYsArgMetIleGlnIleGluTrpIleLysPro 160
 Db 552 TTCCGTGTGAACACCGATTTTGGGCATCAACCGAATGATTCAAATGATGATAAGCCT 611
 Qy 161 GluLeuAlaProValSerSerAspLeuLysTyrThrIleuArgPheArgThrValAsnSer 180
 Db 612 GAGTGGGGCGCTGTTTCATCTGATTTAAATACACACTTCGATTCAGACACTCAACGCT 671
 Qy 181 ThrSerTrpMetGluValAsnPheAlaIleYsAsnArgLysAspLysAsnGlnThrTyrAsn 200
 Db 672 ACCAGCTGATGGAAGTCACTTCCCTAAGAACCTTAAGATTAACCAACGTAAC 731
 Qy 201 LeuThrGlyLeuGlnProPheThrGluTyrValIleAlaLeuArgCysAlaValIleGlu 220
 Db 732 CTCACGGGGCTGCACCTTTTACAGATATGTCATAGCTCTGCGATGTGCGGTCAAGAG 791
 Qy 221 SerLysPheTrpSerAspTrpSerGlnIleLysMetGlyMetThrGluGluGluAlaPro 240
 Db 792 TCMAAGTCTGGAGACTGAGCCAGCAAAAAAGGAAATGACAGAGAAAGAACCTCCA 851
 Qy 241 CysGlyLeuGluLeuTrpArgValIleuLysProAlaGluAlaAspGlyArgArgProVal 260
 Db 852 TGTGGCTGGAACTGTGAGAGTCTTGAAACCAAGCTGAGCGGATGGAAGAGCCAGTG 911
 Qy 261 ArgLeuLeuTrpLysValArgGlyValaProValIleuGluLysThrLeuGlyTyrAsn 280
 Db 912 CGGTGTATGGAAGAAAGCAAGAGAGCCCAAGCTCTAGAGAAAACTTGGCTACAAAC 971
 Qy 281 IleTrpTyrTyrProGluSerAsnThrAsnLeuThrGluThrMetAsnThrThrAsnGln 300
 Db 972 ATATGGTACTATCCAGAAAGCACTAACCTCAAGAAACATGAAACACTTAACAG 1031
 Qy 301 GlnLeuGluLeuHisIleuGlyGlyLysSerPheTrpValSerMetIleSerTyrAsnSer 320
 Db 1032 CAGCTTGAACCTGCATCTGGAGGCGAGAGCTTTTGGGTGTATGATTTCTTATTAATCT 1091
 Qy 321 LeuGlyLysSerProValAlaThrLeuArgIleProAlaIleGlnGluLysSerPheGln 340
 Db 1092 CTTGGGAAGTCTCCAGTGGCCACCTGAGGATTCAGCTTATTCAGAAAAATCATTTGAG 1151
 Qy 341 CysIleGluValMetGlnAlaCysValAlaGluAspGlnLeuValIleYsTrpGlnSer 360
 Db 1152 TGCATTTGAGTCAAGCAGGCTGCTGCTGAGGCCAGCTAGTGTAAAGTGGGAAAGC 1211
 Qy 361 SerAlaLeuAspValAsnThrTrpMetIleGluTrpPheProAspValAspSerGluPro 380
 Db 1212 CCTGCTTACAGACGTGAACATTTGATGATGATGATTTCCGAGTGTGACTCAAGGCC 1271
 Qy 381 ThrThrLeuSerTrpGluSerValSerGlnAlaThrAsnTrpThrIleGlnIleAspLys 400
 Db 1272 ACCAACCTTCTCTGGGAATCTGTGCTCAGGCCAGCAAGCTGAGCATCAGCAAGATAA 1331
 Qy 401 LeuLysProPheTrpCysTyrAsnIleSerValIleProMetLeuHisAspLysValGly 420
 Db 1332 TTAAAACTTTCTGTGTATACATCTCTGTATTCAAATGTTGACAGAACAAAGTTGCG 1391
 Qy 421 GluProTyrSerIleGlnAlaTyrAlaIleYsGluGluValProSerGluGlyProGluThr 440
 Db 1392 GAGCATATTTCCATCCAGCCTTATGCCCAAGAGGCGTTCCATCCAGAGGTCCTGAGACC 1451
 Qy 441 LysValGluAsnIleGlyValIleThrValThrIleThrTrpLysGluIleProLysSer 460
 Db 1452 AAGGTGGAACATTTGGCGTGAAGACGCTCAAGATCATGGAAGAAAGATTTCCCAAGAGT 1511

Qy 461 GluArgLysGlyIleIleCysAsnTyrThrIlePheTyrGlnAlaGluGlyLysGly 480
 Db 1512 GAGAGAAAGGATATCATCTGCACTACCACTTTTCCAAAGCTGAAGGTGGAAGAGA 1571
 Qy 481 PheSerLysThrValAsnSerSerIleuGlnTyrGlyLeuGluSerLeuLysArgLys 500
 Db 1572 TTCTCCAAAGACAGTCAATTCAGACATCTTGCAAGTACGCGCTCGAGTCCCTGAAGAGAA 1631
 Qy 501 ThrSerTyrIleValGlnValMetAlaAsnThrSerAlaGlyIleYsThrAsnGlyThrSer 520
 Db 1632 ACCCTTCAATGTTGACGTGCATGCGCCAGCCAGCTGCGGGGAACGAGCGGACCAAGC 1691
 Qy 521 IleAsnPheLysThrLeuSerPheSerValPheGluIleIleuLysThrSerLeuIle 540
 Db 1692 AATAATTCAGACATTTGTCATTCAGTGTCTTGAAGATATCTCATTAATCTCTGATT 1751
 Qy 541 GlyGlyGlyLeuLeuIleIleuThrValAlaTyrGlyLeuLysLysProAsn 560
 Db 1752 GGTGAGGCGCTTCTTATTTCTATATCTGACAGTGGCATATGGTCTCAAAAAACCCAAC 1811
 Qy 561 LysLeuThrHisLeuCysTrpProThrValProAsnProAlaGluSerSerIleAlaThr 580
 Db 1812 AAATTCATCATCTGTGTGGCCCAAGCTCCCAACCTGCTGAAGATGATAGCCACA 1871
 Qy 581 TrpHisGlyAspAspPheLysAspLysLeuAsnLeuLysGluSerAspAspSerValAsn 600
 Db 1872 TGGCATGAGATGATTTCAAGATTAAGCTTAACCTGAAGAGTGTGAGACTCTGTGAAC 1931
 Qy 601 ThrGluAspArgIleLeuLysProCysSerThrProSerAspLysLeuValIleAspLys 620
 Db 1932 ACAAGAGACAGATCTTAAACCATGTTCCACCCCAAGTCAAGATGTGATGACAG 1991
 Qy 621 LeuValValAsnPheGlyAsnValIleuGlnGluIlePheThrAspGluAlaArgThrGly 640
 Db 1992 TTGGTGTGGAATCTTGGGAATGTTCTGCAAGAAATTTTCAAGATGAAGCCAGAACGGGT 2051
 Qy 641 GlnGluLysGlnPheArgArgGlyLysGluTrp 651
 Db 2052 CAGGA-AAACAAATTTAGAGGGGAAAGAAATGG 2083
 RESULT 12
 ID ACF36434 standard; cDNA; 2481 BP.
 XX ACF36434;
 AC ACF36434;
 DT 18-DEC-2003 (first entry)
 XX
 DE Human type-1 cytokine receptor, GLM-R encoding cDNA.
 XX GLM-R; type-1 cytokine receptor; gene therapy; gene mapping; human;
 KW transgenic; gene; 88.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT CDS 63..2261
 FT /tag= a
 FT /product= "GLM-R"
 FT /note= "type-1 cytokine receptor"
 FT sig_peptide 63..119
 FT /tag= b
 FT mat_peptide 120..2258
 FT /tag= c
 XX
 PN MO2003072740-A2.
 XX
 PD 04-SEP-2003.
 XX
 XX 24-FEB-2003; 2003WO-US005616.
 PF
 XX 25-FEB-2002; 2002US-0359806P.

XX	(GETH) GENENTECH INC.
PA	
XX	
XX	De Sauvage FJ, Ghilardi NP, Goddard A, Godowski PJ, Grimaldi CJ,
PI	Gurney AL, Wood WI;
XX	
XX	WPI; 2003-712721/67.
DR	P-PSDB; ABR82790.
DR	
XX	
PT	New isolated nucleic acid molecule encoding a GLM-R polypeptide, useful
PT	for treating disorders characterized by the over or under abundance of
PT	monocytes or macrophages.
XX	
PS	Claim 3, Fig 1; 156pp; English.
XX	
CC	The invention relates to an isolated nucleic acid molecule encoding a
CC	type-1 cytokine receptor GLM-R polypeptide. The nucleic acid molecules,
CC	polypeptides, antibodies, agonists or antagonist, and compositions are,
CC	useful for treating disorders characterized by the over or under
CC	abundance of monocytes or macrophages. The nucleic acid molecules are
CC	useful as hybridization probes, in chromosome and in gene mapping, and in
CC	generating antisense RNA or DNA. The present sequence represents a cDNA
CC	encoding a human GLM-R polypeptide
XX	
XX	
XX	Sequence 2461 BP; 729 A; 553 C; 603 G; 596 T; 0 U; 0 Other;

Db	570	TGGATGGAAAGCACTTCGCTTAAGAACCGTAAAGATTAAAAACCAAGCTAACCTCAGC	629
QY	203	GIyleuGInProPheThrGIuTYrValIIleAlaLeuArgCYaIaValyleGluSerIys	222
Db	630	GGGCTGCAGCCTTTTACAGAAATATGTCATAGCTCTGCGATGTGCGGTCAAGAGTCAAAAG	689
QY	223	PheTrpSerAspTrpSerGInGluIlyMeGCIyMerThrGIuGIuGIuAlaProCYGIly	242
Db	690	TTCTGGAAATGACTGGAGCCAAAGAAAAATGGAAATGACTGGAGAAAGAGCTCCACGTGTGC	749
QY	243	LeuGIuLeuTPaRgValIleuIysProAlaGIuIIaAspGIaYGAAGProValArgLeu	262
Db	750	CTGGAACCTGTGGAAGGTCTTGAACCCACGCTGAGCGGATGGAAGAAGCCAGTCCGCTTG	809
QY	263	LeuTrpIlySlyAlaArgGIyAlaProValIleuGIuIysThrLeuGIlyTYrAsnIIeTrp	282
Db	810	TTATGGAAAGAGGCAAGAGGAGCCCGAGTCTTAAGAAAAACATTGGCTACAACTATATGG	869
QY	283	TYrTYrProGIuSerAsnThrAsnLeuThrGIuThrMetAsnThrThraSerGInLeu	302
Db	870	TACTATCCAGAAACCACTAACCTCACAAGAAACAATGAACTACTTAACACACAGATT	929
QY	303	GIuIeunHsIleuGIyGIyGluSerPheTrpValSerMetIleSerTYrAsnSerIleuGIly	322
Db	930	GAACTGCATCTGGAGGGCGAGAGCTTTGGGTGTCTATGATTCTTATATTCCTCTTGGG	989
QY	323	LYsSerProValAlaThrLeuArgIleProAlaIleGInGIuIysSerPheGInCYaIle	342
Db	990	AAAGTCTCAGTGGCCACCTCAGGATTCACACTTTCAGAAAAATCATTTCACTGCATT	1049
QY	343	GIuValMetGInAlaCYaValAlaGIuAspGIuLeuValIlyTrpGInSerSerAla	362
Db	1050	GAGGTCAAGCAGGCGCTGCGTTCGAGAGCACGACTAGTGGTGAAGTGGCAAGGCTGCTGT	1109
QY	363	LeuAspValaAsnTrpTrpMetIleGIuTrpPheProAspValaAspSerGIuProThrThr	382
Db	1110	CTAGACGGAACACTGGATATGTAATGGTTTCGGATGTGACTCAGACCCACACACC	1169
QY	383	LeuSerTrpGIuSerValSerGInAlaThrAsnTrpThrIleGInGIuAspIysLeuIys	402
Db	1170	CTTTCCTGGGAATCTGTGTCTCAGGCCACGAACCGAAGATCCAGCAAGATTAATTTAAA	1229
QY	403	ProPheTrpCYrTYrAsnIIeSerValTYrProMetLeuHsAspIysValGIyGIuPro	422
Db	1230	CCTTCTGTGTCCTTAACATCTCTGTGATCCAATGTTGCATGCAAAAGTTGGCGAGCCA	1289
QY	423	TYrSerIleGInAlaTYrAlaIyGIuGIyAlaProSerGIuIyProGIuThrIlyVal	442
Db	1290	TATTCATCCAGGCTTATGCCAAAGAGGCGCTTCATCAGAAAGGCTCGAACAAGAGTG	1349
QY	443	GIuAsnIIleGIyValIlyThrValThrIIeThrTrpIysGIuIleProIysSerGIuArg	462
Db	1350	GGAACATTTGGCGTGGAGACGCTCACGATCCACATGAGAAAGAGATTTCCAAAGTGAAGA	1409
QY	463	LYsGIyIleIleCYaAsnTYrThrIlePheTYrGInAlaGIuGIyGIyLYsGIyPheSer	482
Db	1410	AAGGGAGATCATCTGCAACTACACCATCTTTTACCAAGCTGAAGGTGAAAAAGATTCTCC	1469
QY	483	LYsThrValaAsnSerSerIleLeuGInTYrGIyLeuGIuSerLeuIyAsArgIysThrSer	502
Db	1470	AAGACAGCAATTCACAGCATCTTCACAGACGCGCTGAGTCCCTGMAACGMAAACCTCT	1529
QY	503	TYrIleValIyValMetAlaAsnThrSerAlaGIyGIyThraSerGIyThrSerIIeAsn	522
Db	1530	TACATTTGTCAGGTATGCGACACCAAGCTCTGGGGAAACCAACGGGACCAAGATTAAT	1589
QY	523	PheIysThrLeuSerPheSerValPheGIuIleIleLeuIIeThrSerLeuIleGIyGIy	542
Db	1590	TTCAAGACATTTGTATTCAAGTGTCTTTGAGATTATCCATTAACCTTCTGTATTTGGTGA	1649
QY	543	GIyLeuLeuIIeLeuIIeIleLeuThrValaIaTYrGIyLeuIyIlyAsPProAsnIlyLeu	562


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QY 303 GtUleuHleuGlygluSerPheTrpValSerMetIleSerTyraSerLeuGly 322
DB 970 GAATCATCTGGAGCGGAGAGCTTTGGGTCTATGATTTCTTATATTTCTTTGGG 1029
QY 323 LysSerProValAlaThrLeuAlaGllleProAlaIleGlnGluLysSerPheGlnCysIle 342
DB 1030 AAGTCTCCAGTGGCCACCCCTGAGAGATTCCAGTATTCMAAATAATCATTTTCAGTGCATT 1089
QY 343 GluValMetGlnAlaCysValAlaGluAspGlnLeuValValLysTrpGlnSerAla 362
DB 1090 GAGGATATGACAGCCCTGCTGCTGAGACCACTAGTGTGAAGTGGAAGCTCTGCT 1149
QY 363 LeuAspValAsnThrTrpMetIleGluTrpPheProAspValAspSerGluProThr 382
DB 1150 CTGAGCGTGAACACTTGATGATTTGATGATGTTCCGGATGTGACAGCCAGCCACCACC 1209
QY 383 LeuSerTrpGluSerValSerGlnAlaThrAsnTrpThrIleGlnGlnAspLysLeuLys 402
DB 1210 CTTTCTGGGAATCTGTCTCAGGCCACGAATGACATCCAGCAAGATTAATTAATAA 1269
QY 403 ProPheTrpCysTrpAsnIleSerValTyraProMetLeuHisAspLysValIleGluPro 422
DB 1270 CTTTCTGGTGTATTAACATCTGTGTATCAATGTGATGACAAAGTTGGCGAGCCA 1329
QY 423 TyraSerIleGlnAlaTyraLysGluGlyValProSerGluGlyProGluThrLysVal 442
DB 1330 TATTCATCCAGGCTTATGCCAAAGAGCGTTCCATCAAGAGTCTTGAGACCAAGGTG 1389
QY 443 GluAsnIleGlyValLysThrValThrIleThrTrpLysGluIleProLysSerGluArg 462
DB 1390 GAGAAATGTCGCGTGAAGAGCGTCACGATCACATGAAAGATTCCTCAAGATGTGAGA 1449
QY 463 LysGlyIleIleCysAsnTyraThrIlePheTyraGlnAlaGluGlyLysGlyPheSer 482
DB 1450 AAGGATATCATCTTCGAACATACACATCTTTACCAAGCTGAAGTGGAAGATTTCTCC 1509
QY 483 LysThrValAsnSerSerIleLeuGlnTyraGlyLeuGluSerLeuLysArgLysThrSer 502
DB 1510 AAGACAGTCAATTCAGCATCTTGAGTACGCGCTGGAAGTCCCTGAAGCAAGAACCTCTC 1569
QY 503 TyraIleValGlnValMetAlaAsnThrSerAlaGlyGlyThrMetGlyThrSerIleAsn 522
DB 1570 TACATGTCACAGTCATGCGCACACACAGTCGGGGGAACCAACGGGACACACATAAAT 1629
QY 523 PheLysThrLeuSerPheSerValPheGlnIleIleLeuIleThrSerLeuIleGlyGly 542
DB 1630 TTCAAGACATTCATTCAGTGTCTTGATTAATCTCTCAATACCTCTCTGATTTGGTGA 1689
QY 543 GlyLeuLeuIleLeuIleIleLeuThrValAlaTyraGlyLeuLysLysProAsnLysLeu 562
DB 1690 GGCCTTCTTATCTCATTTATCTGACAGTGCATATGTGTCTCAAAAACCAACCAATTTG 1749
QY 563 ThrHisLeuCysTrpProThrValProAsnProAlaGluSerSerIleAlaThrTrpHis 582
DB 1750 ACCCATCTGTGTTGGCCACCGTTCCCAACCTGCGAAAGTGTATGACACATGGCAAT 1809
QY 583 GlyAspAspPheLysAspLysLeuAsnLeuLysGluSerAspAspSerValAsnThrGlu 602
DB 1810 GGGAGATGATTTCAAGGATTAAGCTTAACCTGAAGAGTCTGATATCTCTGGAACAAGAA 1869
QY 603 AspArgIleLeuLysProCysSerThrProSerAspLysLeuValIleAspLysLeuVal 622
DB 1870 GACAGGATCTTAACCATGTTCCACCCAGTGAACAAGTTGGATGACAAAGTTGGTG 1929
QY 623 ValAsnPheGlyAsnValLeuGlnGluIlePheThrAspGluAlaArgThrGlyGlnGlu 642
DB 1930 GTGAACCTTGGGGAATGTCTGCAAGAAATTTTTCACAGATGAACCGAGAACGGGTCAAGA- 1988
QY 643 LysGlnPheArgArgGlyLysGluTrp 651
DB 1989 AAAACAATTTAGAGGGGAAAAAGAAATGG 2015

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AB083364
ID AB083364 standard; cDNA; 5271 BP.
XX
AC AB083364;
XX
DT 20-JAN-2003 (first entry)
XX
DE Human NR10.4 splicing variant encoding cDNA SEQ ID NO:3.
XX
KW NR10; splicing variant; haematopoietin receptor; immunomodulator;
KW haemostatic; haematopoietic factor; immunological disease;
KW haematopoietic disease; haematopoietic cell regulation; gene; ss.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 7..2301
FT /tag=a
FT /product="NR10.4"
XX
XX
PN MO200277230-A1.
XX
PD 03-OCT-2002.
XX
XX
PF 22-MAR-2002; 2002MO-JP002769.
XX
PR 26-MAR-2001; 2001JP-00087298.
XX
XX
PA (CHUS ) CHUGAI SEIYAKU KK.
XX
PI Maeda M, Yaguchi N, Hasegawa M;
XX
DR WPI; 2003-018925/01.
XX
DR P-PSDB; ABP54364.
XX
XX
PT NR10 splicing variants of haematopoietin receptor proteins and encoded
PT genes, applicable in searching haematopoietic factors and developing
PT remedies for immunological and haematopoietic diseases.
XX
XX
PS Claim 1; Fig 4-5; 250bp; Japanese.
XX
XX
CC The present invention describes haematopoietic receptor NR10 splicing
CC variants (1). (1) have immunomodulator and haemostatic activities. The
CC proteins and encoded genes are applicable in searching for novel
CC haematopoietic factors, and developing remedies for immunological and
CC haematopoietic diseases. The haematopoietin receptor genes participate in
CC in vivo immunomodulation and haematopoietic cell regulation, and in the
CC search for haematopoietic factors capable of functionally binding to the
CC receptors. The present sequence encodes the human NR10.4 protein from the
CC present invention
XX
XX
SQ Sequence 5271 BP; 1312 A; 1302 C; 1318 G; 1339 T; 0 U; 0 Other;

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Alignment Scores:

Pred. No.:	5.28e-314	Length:	5271
Score:	3435.00	Matches:	647
Percent Similarity:	99.85%	Conservative:	1
Best Local Similarity:	99.69%	Mismatches:	1
Query Match:	98.59%	Indels:	1
DB:	8	Gaps:	0

US-10-006-265-2 (1-652) x AB083364 (1-5271)

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QY 3 LeuSerProGlnProSerCysValAsnLeuGlyMetTrpThrTrpAlaLeuTrpMet 22
DB 70 CTTCTCTCCACGCTTCAATGTGTAACTGGGAGATGATGGAACCTGGGCACCTGTGATG 129
QY 23 LeuProSerLeuCysLysPheSerLeuAlaAlaLeuProAlaLysProGluAsnIleSer 42
DB 130 CTCCTCTCATCTTGCAAAATTCACGCTGCGACCTTCCAGCTTAAGCTTAAGAAATTTC 189
QY 43 CysValTyraTyraTyraArgLysAsnLeuThrCysThrTrpSerProGlyLysGluThrSer 62

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XX 22-MAR-2002; 2002WO-JP002769.
 PF
 XX 26-MAR-2001; 2001JP-00087298.
 PR
 XX (CHUS) CHUGAI SEIYAKU KK.
 PA
 XX Maeda M, Yaguchi N, Hasegawa M;
 PI WPI; 2003-018925/01.
 XX P-PSDB; ABP54366.
 DR
 XX NR10 splicing variants of hematopoietin receptor proteins and encoded
 PT genes, applicable in searching hematopoietic factors and developing
 PT remedies for immunological and hematopoietic diseases.
 XX
 PS Claim 1; Fig 10-12; 250pp; Japanese.
 CC The present invention describes hematopoietic receptor NR10 splicing
 CC variants (I). (I) have immunomodulator and haemostatic activities. The
 CC proteins and encoded genes are applicable in searching for novel
 CC haematopoietic factors, and developing remedies for immunological and
 CC haematopoietic diseases. The haematopoietin receptor genes participate in
 CC in vivo immunomodulation and haematopoietic cell regulation, and in the
 CC search for haematopoietic factors capable of functionally binding to the
 CC receptors. The present sequence encodes the human NR10.5 protein from the
 CC present invention
 XX
 SQ Sequence 3072 BP; 849 A; 721 C; 755 G; 747 T; 0 U; 0 Other;
 Alignment Scores:
 Pred. No.: 1,67e-311 Length: 3072
 Score: 3405.00 Matches: 647
 Percent Similarity: 94.05% Conservative: 1
 Best Local Similarity: 93.90% Mismatches: 1
 Query Match: 97.73% Indels: 41
 DB: Gaps: 1
 US-10-006-265-2 (1-652) x ABQ83366 (1-3072)

DB 550 GGCCTGTTTCATCTGATTTAAATACACACTTCGATTCAGACAGTCAACAGTACAGC 609
 QY 183 TTPMGTGLUVALASNPHEALAYSASNARGLYSAPPLYASNGITRTHRYTSENLEUTR 202
 DB 610 TGGATGGAAGTCAACTTCGCTTAAGAACCGTAAGGATTAACCAACGTTACACTCAGC 669
 QY 203 GLYLEUGLNPProPheThrGluTyrValIleAlaLeuArgCysAlaValIlysgIuseTlys 222
 DB 670 GGGCTGACGCTTTTACAAATATGTGCATAGCTCTGCGATGTGCGGTCAAGAGTCAAAAG 729
 QY 223 PHEITPSEASPTTPSerserGlnGluTyrMetGlyMetThrGlnGluGluAlaProCysGly 242
 DB 730 TTCTGGAGTACGTGGAGCCCAAGAAAATGGGAATGACTGAGGAAGAACTCATGTGCG 789
 QY 243 LEUGLLEUTPRArgValLeuIlySPProAlaGluValAspGlyARGArgProValArgLeu 262
 DB 790 CTGGAACGTGTGAAGATCTTGAAACCAAGCTGAGGCGGATGGAAAGAGGCCAGTGGCTTG 849
 QY 263 LEUTPLYSlyAlaArgGlyAlaProValLeuGluLysThrLeuGlyTyrAsnIleTrp 282
 DB 850 TTAATGAAAGAGCAAGAGAGAGCCCAAGTCTTAGAGAAAACACTTGGCTACAAATATGG 909
 QY 283 TYTYRProGluSerAsnThrAsnLeuThrGluThrMetAsnThrThrAsnGlnGlnLeu 302
 DB 910 TACTATCCAGAAAGCAACACTAACTCAGAAAACATGAACACTACTAACCGACGAGCTT 969
 QY 303 GILUEHLIELEUGLYGlyGluSerPheTrpValSerMetIleSerTyrTrpSerserLeuGly 322
 DB 970 GAACGTGCATCTGGAGAGCGAGAGCTTTTGGGTGTATATATTTCTATTAATTTCTTGGG 1029
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 DB 1390 GAGAACATTTGGCGTGAAGCGGTCAAGATCAATGAAAGAAATTTCCAAAGCTGAGAA 1449
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 DB 1450 AAGGATATCATCTGCACATACACATCTTTTACAAAGCTGGAAGTGAAGAAAGATTTCTCC 1509
 QY 483 LYSETHValAsnSerSerIleLeuGlnTyrGlyLeuGluSerLeuLysArgIlySTPThr 502
 DB 1510 AAGACAGTCAATTTCCAGCATCTTGACGTACGCGCTGGAATCTCCGAAAGAAAGACTCTCT 1569
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Job time : 1031.01 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: February 23, 2005, 08:59:57 ; Search time 300.186 Seconds
(without alignments)
3553.966 Million cell updates/sec

Title: US-10-006-265-2

Perfect score: 3484

Sequence: 1 MKLSPQSPSCVLMGMWTAL.....FTDEARTQGEKQFRGKEMD 652

Scoring table:

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Xgapop 10.0, Xgapext 0.5
Ygapop 10.0, Ygapext 0.5
Fgapop 6.0, Fgapext 7.0
Delop 6.0, Delext 7.0

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

Issued_Patents_NA:
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6: /cg2_6/ptodata/1/ina/backfile1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	682.5	19.6	2995	4	US-09-700-820C-17
2	679.5	19.5	3085	3	US-08-795-473B-4
3	679.5	19.5	3085	3	US-09-439-856-4
4	679.5	19.5	3085	4	US-09-023-655-1131
5	678.5	19.5	2369	1	US-07-797-556-1
6	678.5	19.5	2369	1	US-08-308-881-1
7	678.5	19.5	2369	2	US-09-058-263-1
8	678.5	19.5	2369	2	US-09-058-099-1
9	678.5	19.5	2369	3	US-09-058-264-1
10	678.5	19.5	2369	4	US-09-455-962-1
11	678.5	19.5	2369	5	PCT-US95-06530-1
12	677.5	19.4	2754	2	US-08-825-558-5

13	677.5	19.4	2754	3	US-09-312-611-5	Sequence 5, Appli
14	636.5	18.3	1977	2	US-08-825-558-3	Sequence 3, Appli
15	636.5	18.3	1977	3	US-09-312-611-3	Sequence 3, Appli
16	616	17.7	3477	4	US-09-313-942-25	Sequence 25, Appli
17	616	17.7	3507	4	US-09-313-942-23	Sequence 23, Appli
18	505.5	14.5	2943	4	US-07-923-976-3	Sequence 3, Appli
19	505.5	14.5	2943	4	US-09-023-655-1086	Sequence 1086, Ap
20	503.5	14.5	3024	1	US-07-923-976-7	Sequence 7, Appli
21	487	14.0	2563	6	5422248-1	Patent No. 5422248
22	487	14.0	2563	6	5422248-1	Patent No. 5422248
23	464.5	13.3	3293	1	US-07-923-976-1	Sequence 1, Appli
24	461	13.2	2855	1	US-07-923-976-5	Sequence 5, Appli
25	401.5	11.5	3182	1	US-07-923-976-5	Sequence 5, Appli
26	401.5	11.5	3182	1	US-07-943-843-1	Sequence 1, Appli
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33	377	10.8	4040	2	US-08-915-455-1	Sequence 1, Appli
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44	244	7.0	2589	1	US-08-653-740-6	Sequence 6, Appli
45	244	7.0	2589	2	US-09-073-594-6	Sequence 6, Appli

ALIGNMENTS

RESULT 1

US-09-700-820C-17
; Sequence 17, Application US/09700820C
; Patent No. 6610485

GENERAL INFORMATION:

APPLICANT: Tsuchiya, Masayuki
APPLICANT: Saito, Makiyoshi
TITLE OF INVENTION: NOVEL METHOD FOR GENE CLONING
FILE REFERENCE: 06501-07001
CURRENT APPLICATION NUMBER: US/09/700, 820C
PRIOR FILING DATE: 1998-05-20
PRIOR APPLICATION NUMBER: JP 10/138652
PRIOR FILING DATE: 1998-05-20
PRIOR APPLICATION NUMBER: JP 10/279876
NUMBER OF SEQ ID NOS: 39
SEQ ID NO 17

LENGTH: 2995

TYPE: DNA

ORGANISM: Mus musculus

FEATURE:

NAME/KEY: CDS

LOCATION: (29) .. (2839)

US-09-700-820C-17

DB:

Alignment Scores:

Pred. No.: 2,846-65
Score: 682.50
Percent Similarity: 47.24%
Best Local Similarity: 28.35%
Query Match: 19.59%
Length: 2995
Matches: 180
Conservative: 120
Mismatch: 282
Indels: 54
Gaps: 17


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COUNTRY: USA
ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: MS-DOS EDITOR
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/795,473B
FILING DATE: 11-FEB-1997
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Davidson, Clifford M.
REGISTRATION NUMBER: 32,728
TELEPHONE: (212)-997-1028
TELEFAX: (212)-997-1037
TELECOMMUNICATION INFORMATION:
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 3085 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: unknown
US-08-795-473B-4

Alignment Scores:
Pred. No.: 6,45e-65 Length: 3085
Score: 679.50 Matches: 175
Percent Similarity: 46.75% Conservative: 113
Best Local Similarity: 28.41% Mismatches: 261
Query Match: 19.50% Indels: 67
Gaps: 16

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QY 71 ThrTyAlaPheGlyGlu-----LysHisAsp-----AsnCysThrThrAsn 84
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QY 105 AspAsnTyThrIleGluValGluIleAsnGlyAspGlyValIleLysSer---His 123
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QY 124 MetThrTyTrpArgLeuGluIleAsnIleAlaTyThrGluProGlyIlePheArgVal 143
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QY 482 SerLysThrValAsnSerSerIleLeuGlnTyRgylLeuGluSerLeuLysArgIleThr 501
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QY 522 AsnPheLysThrLeuSerPheSerValPheGluIleIleLeuIleThrSerLeuIleGly 541
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 / Patent No. 641009
 / GENERAL INFORMATION:
 / APPLICANT: Galun, Elchan
 / APPLICANT: Nahot, Orit
 / APPLICANT: Blum, Herbert E.
 / TITLE OF INVENTION: A Pharmaceutical Composition for Treating
 / TITLE OF INVENTION: Hepatitis B Virus (HBV) Infection
 / NUMBER OF SEQUENCES: 10
 / CORRESPONDENCE ADDRESS:
 / ADDRESSEE: Davidson, Davidson and Kappel, LLC
 / STREET: 1140 Avenue of the Americas
 / CITY: New York
 / STATE: New York
 / COUNTRY: USA
 / ZIP: 10036
 / COMPUTER READABLE FORM:
 / MEDIUM TYPE: 3.5 inch disk
 / COMPUTER: IBM PC compatible
 / OPERATING SYSTEM: PC-DOS/MS-DOS
 / SOFTWARE: MS-DOS EDITOR
 / CURRENT APPLICATION DATA:
 / APPLICATION NUMBER: US/09/439,856
 / FILING DATE:
 / CLASSIFICATION:
 / PRIOR APPLICATION DATA:
 / APPLICATION NUMBER: 08/795,473
 / FILING DATE: 11-FEB-1997
 / ATTORNEY/AGENT INFORMATION:
 / NAME: Davidson, Clifford M.
 / REGISTRATION NUMBER: 32,728
 / TELECOMMUNICATION INFORMATION:
 / TELEPHONE: (212)-997-1028
 / TELEFAX: (212)-997-1037
 / INFORMATION FOR SEQ ID NO: 4:
 / SEQUENCE CHARACTERISTICS:
 / LENGTH: 3085 base pairs
 / TYPE: nucleic acid
 / STRANDEDNESS: single
 / TOPOLOGY: unknown
 / US-09-439-856-4
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 Score: 679.50 Matches: 175
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 Best Local Similarity: 28.41% Mismatches: 261
 Query Match: 19.50% Indels: 67
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 Db 1594 AGGGAATCTGTAAAGAAATATATACTAGTGTGTGTGTATTCAGATGAACACCCCTGT 1653
 Qy 382 ThrLeuSerTrpGluSerValSerGlnAlaThrAsnTrpThrIleGlnGlnAspLysLeu 401
 Db 1654 ATCAAGACTGGCAACAGAAAGATGTGATCCGTGCATCGCACTTATTAAGGGAACCTTA 1713
 Qy 402 LysProPheTrpCysTyrAsnIleSerValTyrPrometLeuHisAspLysValGlyGlu 421

```

Db      1714 GCAGAGCAAAATGCTATTGTAACAGTACTCCAGATATGATGATGACCAAGGAGC 1773
Qy      422 ProTyrSer11eGlnAlaTyrAlaYsgluYvalProSerGluYProGluThrIys 441
Db      1774 CCTGATCATTAAGGACATACCTTAAACAAAGCTCCACCTTCCAAAGAGACCTACTGTGCG 1833
Qy      442 ValGluAen11eGlyValYsThrValThriethrTblyGlu11leProIysSerGlu 461
Db      1834 ACAAAAAAGTAGGAAAAACAGAGCTGCTTAGAGTGAGACCACTTCTTGATGTT 1893
Qy      462 ArgIysGly11e11eCysAenTyrThri11ePheTyrGlnAlaGly11eYsGlyPhe 481
Db      1894 CAGATGATTTATCAGAAATATATCTATATTTATAGAACATCATGTAAGTAAGTAAGT 1953
Qy      482 SerIysThrValAenSerSer11eGluTnTyrGlyLeuGluSerLeuYsArgIysThr 501
Db      1954 GCTGTGAATGTGATTTCTCCACACAGATATACATGCTCTTGTGACTAGTACACA 2013
Qy      502 SerTyr11eValGlnValMetAlaAenThrsEralaGlyIysTyrThraGlyThrsErl 521
Db      2014 TTGTACATGATGACGATGACGATACACAGATGAAGTGAGGAGAGATGTCAGAAATTC 2073
Qy      522 AenPheIysThrLeuSerPheSerValPheGlu11e11eLeu11eThrsErl11eGly 541
Db      2074 ACTTTTACTACCCCAAGATTGCTCAGAGAGAAATTTGAAGCATGCTGCTGCTTTCG 2133
Qy      542 GlyIysLeuLeu11eLeu11e11eLeuThraValAlaTyrGlyLeuYsLeuYsProAenIys 561
Db      2134 TTAGCATTCCTTATGACAACTCTTCTGGAGTGCTGCTCTTAAATGAAGCAACCTTA 2193
Qy      562 LeuThri11eLeuCystrProThraValProAenProAlaGluSerSer11e11eThr 581
Db      2194 ATTAACAAAAACATGCTGCTTAATGTTCCAGATTCCTTCAAGAGCATATGTCAGATGG 2253
Qy      582 -----HisGlyAenPheIysAenPheIysAenPheIysAenPheIysAenPheIys 590
Db      2254 TCACCTCAGACTCCTCCAGAGCAAAATTTAATTCAAAAGATCAATATGATTCAGATGGC 2313
Qy      590 ----- 590
Db      2314 AATTCACTGATGATGATGTTGTGGAATAGAACAAATGACAAAAGCCTTTTCAGAA 2373
Qy      591 AenLeuYsGluSerAenPhe-----AenSerValAenThriGlu 602
Db      2374 GATCTGAATCATGATGACCTGTTCAAAAAAGAAAAAATTAATATCTGAA 2421

RESULT 4
US-09-023-655-1131
; Sequence 1131, Application US/09023655
; Patent No. 6607879
; GENERAL INFORMATION:
; APPLICANT: Cocks, Benjamin G.
; APPLICANT: Susan G. Stuart
; APPLICANT: Jeffrey J. Seilhamer
; TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF BLOOD CELL GENE
; TITLE OF INVENTION: EXPRESSION
; NUMBER OF SEQUENCES: 1508
; CORRESPONDENCE ADDRESS:
; ADDRESS: INCYTE PHARMACEUTICALS, INC.
; STREET: 3174 PORTER DRIVE
; CITY: PALO ALTO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/023,655
; FILING DATE: HEREMITH

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; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Zeller, Karen J.
; REGISTRATION NUMBER: 37,071
; REFERENCE/DOCKET NUMBER: PA-0001 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650) 855-0555
; TELEFAX: (650) 845-4166
; INFORMATION FOR SEQ ID NO: 1131:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3085 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: GENBANK
; CLONE: g186353
; US-09-023-655-1131

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Alignment Scores:
Pred. No.: 6,45e-65 Length: 3085
Score: 679.50 Matches: 175
Percent Similarity: 46.75% Conservative: 113
Best Local Similarity: 28.41% Mismatches: 261
Query Match: 19.50% Indels: 67
DB: 4 Gaps: 16

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US-10-006-265-2 (1-652) x US-09-023-655-1131 (1-3085)

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Qy      35 ProAlaIysProGluAen11eSerCyValTyrTyrTyrAlaYsAenLeuThrCysThr 54
Db      631 CCAAAAAAAGCTAAATAATTTGATGTCATGTGAACGAGGAGAAATAAGATGATGAG 690
Qy      55 TrpSerProGlyYsGluThrSerTyr---ThrGlnTyrThraValys-----Arg 70
Db      691 TGGATGCTGAGAGGAAACACACTTGAGCAAACTTCACTTAATAATCTGAATGGCA 750
Qy      71 ThrTyrAlaPheGlyGlu-----LysHisAenPhe-----AenCystrThraAen 84
Db      751 ACACACAAGTTTGTGATGTCGAAGCAAAAGTGAACACCCCACTCATGATGATGAT 810
Qy      85 SerSerThrsErlAenArgAlaSerCysSerPhePheLeuProArgIleThri11ePro 104
Db      811 TATCTACT-----CTGATTTTTC----- 831
Qy      105 AenAenTyrThri11eGluValGluAlaGluAenGlyVal11eIysSer---His 123
Db      832 ---AACATGAAAGCTGGTGAAGAGAGAGATCCCTTGGGAAGTTTACATCATGATCAT 888
Qy      124 MetThrTyrTPAArgLeuGluAen11eAlaYsThriGluProProYs11ePheArgVal 143
Db      889 ATCAATTTTATCTCTGATATTAAGTC---AAGCCCAATCCGACATATTTATTCAGTC 945
Qy      144 LysProValLeuGlyIysYsArgMet11eGln11eGluTnTyrIleYsProGluLeuAla 163
Db      946 ATCAACTCAGAGAAAGCTGATGATCTTAATAATGACATGACCAACCAAGATTAAG 1005
Qy      164 ProValSerSerAenPheIysTyrThriLeuArgPheThraValAenSerThrsTyr 183
Db      1006 AGTGTATTAATA---CTTAATAATTAACATTCATATAGAGCAAAAGATGCTCAACTGG 1062
Qy      184 MetGluValAenPheAlaYsAenArgIysAenGlyAenGlnTyrTyrAenLeuThriGly 203
Db      1063 AGCCAGATCTCT---CTGAAGACACAGCATCCCGGATCTTATTCATCTGTCAGAGAC 1119
Qy      204 LeuGlnProPheThriGluTyrVal11eAlaLeuArgCysAlaValYsGluSerIys--- 222
Db      1120 CTTAACCTTTTACAGATATGTTGATGATGATGATGATGATGATGATGATGATGATGATGAT 1179

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QY 223 PheTrpSerAspTrpSerGlnGlnIleuValMetThrGlnGlnIleuValProCys--- 241
Db 1180 TACTGGAGTGACGCGATGAAGAAGCAAGGGATCACCTATGAAGATGACCATGTAA 1239
QY 242 GlyLeuGlnLeuTrpArgValIleuLysProAlaGlnIleuAspGlyArgArgProValArg 261
Db 1240 GCACCAAGTTCTTCGATATAAAATAGATCCATCCATACCTACAGGCTACACAGACCTGACAA 1299
QY 262 LeuLeuTrpLysValIleuValIleuValIleuValIleuValIleuValIleuValIleuVal 281
Db 1300 CTGCTGTGGAAGACATGCTCTCTCTTTGAAGCCAAAGAAATCTTGAGTTATGAAAGTG 1359
QY 282 TrpTrpTrpProGlnSerAsnThrAsnLeuThrGlnThrAsnThrThrAsnGlnGln 301
Db 1360 ACTCTCAACAAGATGAATACATCATTTACAAATATACAGTATATGCCACA-----AAA 1413
QY 302 LeuGlnLeuIleuGlnGlyGlnSerPheTrpValSerMetIleSerTrpAsnSerLeu 321
Db 1414 CTGACAGTAAATCTCAAAATGATCGCTATCTAGCAACCTTAACAGTAAAGAAATCTTGTT 1473
QY 322 GlyLysSerProValAlaThrLeuArgIleProAlaIleGlnGlnLysSerPheGlnCys 341
Db 1474 GGCAAATTCAGATCAGCTGTTTAACTATCCCTGCTGACTTTCAGCTTCACTCACTCACT 1533
QY 342 IleGlnValMetGlnIleCysValIleGlnAspGlnLeuValIleLysTrpGlnSerSer 361
Db 1534 GTAAATGATCTTAAGATCTCCCAAGATACATGCTTTGGGATGAGATGATCACTCACTCA 1593
QY 362 AlaLeuAspValAsnThrTrpMetIleGlnTrpPheProAspValAspSerGluProThr 381
Db 1594 AGGGAATCTGTAAAGAAATATATATCTGATGCTGTGTATATCAGTAAAGCACTCTGT 1653
QY 382 ThrLeuSerTrpGlnSerValSerGlnAlaThrAsnTrpThrIleGlnIleAspLysLeu 401
Db 1654 ATACAGACTGGCAACAAGATGGTACCGTGCATGCCACTTATTAAGAGGAATTA 1713
QY 402 LysProPheTrpCysTrpAsnIleSerValTrpProMetLeuIleAspLysValGlyGln 421
Db 1714 GCAGAGCAAAATGCTATTTGATTAACAGTATCTGCTGCTGATGATGATGATGATGATGAT 1773
QY 422 ProTrpSerIleGlnIleValIleValIleValIleProSerGlnGlyProGlnThrLys 441
Db 1774 CCTGAATCCATAAGGATCTCTTAAACAAGCTCCCAAGCAAGCTTCTGTTGCG 1833
QY 442 ValGlnAsnIleGlyValLysThrValThrIleThrTrpGlnIleProLysSerGlu 461
Db 1834 ACAAAAAGATGAGAAAAACAAGCTGCTTGAAGTGGACCAACTCTCTGTTGATTT 1893
QY 462 ArgLysGlyIleIleCysAsnTrpThrIlePheTrpGlnIleGlnGlyLysGlyPhe 481
Db 1894 CAGAAATGATTTATCAGAATTTATCTATTTTATGAAACCATTCATGGAATGAAACT 1953
QY 482 SerLysThrValAsnSerSerIleLeuGlnTrpGlyLeuGlnSerLeuLysValGlyThr 501
Db 1954 GCTGTGATGTGATCTCTCCACACAGATATACATTCCTCTTGTGACTGATGACACA 2013
QY 502 SerTrpIleValIleGlnIleAlaAsnThrSerAlaGlyGlyThrAsnGlnTrpSerIle 521
Db 2014 TTGTACATGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2073
QY 522 AsnPheLysThrLeuSerPheSerValPheGlnIleIleLeuIleThrSerLeuIleGly 541
Db 2074 ACTTTTACTACCCCAAAAGTTTGCTCAAGAGAAATGAAACCATTCATGCGCTGTTGCG 2133
QY 542 GlyGlyLeuLeuIleLeuIleIleLeuThrValAlaTrpGlyLeuLysProAsnLys 561
Db 2134 TTAGCATCTCTATGACACTCTTCTGAGGTGCTGTTCTTATATAGCGAGACTTA 2193
QY 562 LeuThrIleLeuCysTrpProThrValProAsnProLagLysSerIleAlaIleTrp 581
Db 2194 ATTAATAAAACACATCTGGCTTAATGTCCAGATCTTCAAAAGATCATTAATGCGCAGTGG 2253
QY 582 -----HISGlyAspAspPheLysAspLysLeu----- 590

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Db 2254 TCACCTCACACTCTCCAAAGCACACATTTTAAATCAAAAAGATCAAAATGATTCAGATGCG 2313
QY 590 ----- 590
Db 2314 AATTTCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2373
QY 591 AsnLeuLysGlnSerAsp-----AspSerValAsnThrGln 602
Db 2374 GATCTGAATTCATGTGACCTGTTCAAAAAGAAATTAATTCGAA 2421

RESULT 5
US-07-797-556-1
; Sequence 1, Application US/07797556
; Patent No. 5262522
; GENERAL INFORMATION:
; APPLICANT: Geating, David P.
; TITLE OF INVENTION: Receptor for Oncostatin M and Leukemia
; TITLE OF INVENTION: Inhibitory Factor
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSER: Immunex Corporation
; STREET: 51 University Street
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/797,556
; FILING DATE: 19911122
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Seese, Kathryn A.
; REGISTRATION NUMBER: 32,172
; REFERENCE/DOCKET NUMBER: 2607
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 206-587-0430
; TELEFAX: 206-587-0606
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2369 base pairs
; TYPE: NUCLEIC ACID
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA to mRNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE: N-terminal
; ORIGINAL SOURCE:
; TISSUE TYPE: human placenta
; IMMEDIATE SOURCE:
; CLONE: B10G/pDC303
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 244..2369
; FEATURE:
; NAME/KEY: mat_peptide
; LOCATION: 310..2369
; FEATURE:
; NAME/KEY: sig_peptide
; LOCATION: 244..309
; US-07-797-556-1

Alignment Scores:
Pred. No.: 5,36e-65 Length: 2369
Score: 678.50 Matches: 169
Percent Similarity: 48.44% Conservative: 110
Best Local Similarity: 29.34% Mismatches: 258

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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/249,553
FILING DATE: 26-MAY-1994
ATTORNEY/AGENT INFORMATION:
NAME: Seese, Kathryn A.
REGISTRATION NUMBER: 32,172
REFERENCE/DOCKET NUMBER: 2614-A
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 587-0430
TELEFAX: (206) 233-0644
TELEX: 756822
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 2369 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA to mRNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: N-terminal
ORIGINAL SOURCE:
TISSUE TYPE: human placenta
IMMEDIATE SOURCE:
CLONE: B10G/pDC303
FEATURE:
NAME/KEY: CDS
LOCATION: 244..2369
NAME/KEY: mat_peptide
LOCATION: 310..2369
FEATURE:
NAME/KEY: sig_peptide
LOCATION: 244..309
US-08-308-881-1

Alignment Scores:
Pred. No.: 5.36e-65 Length: 2369
Score: 678.50 Matches: 169
Percent Similarity: 48.44% Conservative: 110
Best Local Similarity: 29.34% Mismatches: 258
Query Match: 19.47% Indels: 39
DB: Gaps: 14

US-10-006-265-2 (1-652) x US-08-308-881-1 (1-2369)
QY 35 ProValIserSerAspLeuIleuThrIleuArgpheaArgThrValIasnSerThr 54
DB 619 CCAGAAAACCTTAAATTTGAGTTGATGTGAACGAGGGAGAAAGAAATGAGGTGTGAG 678
QY 55 TrpSerProGlyIleuSerIleuThrSerIleuThrGlnIleuThrValIleu 70
DB 679 TGGGATGGTGGAGGAAACACACTTGGAGACAACTTCACTTAAATGTGAATGGCA 738
QY 71 ThrTyrAlaPheGlyIleu-----LysHisAsp-----AsnCysThrThrAsn 84
DB 739 ACACACAGAGTTGCTGATTCGAAGCAAAACGTGACACCCCACTCATGCTGATGAT 798
QY 85 SerSerThrSerIleuAsnIleuAlaSerCysSerPhePheIleuProArgIleuThrIleuPro 104
DB 799 TATTTCTACT-----GTGTATTTGTCT----- 819
QY 105 AspAsnTyrThrIleuGluValIleuAlaGluAsnGlyAspGlyValIleuLysSer---His 123
DB 820 ---AACATTGAAGTCTGGGTGAGAGAGAGAAATGCCCTTGGGAAGGTATACATGATCAT 876
QY 124 MetThrTyrTrpArgIleuAsnIleuAlaLysThrGluProProIleuLysIleuPheArgVal 143
DB 877 ATCAATTTGATCCTGTATATAAGTG---AAGCCCAATCCGCACTATATTTATCAGTG 933
QY 144 LysProValIleuGlyIleuLysArgMetIleuGlnIleuIleuTrpIleuSerProGluLeuAla 163
DB 934 ATCAACTCAGAGGAACGTCTAGATCTTAAATTTGACATGACCAACCAAGTATTTAAG 993

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QY 164 ProValIserSerAspLeuIleuThrIleuArgpheaArgThrValIasnSerThrSerTrp 183
DB 994 AGGTGTTATATA---CTAATAATTAACATTCATATAGAACCAAGATCCCTCACTTG 1050
QY 184 MetGluValIasnPheAlaLysAsnArgLysAspLysAsnGlnIleuThrTyrAsnLeuThrGly 203
DB 1051 ACCCAGATTCCT---CCTGAAGACACAGCATCCACCCGATCTTCACTCATCTCCAAAGAC 1107
QY 204 LeuGlnProPheThrGlnIleuThrValIleuAlaLeuArgCysValIleuLysIleuSer--- 222
DB 1108 CTTAAACCTTTTACAGAAATGATGTGTTAGCATTCGCTGATGAGAAAGATGTGAAGGGA 1167
QY 223 PheTrpSerAspTrpSerGlnIleuLysMetGlyMetThrGlnIleuGluIleuLysProCys--- 241
DB 1168 TACTGAGAGTCTGAGTGAAGTAAGAACAGTGGGATCACCCTTAAGATAGACATCTAATA 1227
QY 242 GlyLeuGluIleuTrpArgValIleuLysProAlaGluAlaAspGlyValArgpProValArg 261
DB 1228 GCACCAAGTTTCTGGTATATAATGATCCATCCATCTCAAGCTCAAGAACTGATACAA 1287
QY 262 LeuLeuTrpIleuLysAlaArgGlyAlaProValIleuGluLysThrLeuGlyTyrAsnIle 281
DB 1288 CTCGTGTGGAAGACATTCCTCTTTTGAAGCCAAATGCAAAATCTTGGATATGAAAGTG 1347
QY 282 TrpTyrTyrProGlyIleuSerAsnThrAsnLeuThrGlnIleuThrMetAsnThrThrAsnGln 301
DB 1348 ACTCTCAACAAGATGGAATATCAATTTACAAATTTACACAGTTAAGCCCA-----AAA 1401
QY 302 LeuGluLeuHisLeuGlyIleuSerPheTrpValSerMetIleuSerTyrAsnSerLeu 321
DB 1402 CTGACAGTAAATCTCAAAATGATGCTATCTAGCAACCCCTAAGCAAGTAAATCTGTGT 1461
QY 322 GlyLysSerProValAlaThrIleuArgIleuProAlaIleuGlnLysSerPheGlnCys 341
DB 1462 GGCAAATCAGATGACGCTGTTTAACTATCCCTGCTGTGACTTTCAMGCTACTACCTT 1521
QY 342 IleGluValMetGlnAlaCysValAlaGluAspGlnLeuValIleuLysTrpIleuSer 361
DB 1522 GTAAATGATCTTAAAGCATTCGCCAAAGATTAACGCTTTGGGTGAAGTACTGCA 1581
QY 362 AlaLeuAspValIasnThrTrpMetIleuIleuTrpPheProAspValIaspSerIleuProThr 381
DB 1582 AGGGAATCTGTAAAGAAATATATATCTTGAAGTGTGTGTATCTAGATTAAGCACCTCTGT 1641
QY 382 ThrLeuSerTrpGluSerValSerGlnAlaThrAsnTrpThrIleuGlnIleuAspLysIleu 401
DB 1642 ATCACAGACTGGCAACAAAGATGTGATCCGTGCATCGCACTTATTTAAGAGGAACTTA 1701
QY 402 LysProPheTrpCysTyrAsnIleuSerValTyrPrometLeuHisAspLysValGlyIleu 421
DB 1702 GCAGAGAGCAATGCTATTTGATTAACAGTTACTCCAGTATATGCGATGAGACCAAGGAAC 1761
QY 422 ProTyrSerIleuGlnAlaTyrAlaLysGluGlyValProSerGluGlyProGluThrLys 441
DB 1762 CCTGAATCATTAAGGAGCATACCTTAAACAGCTCCACCTTCCAAAGSACCTACTGTGCG 1821
QY 442 ValGluAsnIleuGlyValIleuThrValThrIleuTrpLysGluIleuProLysSerGlu 461
DB 1822 ACAAAAAGATGAGGAAAAACAAGCTGTCTTAAGGTGGACCAACTTCTTGTGATGTT 1881
QY 462 ArgLysGlyIleuIleuCysAsnTyrThrIleuPheTyrGlnAlaGluGlyGlyLysGlyPhe 481
DB 1882 CAGATGATGTTTATATCAAAATTTATCTATATTTTATAGAACATCATTTGAAATGAAACT 1941
QY 482 SerLysThrValIasnSerSerIleuGlnIleuGlyLysSerIleuLysArgLysThr 501
DB 1942 GCTGTAATGATGATCTTCCACACAGAAATATATCATTTGCTCTTGTGACTGATGACACA 2001
QY 502 SerTyrIleuAlaGlnValMetAlaAsnThrSerAlaGlyGlyThrAsnGlyThrSerIle 521
DB 2002 TTGTATCATGTATCAGATGAGCATATACAGATGGAAGGTGGAAGATGTGTCACGAATTC 2061

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Oy 522 Asn|Phe|Thr|Leu|Ser|Phe|Ser|Val|Phe|Glu|Ile|Ile|Leu|Ile|Thr|Ser|Leu|Ile|Gly 541
Db 2062 ACTTTTACTTACCCCAAGTTTCTCTCAAGAGAAATTGAAGCAATGCTCTGCTGTTTGC 2122
Oy 542 Gly|Gly|Leu|Leu|Ile|Leu|Ile|Leu|Thr|Val|Ala|Arg|Gly|Leu|Ile|Phe|Pro|Asn|Iys 561
Db 2122 TTAGCATTCCTATTGACAACACTCTTCTGGAGTGCCTGTTCTTAAATGAAGAGACCTA 2189
Oy 562 Leu|Thr|His|Leu|Cys|Tyr|Pro|Thr|Val|Pro|Asn|Pro|Ala|Glu|Ser|Ser|Ile|Ala|Thr|Tyr 581
Db 2182 ATTAATAAAACACATCTGGCTGCTAATGTTCCAGATCCTTCAAAAGCATATTGCCCAGATGG 2241
Oy 582 -----His|Gly|Asp|Asp|Phe|Iys|Asp|Ile|Leu 590
Db 2242 TCACCTCACACTCTCTCAAGGACACATTTTAATTCAAAAGATCAATG 2289

RESULT 7
US-09-058-263-1
Sequence 1, Application US/09058263
Patent No. 5891997
GENERAL INFORMATION:
APPLICANT: Mosley, Bruce
APPLICANT: Cosman, David J.
TITLE OF INVENTION: Receptor for Oncostatin M
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: Immunex Corporation
STREET: 51 University Street
CITY: Seattle
STATE: WA
COUNTRY: USA
ZIP: 98101

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Macintosh
OPERATING SYSTEM: Apple 7.1
SOFTWARE: Microsoft Word, Version 5.1a
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/058,263
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/308,881
FILING DATE: 12-SEP-1994
APPLICATION NUMBER: US 08/249,553
FILING DATE: 26-MAY-1994
ATTORNEY/AGENT INFORMATION:
NAME: Seege, Kathryn A.
REGISTRATION NUMBER: 32,172
REFERENCE/DOCKET NUMBER: 2614-A
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 587-0430
TELEFAX: (206) 233-0644
TELEX: 756822
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 2369 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA to mRNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: N-terminal
ORIGINAL SOURCE:
TISSUE TYPE: human placenta
IMMEDIATE SOURCE:
CLONE: B10G/pBC303
FEATURE:
NAME/KEY: CDS
LOCATION: 244..2369
FEATURE:
NAME/KEY: mat_peptide

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LOCATION:	310..2369		
FEATURE:			
NAME/KEY:	big_peptide		
LOCATION:	244..309		
US-09-058-263-1			
Alignment Scores:			
Pred. No.:	5,366-65	Length:	2369
Score:	678.50	Matches:	169
Percent Similarity:	48.44%	Conservative:	110
Best Local Similarity:	29.34%	Mismatches:	258
Query Match:	19.47%	Indels:	39
DB:	2	Gaps:	14
US-10-006-265-2 (1-652) x US-09-058-263-1 (1-2369)			
QY	35	ProAlaLysProGluAsnIleSerCysValTyrTyrArgLysAsnLeuThrCysThr	54
DB	619	CCAGAAAACTTAAATTTGGATTGTCATTGGAAAGGAGGAAAGAAATAGAGTGTGAG	678
QY	55	TTPSerProGlyLysGluThrSerTyr---ThrGlnTyrThrValLys-----Arg	70
DB	679	TGGATGTGGAGAAAGGAAACACACTGGAGACAAACTTCATTAAATCTGAATGGCGA	728
QY	71	ThrTyrAlaPheGlyGlu-----LysHisAsp-----AsnGlyThrThrAsn	84
DB	739	ACACCAAGTTTGGTCGATGGTCAAGCAAAACCTGACCCCACTTCATGCACTGTGAT	798
QY	85	SerSerThrSerGluAsnArgLysSerCysSerPhePheLeuProArgLethrIlePro	104
DB	799	TATTTTACT-----GCTATTTTGTG-----	819
QY	105	AspAsnTyrThrIleGluValGluAlaGluAsnGlyAspGlyValIleLysSer---His	123
DB	820	---AACATTGAAGCTGGGTAGAACACAGAGATGCCCTTGGGAAGSTTACATCAGATCAT	876
QY	124	MetThrTyrTTPArgLysGluAsnIleAlaLysThrGluProProLysIlePheArgVal	143
DB	877	ATCATTTTGGATCCGTATATTAAGTG--AAGCCCAATCCGCCACATATTATTCAGTG	933
QY	144	LysProValLeuGlyIleLysArgMetIleGlnIleGluTProIleLysProGluLeuAla	163
DB	934	ATCAACTGAGAGAACTGTCTAGTATCTTAAATTTGACATGGACCAACCCAGATTAAG	993
QY	164	ProValSerSerAspLeuLysTyrThrThrArgPheArgThrValAsnSerThrSerTTP	183
DB	994	AGTGTATTAATA---CTAAATATATACATTCAATAGACCAAGATGCCCTCAACTGG	105
QY	184	MetGluValAsnPheAlaLysAsnArgLysAspLysAsnGlnThrTyrAsnLeuThrGly	203
DB	1051	AGCCAGATTCTCT---CCTGAAGACACACGATCCACCCGATCTTCCTCACTGTCCAAAGAC	110
QY	204	LeuGlnProPheThrGlnTyrValIleAlaLeuAlaGlyGlyAlaValIleGluSerLys---	222
DB	1108	CTTAAACCTTTTACAGAAATATGTGTTTAGGATTCCTGTATGAGAAAGAAATGTAAAGGA	116
QY	223	PheTTPSerAspTTPSerGlnGluLysMetGlyMetThrGluGluGluAlaProCys---	241
DB	1168	TACTGGAAGTCTGGAGTGAAGAAACCAAGTGGATCACCCTATGAAAGATAGACATTAAG	122
QY	242	GlyLeuGluLeuTTPArgValLeuLysProAlaGluAlaAspGlyArgArgProValArg	261
DB	1228	GCACCAAGTTTCTGGTATTAATAATAGATCATCCATCCATCTCAAGCTACAGAACTGACAA	128
QY	262	LeuLeuTTPLysLysAlaArgGlyAlaProValLeuGluLysThrLeuGlyTyrAsnIle	281
DB	1288	CTCGTGTGAAGACATTGCCCTCTTTTGAAGCCATGGAAAAATCTTGATTTAGAAAGTG	134
QY	282	TrpTyrTyrProGluSerAsnThrAsnLeuThrGluThrMetAsnThrThrAsnGlnGln	301
DB	1348	ACTCTCACAAAGATGGAATTCACATTACAAATTAACAGATTAAAGCCACA-----AAA	140
QY	302	LeuGluLeuLysLeuGlyGlyLysSerPheThrValSerMetIleSerTyrAsnSerLeu	321

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Db      1462 GGGAAATCGAGATCGACCTGTTTAACTATCCCTGCTGATGCTTCAAGCTACTCAACCT 1521
Qy      342 IleGluValMetGlnIaCysValAlaGluAspGlnIleuValValIlystrPginSerSer 361
Db      1522 GTPATGATCTTAAACATCTCCCAAGAAATACATGCTTGGGTGGAATGATGACTCCCA 1581
Qy      362 AlaIleuAspValaSerThrTrpMetIleGluTrpPheProAspValaIpsSerGluProthr 381
Db      1582 AGCGAATCTGTAAAGAAATATATATGATGATGCTGTGTATTCAGATTAAGACACCTGT 1641
Qy      382 ThrIleuSerTrpGluSerValSerGlnAlaThrAsnTrpThrIleGlnIleAspIlySleu 401
Db      1642 ATCAGACACTGCGCAGACAGAAAGTGTACCGTGCATCGCACCTATTTAAAGAGGAACTTA 1701
Qy      402 LysProPheTrpCysTrpIleuSerValIlyrProMetLeuHisAspIlySValGlyGlu 421
Db      1702 GCGAGAGCAAAATCTTATTGATPACAGTACTCCAGTATATGCTATGATGACACGAGAAC 1761
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? COUNTRY: USA
? ZIP: 98101
? COMPUTER READABLE FORM:
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? COMPUTER: Apple Macintosh
? OPERATING SYSTEM: Apple 7.1
? SOFTWARE: Microsoft Word, Version 5.1a
? CURRENT APPLICATION DATA:
? APPLICATION NUMBER: US/09/059,099
? FILING DATE:
? CLASSIFICATION:
? PRIOR APPLICATION DATA:
? APPLICATION NUMBER: US/08/308,881
? FILING DATE: 12-SEP-1994
? APPLICATION NUMBER: US 08/249,553
? FILING DATE: 26-MAY-1994
? ATTORNEY/AGENT INFORMATION:
? NAME: Seese, Kathryn A.
? REGISTRATION NUMBER: 32,172
? REFERENCE/DOCKET NUMBER: 2614-A
? TELECOMMUNICATION INFORMATION:
? TELEPHONE: (206) 587-0430
? TELEFAX: (206) 233-0644
? TELEX: 756822
? INFORMATION FOR SEQ ID NO: 1:
? SEQUENCE CHARACTERISTICS:
? LENGTH: 2369 base pairs
? TYPE: nucleic acid
? STRANDEDNESS: single
? TOPOLOGY: linear
? MOLECULE TYPE: CDNA to mRNA
? HYPOTHEICAL: NO
? ANTI-SENSE: NO
? FRAGMENT TYPE: N-terminal
? ORIGINAL SOURCE:
? TISSUE TYPE: human placenta
? IMMEDIATE SOURCE:
? CLONE: B10G/PDC303
? FEATURE:
? NAME/KEY: CDS
? LOCATION: 244..2369
? FEATURE:
? NAME/KEY: mat_peptide
? LOCATION: 310..2369
? FEATURE:
? NAME/KEY: g1g_peptide
? LOCATION: 244..309
? US-09-059-099-1
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? Alignment Scores:
? Pred. No.: 5,36e-65 Length: 2369
? Score: 678.50 Matches: 169
? Percent Similarity: 48.44% Conservative: 110
? Best Local Similarity: 29.34% Mismatches: 258
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Qy      55 TrpSerProGlyIlyGlnIlyrSerIlyr-----ThrGlnTrpThrValys-----Arg 70
Db      679 TGGGATGTGGAGGAAACACACTTGAGACAAACTTAAATCTGAATGGCA 738
Qy      71 ThrTrpAlaPheGlyGlu-----LysHisAsp-----AsnCysThrThrAsn 84
Db      739 ACACAGAAGTTTGCTGATTCGAAGCAAAACGTGACACCCCACTCATGACTGTGAT 798
Qy      85 SerSerThrSerGluAsnArgAlaSerCysSerPhePheLeuProArgIleThrIlePro 104

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MOLECULE TYPE: cDNA to mRNA
 HYPOTHETICAL: NO
 ANTI-SENSE: NO
 FRAGMENT TYPE: N-terminal
 ORIGINAL SOURCE:
 TISSUE TYPE: human placenta
 IMMEDIATE SOURCE:
 CLONE: B10G/PDC303
 FEATURE:
 NAME/KEY: CDS
 LOCATION: 244..2369
 NAME/KEY: NAME/KEY: mat peptide
 LOCATION: 310..2369
 FEATURE:
 NAME/KEY: sig peptide
 LOCATION: 244..309
 US-09-058-264-1

Alignment Scores:

Pred. No.:	5,366-65	Length:	2369
Score:	678.50	Matches:	169
Percent Similarity:	48.44%	Conservative:	110
Best Local Similarity:	29.34%	Mismatches:	258
Query Match:	19.47%	Indels:	39
		Gaps:	14

US-10-006-265-2 (1-652) x US-09-058-264-1 (1-2369)

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QY 35 ProAlaLysProGluAsnIleSerCysValTyrTyrTyrArgLysAsnLeuThrCysThr 54
Db 619 CCGAAAAAAGCTTAAATTTGAGTTCATTTGACAGGGGAAATAAGGTGTGAG 678
QY 55 TrpSerProGlyLysGluThrSerTyr---ThrGlnTyrThrValys-----Arg 70
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Db 820 ---AACATTGAAGTCTGGGTAGAGACAGAGAAATGCCCTTGGGAAGTTTACATCAGATCAT 876
QY 124 MetThrTyrTrpArgLeuGluAsnIleAlaLysThrGluProProLysIlePheArgVal 143
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RESULT 10

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 ; Sequence 1, Application US/09455962
 ; Patent No. 6524817
 ; GENERAL INFORMATION:
 ; APPLICANT: Mosley, Bruce
 ; APPLICANT: Cosman, David J.
 ; TITLE OF INVENTION: Receptor for Oncostatin M
 ; NUMBER OF SEQUENCES: 11
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Immunex Corporation
 ; STREET: 51 University Street
 ; CITY: Seattle
 ; STATE: WA
 ; COUNTRY: USA
 ; ZIP: 98101
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: Apple Macintosh
 ; OPERATING SYSTEM: Apple 7.1
 ; SOFTWARE: Microsoft Word, Version 5.1a
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/09/455,962
 ; FILING DATE:
 ; CLASSIFICATION:
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 09/058,264
 ; FILING DATE:
 ; APPLICATION NUMBER: US 08/249,553
 ; FILING DATE: 26-MAY-1994
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Seese, Kathryn A.
 ; REGISTRATION NUMBER: 32,172
 ; REFERENCE/DOCKET NUMBER: 2614-A
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (206) 587-0430
 ; TELEFAX: (206) 233-0644
 ; TELEX: 756822
 ; INFORMATION FOR SEQ ID NO: 1:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 2369 base pairs
 ; TYPE: nucleic acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: cDNA to mRNA
 ; HYPOTHETICAL: NO
 ; ANTI-SENSE: NO
 ; FRAGMENT TYPE: N-terminal
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 ; TISSUE TYPE: human placenta
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 ; CLONE: B106/pDC303
 ; FEATURE:
 ; NAME/KEY: CDS
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 ; LOCATION: 244..309
 ; US-09-455-962-1
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 Pred. No.: 5,366-65 Length: 2369
 Score: 678..50 Matches: 169
 Percent Similarity: 48.44% Conservative: 110
 Best Local Similarity: 29.34% Mismatches: 258
 Query Match: 19.47% Indels: 39
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 ; Sequence 1, Application PC/TUS9506530
 ; GENERAL INFORMATION:
 ; APPLICANT: Mosley, Bruce
 ; APPLICANT: Cosman, David J.
 ; TITLE OF INVENTION: Receptor for Oncostatin M
 ; NUMBER OF SEQUENCES: 11
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Immunex Corporation
 ; STREET: 51 University Street
 ; CITY: Seattle
 ; STATE: WA
 ; COUNTRY: USA
 ; ZIP: 98101
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patentin Release #1, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: PCT/US95/06530
 ; FILING DATE:
 ; CLASSIFICATION:
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 08/308,881
 ; FILING DATE: 09-SEP-1994
 ; APPLICATION NUMBER: US 08/249,553
 ; FILING DATE: 26-MAY-1994
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Anderson, Kathryn A.

; REGISTRATION NUMBER: 32,172
 ; REFERENCE/DOCKET NUMBER: 2614-MO
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (206) 587-0430
 ; TELEFAX: (206) 233-0644
 ; TELEX: 756822
 ; INFORMATION FOR SEQ ID NO: 1:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 2369 base pairs
 ; TYPE: nucleic acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: cDNA to mRNA
 ; HYPOTHETICAL: NO
 ; ANTI-SENSE: NO
 ; FRAGMENT TYPE: N-terminal
 ; ORIGINAL SOURCE:
 ; TISSUE TYPE: human placenta
 ; IMMEDIATE SOURCE:
 ; CLONE: B10G/pDC303
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 ; NAME/KEY: CDS
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 ; FEATURE:
 ; NAME/KEY: mat_peptide
 ; LOCATION: 310..2369
 ; FEATURE:
 ; NAME/KEY: sig_peptide
 ; LOCATION: 244..309
 ; PCT-US95-06530-1
 Alignment Scores:
 Pred. No.: 5,366-65 Length: 2369
 Score: 678.50 Matches: 169
 Percent Similarity: 48.448 Conservative: 110
 Best Local Similarity: 29.348 Mismatches: 238
 Query Match: 19.478 Indels: 39
 DB: 5 Gaps: 14
 US-10-006-265-2 (1-652) x PCT-US95-06530-1 (1-2369)
 Qy 35 ProAlaLysProGluAsnIleSerCysValIleThrValGlyAsnLeuThrCysThr 54
 Db 619 CCAGAAAACCTTAATAATTTGATGCTGTAACGAGGAGAAATGAGTGTGAG 678
 Qy 55 TrpSerProGlyLysGluThrSerIleThrGlnIleThrValLys-----Arg 70
 Db 679 TGGGATGTGGAGGAGGAAACACACTTGAGACAACTTCAATTAATCTGAATGGCA 738
 Qy 71 ThrTyrAlaPheGlyGlu-----LysHisAsp-----AsnCysThrThrAsn 84
 Db 739 ACACACAGATGTTGCTGATTCGACAAAGCAAAACGACACCCACCTCATGCTGTGAT 798
 Qy 85 SerSerThrSerGluAsnArgAlaSerCysSerPhePheLeuProArgIleThrIlePro 104
 Db 799 TATTCTACT-----GTGATTTTGTG----- 819
 Qy 105 AspAsnIleThrIleGluValGluAlaGluAsnGlyAspGlyValIleLysSer---His 123
 Db 820 ---AACATTGAGTCTGGGTGAGAGCAGAGATGCCCTTGGAGAGGTATCATCATGATCAT 876
 Qy 124 MetThrTyrTrpArgLeuGluAsnIleAlaValThrGluProProLysIlePheArgVal 143
 Db 877 ATCAATTTGATTCCTGATATTAAGG---AAGCCCAATCCCGCCACATATATTATCAGTG 933
 Qy 144 LysProValLeuGlyIleLysArgMetIleGlnIleGluTyrIleLysProGluLeuAla 163
 Db 934 ATCAACTCAGAGAGACTGTCTAGTATCTTAATAATGACATGACCAACCAAGATTAAG 993
 Qy 164 ProValSerSerAspLeuLysTyrThrIleAsnArgPheArgThrValAsnSerThrSerTrp 183
 Db 994 AGTGTATATAATA---CTAAATAATATAACATTCATATATAGACCAAAAGATGCTCAACTTGG 1050

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Qy 184 MetGluValAsnPheAlaLysAsnArgLysAspLysAsnGlnThrTyrAsnLeuThrGly 203
Db 1051 AGCCAGATTCCCT---CTGGAAGACACAGATCCACCACATCTTCATTCTCCTCCAAAGC 1107
Qy 204 LeuGlnProPheThrGlyTyrValIleAlaLeuArgCysAlaValLysGlnSerLys--- 222
Db 1108 CTTAAACCTTTTACAGAAATATGTGTTAGGATTCCTGATGAGAGAAATGTAAGGGA 1167
Qy 223 PheTyrPseAspTrpSerGlnGluLysMetGlnThrGlnGluAlaProCys--- 241
Db 1168 TACTGGAGTCTGAGTGAAGAGACAGATGGATCACCCTATGAAGATGAGACATCTAA 1227
Qy 242 GlyLeuGluLeuTrpArgValLeuLysProAlaGlnAlaAspGlyArgArgProValArg 261
Db 1228 GCACCAATTTCTGTTATTAATATATATCTCCATCTCAAGCTTACAGAACTTACAA 1287
Qy 262 LeuLeuTrpLysLysAlaArgGlyAlaProValLeuGlnLysLeuThrLeuGlyTyrAsnIle 281
Db 1288 CTCGGTGGAAAGACATTCCTCTTTTGAAGCCCAATGAGAAATCTTGATATGAGTG 1347
Qy 282 TrpTyrTyrProGluSerAsnThrAsnLeuThrGlnThrMetAsnThrThrAsnGlnGln 301
Db 1348 ACTCTCACAGATGAGAAATCACATTACAAATTAACAGATTAAATGCCA---AAA 1401
Qy 302 LeuGluLeuHisLeuGlyGlyLysSerPheTrpValSerMetLysSerTyrAsnSerLeu 321
Db 1402 CTGACAGTAAATCTCACAAATGATGCTATCTAGAACCTTACAGTAAAGAAATTTGTT 1461
Qy 322 GlyLysSerProValAlaThrLeuArgLysProAlaIleGlnGluLysSerPheGlnCys 341
Db 1462 GGCAAATCAGATGAGCTGTTTAACTATCCCTGCTGATCTTCAAGCTTACCTACCT 1521
Qy 342 IleGluValMetGlnAlaCysValAlaGluLysGlnLeuValValLysTrpGlnSerSer 361
Db 1522 GTAATGATCTTAAAGCATTTCCCAAGATTAACATCTTGGTGAATGAGACTTCA 1581
Qy 362 AlaLeuSerValAsnThrTrpMetLysGlnTrpPheProAspValAspSerGlnProThr 381
Db 1582 AGGGAATCTGTAAAGAAATATATATCTTACTGATGCTGTCTTATCAGATTAAGACCCCTGT 1641
Qy 382 ThrLeuSerTrpGluSerValSerGlnAlaThrAsnTrpThrIleGlnGlnAspLysLeu 401
Db 1642 ATCACAGATCGCAACAAGAGATGCTACCGATCCGATCTTAAAGAGGGAACCTTA 1701
Qy 402 LysProPheTrpCysTyrAsnLysSerValTyrProMetLysHisAspLysValGlyGlu 421
Db 1702 GCAGAGAGCAAAATCTATTGTATACAGTACTCCAGATATGCGTGAAGGACGACGAGC 1761
Qy 422 ProTyrSerIleGlnAlaTyrAlaLysGlnGlyValProSerGlnGlyProGluThrLys 441
Db 1762 CTTGAATCTTAAGGACATCTTAAACAGCTCCACCTTCAAGAGGACCTACTGTTGG 1821
Qy 442 ValGluAsnIleGlyValLysThrValThrIleThrTrpLysGlnLeuProLysSerGlu 461
Db 1822 ACAAAAAGAGGAGAAAAGAGAGCTGCTTAGAGTGGAACAACCTCGTTGATGATTT 1881
Qy 462 ArgLysGlyIleIleCysAsnTyrThrIlePheTyrGlnAlaGluGlyLysGlyPhe 481
Db 1882 CAGATGATTTTATCAGAAATTAATATATTTATATAGAACCATCATGGAATGAAACT 1941
Qy 482 SerLysThrValAsnSerSerIleLeuGlnTyrGlnLeuGlnSerLeuLysArgLysThr 501
Db 1942 GCTGTGAATGTGATTTCTTCCACACAGAAATATACATTTGCTCTTTGACTAGTACACA 2001
Qy 502 SerTyrIleValGlnValMetAlaAsnThrSerAlaGlyTyrAsnGlyThrSerIle 521
Db 2002 TTGTAATCGTGAATGAGACATACACAGATGAGAGTGGAGAGATGCGCAAGATTC 2061
Qy 522 AsnHelysThrLeuSerPheSerValPheGluIleIleLeuIleThrSerLeuIleGly 541
Db 2062 ACTTTTACTACCCCAAAATTTGCTCAAGAGAAATTAAGCCATAGTCTGCTGTTGC 2121
Qy 542 GlyGlyLeuLeuIleLeuIleIleLeuThrValAlaTyrGlyLeuLysLysProAsnLys 561

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Db 2122 TTAGATTCCTATTGACAACCTCTCTGGAGTGGCTTCTGCTTAAATTAAGGAGACCTA 2181
Qy 562 LeuThrHisLeuCysTrpProThrValProAsnProAlaGlnSerSerIleAlaThrTrp 581
Db 2182 ATTAACAAACATCTGCTTAATGTTCCAGATCTTCAAGAGATGATGCGCAGTGG 2241
Qy 582 -----HisGlyAspAspPheLysAspLysLeu 590
Db 2242 TCACCTCACTCTCCAGGACAAATTTTATTAACAAAGATCAAAATG 2289

RESULT 12
US-08-825-558-5
; Sequence 5, Application US/08825558
; Patent No. 5965724
; GENERAL INFORMATION:
; APPLICANT: SHARKEY, ANDREW
; APPLICANT: SMITH, STEPHEN K.
; APPLICANT: DELLOW, KIMBERLEY A.
; TITLE OF INVENTION: Gp 130 Lacking the Transmembrane Domain
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: STERN, KESSLER, GOLDSTEIN & FOX
; STREET: 1100 NEW YORK AVENUE
; CITY: WASHINGTON
; STATE: DC
; COUNTRY: USA
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/825,558
; FILING DATE: 19-MAR-1997
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: ESMOND, ROBERT W.
; REGISTRATION NUMBER: 32,893
; REFERENCE/DOCKET NUMBER: 0623_0530001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)371-2600
; FAX: (202)371-2540
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2754 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..2754
; US-08-825-558-5

Alignment Scores:
Pred. No.: 8.92e-65 Length: 2754
Score: 677.50 Matches: 175
Percent Similarity: 46.75% Conserved: 113
Best Local Similarity: 28.41% Mismatches: 261
Query Match: 19.45% Indels: 67
DB: Gaps: 16

US-10-006-265-2 (1-652) x US-08-825-558-5 (1-2754)
Qy 35 ProAlaLysProGluAsnLysSerCysValTyrTyrArgLysAsnLeuThrCysThr 54
Db 376 CCGAAGAAACCTTAAGAAATTTGAGTGGATTTGACAGAGGAGAAAGAAATGAGGTGAG 435
Qy 55 TrpSerProGlyLysGlnThrSerTyr---ThrGlnTyrThrValLys-----Arg 70
Db 436 TGGGATGTGTGAAGGAGAAACACACTTGAGACAAACTCTTAAATGTAATGGCA 495

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REFERENCE/DOCKET NUMBER: 0623.0530002
TELEPHONE: (202)371-2600
TELEFAX: (202)371-2540
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 2754 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
TOPOLOGY: linear
MOLECULE TYPE: CDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 1..2754
US-09-312-611-5

Alignment Scores:
Pred. No.: 8,92e-65 Length: 2754
Score: 677.50 Matches: 175
Percent Similarity: 46.75% Conservative: 113
Best Local Similarity: 28.41% Mismatches: 261
Query Match: 19.45% Indels: 67
Gaps: 16

US-10-006-265-2 (1-652) x US-09-312-611-5 (1-2754)

QY 35 ProAlaLysProGluAsnLysSerCyValTyrTyrArgLysAsnLeuThrCysThr 54
DB 376 CCAAGAAAACTTAAATTTGAGTTCATTTGAAACGAGCGAAGAAATGAGGTGTGAG 435
QY 55 TTPSerProGluLysGluThrSerTyr---ThrGlnTyrThrValLys-----Arg 70
DB 436 TGGAGTGGTGAAGGAAACACACTTGGACAACTTCACTTAAATCTGAATGGCA 495
QY 71 ThrTyrAlaPheGluGlu-----LysHisAsp-----AsnCySerThrAsn 84
DB 496 ACACAGAGTTTGCATGATTGCAAGCAAAAGCTGACACCCCACTCATGCTTGAT 555
QY 85 SerSerThrSerGluAsnArgLysSerCysSerPhePheLeuProArgLleThrIlePro 104
DB 556 TATCTACT-----GTGATTTTGTG----- 576
QY 105 AsnAsnTyrThrIleGluValGluValGluAsnGlyAspGlyValIleLysSer---His 123
DB 577 ---AACATTGAAGTGTGGTAGAGCAAGATGCGCTTGGAGGTTACATCATCAT 633
QY 124 MetThrTyrTyrArgLeuGluAsnIleAlaLysThrGluProProLysIlePheArgVal 143
DB 634 ATCATTTTGCATCCCTATATAAAGTG---AAGCCCATCCGCCCATATATTATCAGTG 690
QY 144 LysProValLeuGlyIleLysArgMetIleGlnIleGluTyrIleLysProGluLeuAla 163
DB 691 ATCAACTGAGAGCACTGCTAGTATCTTAAATATGACATGGACCAACCAAGTATTAG 750
QY 164 ProValSerSerAspLeuLysTyrThrLeuArgPheArgThrValAsnSerThrSerTrp 183
DB 751 AGTGTATATAA---CTAAATATATAACTCATATAGACCAAGATGCCCTCAACTGG 807
QY 184 MetGluValAsnPheAlaLysAsnArgLysAspLysAsnGlnThrTyrAsnLeuThrGly 203
DB 808 AGCCGATTTCC---CTGGAAGACACAGATCCACCATCTTCATTCATCTCCAAAGC 864
QY 204 LeuGlnProPheThrGluTyrValIleAlaLeuArgCysAlaValLysGluSerLys--- 222
DB 865 CTTAAACCTTTTACAGATATGTGTAGATTGCTGTATGAAGAAAGATGTAAGGA 924
QY 223 PheTrpSerAspTrpSerGlnGluLysMetGlyMetThrGluGluAlaProCys--- 241
DB 925 TACTAGAGTGAAGTGAAGCAAGCAAGTGGATCACCCTATGAAGATGACACTTAA 984
QY 242 GlyLeuGluLeuTyrArgValLeuLysProAlaGluAlaAspGlyArgArgProValArg 261
DB 985 GCACCAAGTTTCTGTATATAATATAGATCCATCCACTCAAGGCTACAGAACTGTACA 1044

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QY 262 LeuLeuTyrLysLysAlaArgGlyAlaProValLeuGluLysThrLeuGlyTyrAsnIle 281
DB 1045 CTCGTGTGAAGACATTCCTCTTTTGAAGCCAAATGGAATCTTGATTAAGAGTG 1104
QY 282 TrpTyrTyrProGluSerAsnThrAsnLeuThrGluThrMetAsnThrThrAsnGln 301
DB 1105 ACTCTCAAAATGGAATACATTTACAAAATTAACAGATTAATGCCACG-----AAA 1156
QY 302 LeuGluLeuHisLeuGlyGlyLysSerPheTrpValSerMetLysSerTyrAsnSerLeu 321
DB 1159 CTGACAGTAATCTCACAAATGATGCTATCTACCAACCTTAACAGTAAGAAATCTGT 1218
QY 322 GlyLysSerProValAlaThrLeuArgLleProAlaIleGlnGluLysSerPheGlnCys 341
DB 1219 GGCAAATGATGATGACGCTGTATTACTATCCCTGCTGTGACTTCAAGCTACACCT 1278
QY 342 IleGluValMetGlnAlaCysValAlaGluAspGlnLeuValValLysTrpGlnSerSer 361
DB 1279 GTAATGATCTTAAAGCATTTCCCAAGATTAACATGCTTTGGTGGATGACTATCCA 1338
QY 362 AlaLeuAspValAsnThrTyrMetIleGluTyrPheProAspValAspSerGluProThr 381
DB 1339 AGGGAATCTGTAAGAAATATATATCTGAGTGTGTGTATCATGATTAAGACACCTGT 1398
QY 382 ThrLeuSerTrpGluSerValSerGlnAlaThrAsnTrpThrIleGlnGlnAspLysLeu 401
DB 1399 ATCAAGACTGCAACAGAAAGATGTACCGCTGATCGACCTTATTAAGAGGAACCTTA 1458
QY 402 LysProPheTrpCysTyrAsnLysSerValTyrProMetLeuHisAspLysValGlyVal 421
DB 1459 GCAGAGACAAATGCTATTTTATATACAGTTACTCAGATATGCTGATGACACGGAAGC 1518
QY 422 ProTyrSerIleGlnAlaTyrAlaLysGluGlyValProSerGluGlyProGluThrLys 441
DB 1519 CCGATATCATTAAGAGCATACCTTAACAAAGCTCACCTTCAAGAGCACTATGCTGG 1578
QY 442 ValGluLeuIleGlyValLysThrValThrIleThrTyrLysGluIleProLysSerGlu 461
DB 1579 ACAAAAAGAGTGAAGAAAGCAAGAGCTGTCTTAAGTGGGCAACCTCCGTGATGTT 1638
QY 462 ArgLysGlyIleLysAsnTyrThrIlePheTyrGlnAlaGluGlyLysGlyPhe 481
DB 1639 CAGATGATTTATCAGAAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1698
QY 482 SerLysThrValAsnSerSerIleLeuGlnTyrGlyLeuGlnSerLeuLysArgLysThr 501
DB 1699 GCTGGAATGTGATTTCTCCACACAGAAATATACATTTGCTCTTGTGACATGACACA 1758
QY 502 SerTyrIleValGlnValMetAlaAsnThrSerAlaGlyLysThrAsnGlyThrSerIle 521
DB 1759 TTGTACATGTGACCAATGCGACATACAGATGAGGTGGAGATGTCAGAAATTC 1818
QY 522 AsnPheLysThrLysSerPheSerValPheGluIleIleLeuIleThrSerLeuIleGly 541
DB 1819 ACTTTTACTACCCCAAGTTTGTCAAGAGAAATTAAGCAATGATGCTGCTGTTC 1878
QY 542 GlyLysLeuLeuIleLeuIleLeuThrValAlaTyrGlyLeuLysLysProAsnLys 561
DB 1879 TTACATTTCCATTTGACAACTCTCTGGAGTGTGTCGCTTAAATTAAGCGAGACTA 1938
QY 562 LeuThrHisLeuCysTrpProThrValProAsnProAlaGluSerSerIleAlaThrTrp 581
DB 1939 ATTAAAAACACATCTGCGCTTAAGTTCCAGATCTTCAAAAGTCTATATATGCCAGTGG 1998
QY 582 -----HisGlyAspAspPheLysAspLysLeu----- 590
DB 1999 TCACCTACACTCTCCAAAGGACAAATTTTAATTAATTAATTAATTAATTAATTAAT 2058
QY 590 ----- 590
DB 2059 AATTTCACATAATGTAATGTTGTGAAATTAAGAAATGACAAAGACCTTTCCAGAA 2118

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QY      591 AsnLeuLysGluSerAsp-----AspSerValAsnThrGlu 602
Db      2119 GATCTGAATCATCTGGACCTGTTCAAAAGAAAATAATTAATCTGA 2166

RESULT 14
US-08-825-558-3
/ Sequence 3, Application US/08825558
/ Patent No. 5965724
/ GENERAL INFORMATION:
/ APPLICANT: SHARKEY, ANDREW
/ APPLICANT: SMITH, STEPHEN K.
/ APPLICANT: DELLOW, KIMBERLEY A.
/ TITLE OF INVENTION: Gp 130 Lacking the Transmembrane Domain
/ NUMBER OF SEQUENCES: 14
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: STERN, KESSLER, GOLDSTEIN & FOX
/ STREET: 1100 NEW YORK AVENUE
/ CITY: WASHINGTON
/ STATE: DC
/ COUNTRY: USA
/ ZIP: 20005
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: PatentIn Release #1.0, Version #1.30
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/825,558
/ FILING DATE: 19-MAR-1997
/ CLASSIFICATION: 536
/ ATTORNEY/AGENT INFORMATION:
/ NAME: ESMOND, ROBERT W.
/ REGISTRATION NUMBER: 32,893
/ REFERENCE/DOCKET NUMBER: 0623.0530001
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (202)371-2600
/ TELEFAX: (202)371-2540
/ INFORMATION FOR SEO ID NO: 3:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 1977 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: both
/ TOPOLOGY: linear
/ MOLECULE TYPE: cDNA
/ FEATURE:
/ NAME/KEY: CDS
/ LOCATION: 1..1974
/ US-08-825-558-3

Alignment Scores:
Pred. No.:      1,94e-60      Length:      1977
Score:          46.53%      Matches:      163
Percent Similarity: 28.53%      Conservative: 105
Best Local Similarity: 18.27%      Mismatches: 237
Query Match:      2          Indels:      72
                        Gaps:      15

US-10-006-265-2 (1-652) x US-08-825-558-3 (1-1977)
QY      35 ProAlaLysProGluAsnLysSerCysValTyrTyrTyrArgLysAsnLeuThrCysThr 54
Db      376 CCAGAAACCTTAATAATTTGAGTTGATGTGAACGAGGGAAGAAATGAGAGTGTGAG 435
QY      55 TrpSerProGluLysGluThrSerTyr---ThrGlnTyrThrValLys-----Arg 70
Db      436 TGGGATGGTGAAGGGAACACCTTGAGACAAACTTCACTTAAATCTGAATGGGCA 495
QY      71 ThrTyrAlaPheGluGlu-----LysHisAsp-----AsnCysThrThrAsn 84
Db      496 ACACACAGATTTCGATTGTCACAAAGCAAAACGTGACACCCCACTCATCTGTTGAT 555
QY      85 SerSerThrSerGluAsnArgAlaSerCysSerPhePheLeuProArgIleThrIlePro 104

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Db      556 TATTTCTACT-----GTGATTTTGTG----- 576
QY      105 AspAsnTyrThrIleGluValGluLysAsnGlyAspGlyValIleLysSer---His 123
Db      577 ---AACATTGAAGTCTGGGTAGACAGAGAAATGCCCTTGGGAAGTTACATCATCAT 633
QY      124 MetThrTyrTrpArgLysGluAsnIleAlaLysThrGluProProLysIlePheArgVal 143
Db      634 ATCAATTTGATCGTGATATATAAGTG---AAGCCCAATCCGCCACATATATTATCAGTG 690
QY      144 LysProValLeuGlyIleLysArgMetIleGlnIleGluTrpIleLysProGluLeuAla 163
Db      691 ATCAACTCAGACAGACTGTCTAGTATCTTAAATTAATGACATGAGCAACCACTCAATTAAG 750
QY      164 ProValSerSerAspLeuLysTyrThrLeuArgPheArgThrValAsnSerThrSerTrp 183
Db      751 AGTGTTATATA---CTAATAATTAACATTCATATATAGACCAAAAGATCCCTCACTTG 807
QY      184 MetGluValAsnPheAlaLysAsnArgLysAspLysAsnGlnThrTyrAsnLeuThrGly 203
Db      808 AGCCAGATTTCCT---CCTGAGACACAGCATCCACCCGATCTTCATCTCATCCCAAGAC 864
QY      204 LeuGlnProPheThrGluTyrValIleAlaLeuArgCysAlaValLysGluSerLys--- 222
Db      865 CTTAAACCTTTTACAGAAATATGTGTAGATTCCTGTATGACAGAAAGATGTAAAGGA 924
QY      223 PheTrpSerAspTrpSerGlnGluLysMetGlyMetThrGluGluGluAlaProCys--- 241
Db      925 TACTGAGTGACTGGAGTGAAGCAAGTGGGATCACCCTAATGATATGACATCTTAA 984
QY      242 GlyLeuGluLeuTrpArgValLeuLysProAlaGluAlaAspGlyArgArgProValArg 261
Db      985 GCACCAAGTTCTCGTATTAATAATAGATCATCCATCAAGCTTCAAGCTACAGACTGACAA 1044
QY      262 LeuLeuTrpLysLeuAlaArgGlyAlaProValLeuGluLysThrLeuGlyTyrAsnIle 281
Db      1045 CTCGGTGAAGACATGTCCTCTTTTGAAGCCAAATGGAATAATCTGGATTAAGAAGG 1104
QY      282 TrpTyrTyrProGluSerAsnThrAsnLeuThrGluThrMetAsnThrThrAsnGln 301
Db      1105 ACTCTCACAAGATGGAATATCACTTTACAAATTTACACAGTTAAAGCCCA-----AAA 1158
QY      302 LeuGluLeuIleLeuGlyLysGluSerPheTrpValSerMetLysSerTyrAsnSerLeu 321
Db      1159 CTGACAGTAACTCTCAAAATGATCGCTATCTAGCAACCCCTAAGATGAATCTTGTG 1218
QY      322 GlyLysSerProValAlaThrLeuArgIleProAlaIleGlnGluLysSerPheGlnCys 341
Db      1219 GGCAAATCGATGACAGCTGTTTAACTATCTATCCCTGCTGACTTTCAAAGCTTCAACCT 1278
QY      342 IleGluValMetGlnAlaCysValAlaGluAspGlnLeuValValLysTrpGlnSerSer 361
Db      1279 GTAAATGATCTTAAAGCATATCCCAAAAGATACATGCTTTGGGTGAATGAGACTCTCA 1338
QY      362 AlaLeuAspValAsnThrTrpMetIleGluTrpPheProAspValAspSerGluProThr 381
Db      1339 AGGGAATCTGAAGAATATATACTGAGTGCTGTGTGTATGATGAATGAACACCCCTGT 1398
QY      382 ThrLeuSerTrpGluSerValSerGlnAlaThrAsnTrpThrIleGlnIleAspLysLeu 401
Db      1399 ATCACAGACTGCAACCAAGAGATGTACCCGTGACCTGCACTTAATTAAGAGGAACCTTA 1458
QY      402 LysProPheTrpCysTyrAsnLysSerValTyrPrometLeuHisAspLysValGluGlu 421
Db      1459 GCAGAGAGCAATTCGATTGTGAACAAGTTACTCCAGTATAGCTGATGAGACCAAGAAC 1518
QY      422 ProTyrSerIleGlnAlaTyrAlaLysGluGlyValProSerGluGlyProGluThrLys 441
Db      1519 CCGAATCATTAAGGCACTAATCTTAAACAGGTCCACCTTCAAGAGACTCATGTGTCGG 1578
QY      442 ValGluAsnIleGlyValLysThrValThrIleThrTrpLysGluIleProLysSerGlu 461
Db      1579 ACAAAAAAGTAGGAAAAAAGCAAGCTGTCTTAGGTGGACCAACTTCCTGTGATGTT 1638

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Db 1219 GCGAAATCAGATGACGCTGTTTAACCTATCCCTGCTGATGCTTTCAGCTCAACCTCCT 1278
QY 342 ILeGIuValMeGIuAlaCyValAlaGIuAspGIuLeuValValIySTrGIuSerSer 361
Db 1279 GTAAATGATCTTAAAGCATTCCTCCCAAGATACAGTCTTGGGTGAGATGACTACTCCA 1338
QY 362 AlaleuAspValAsnThrTrpMetIleGIuTrpPheProAspValAspSerGIuProThr 381
Db 1339 AGGGAATCTGTAAAGAAATATATATATCTGAGTGGTGTGTATTCAGATTAAGCACCTGT 1398
QY 382 ThrLeuSerTrpGIuSerValSerGIuAlaThrAsnTrpThrIleGIuInAspIySLeu 401
Db 1399 ATCAGACACTGGCACAAGAAAGATGATGATCCGTGATCGACCTATTTAAGAGGAACTTA 1458
QY 402 LysProPheTrpCysTrpAsnIleSerValTrpProMetLeuHisAspIySValGIyGIu 421
Db 1459 GCGAGAGCAAAATGCTATTGATTAACGTTACTCCAGTATATGCTGATGACCAAGAAC 1518
QY 422 ProTrSerIleGIuAlaTrpAlaIySLeuGIyValProSerGIuGIyProGIuThrIyS 441
Db 1519 CTGAATCCATTAAGCATATCCTTAACAGATCCACCTTCCAAGACCTTACTGTTCCG 1578
QY 442 ValGIuAsnIleGIyValIySThrValThrIleThrTrpIySLeuIleProIySLeu 461
Db 1579 ACAAAAAAGTAGGAAAAAGAAAGCTGCTTGAAGTGGACCAACTTCTGTTGATGTT 1638
QY 462 ArgIySLeuIleIleCysAsnTrpThrIlePheTrpGIuAlaGIuGIyGIySLeuPhe 481
Db 1639 CAGAAATGATTTTACAGAAATTTATCTATTTTATTAAGAACCATCATGGAATGAACCT 1698
QY 482 SerIySThrValAsnSerSerIleLeuGIuTrpGIyLeuGIuSerLeuIySArgIySThr 501
Db 1699 GCTGTGAATGTGATTCCTCCACACAGATATACATTCCTTCTTGAAGTACACACA 1758
QY 502 SerTrpIleValGIuValMetAlaAsnThrSerAlaGIyGIyThrAsnGIyThrSerIle 521
Db 1759 TTGTACATGGTACGAATGCGACATACACAGATGAAGTGGAAAGTGTCCAGAAATTC 1818
QY 522 AsnPheIySThrLeuSerPheSerValPheGIuIleIleLeuIleThrSerLeuIleGIy 541
Db 1819 ACTTTTACTACCCCAAGTTT----- 1839
QY 542 GIyGIyLeuLeuIleLeuIleIleLeuThrValAlaTrpGIyLeuIySLeuProAsnIyS 561
Db 1840 -----GAA 1842
QY 562 LeuThrHisLeuCySTrProThrValProAsnProAlaGIuSerSerIleAlaThrTrp 581
Db 1843 TTAAAAAACAC-ATCTGGCTTAATGTTCAGATCCTTCAAAAGATCATATTGCCAGTGG 1901
QY 582 -----HisGIyAspAspPheIySAspIySLeu 590
Db 1902 TCACCTCACACTCCTCCAGGACCAATTTTAATTCAAAGATCAAAATG 1949

Search completed: February 23, 2005, 19:35:55
Job time : 343.186 secs

GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Run on: February 23, 2005, 09:15:27 ; Search time 1015.05 Seconds

(without alignments)
3796.488 Million cell updates/sec

Title: US-10-006-265-2

Perfect score: 3484

Sequence: 1 MKLSPQSCVNLGMMWTAL.....FTDEARTQEQKFRGKEMD 652

Scoring table:

	BLOSUM62
Xgapop 10.0 , Xgapext 0.5	
Ygapop 10.0 , Ygapext 0.5	
Fgapop 6.0 , Fgapext 7.0	
Delop 6.0 , Delext 7.0	

Searched: 5384158 seqs, 2955248155 residues

Total number of hits satisfying chosen parameters: 10768316

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:

-MODEL=frame+g2n.model -DEV=xlh
-DB=cn2_1/USPTO.spool/US1006265/runat_18022005_094659_22236/app_query.fasta_1.2069
-LOOPEXT=0 -LOOPEXT=0 -UNIT=bits -START=1 -END=1 -MATRIX=blomum62
-TRANS=human40.cdi -LIST=45 -DOCALLIGN=200 -THR SCORE=pct -THR MAX=100
-THR MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=pct -NORM=ext -HEAPSIZE=500 -MNLLEN=0
-MAXLEN=200000000 -USER=US1006265_@CN2_1_1175@runat_18022005_094659_22236
-NCPU=6 -ICPU=3 -NO MMAP -LARGEQUERY -NEG SCORES=0 -WAIT -DSPBIOCK=100
-LONGLOG -DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5
-FGAPOP=6 -FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

Published Applications NA:*

- 1: /cn2_6/ptodata/1/pubpna/US07_PUBCOMB.seq:*
- 2: /cn2_6/ptodata/1/pubpna/PCT_NEW_PUB.seq:*
- 3: /cn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq:*
- 4: /cn2_6/ptodata/1/pubpna/US06_PUBCOMB.seq:*
- 5: /cn2_6/ptodata/1/pubpna/US07_NEW_PUB.seq:*
- 6: /cn2_6/ptodata/1/pubpna/PCTUS_PUBCOMB.seq:*
- 7: /cn2_6/ptodata/1/pubpna/US08_NEW_PUB.seq:*
- 8: /cn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq:*
- 9: /cn2_6/ptodata/1/pubpna/US09A_PUBCOMB.seq:*
- 10: /cn2_6/ptodata/1/pubpna/US09B_PUBCOMB.seq:*
- 11: /cn2_6/ptodata/1/pubpna/US09C_PUBCOMB.seq:*
- 12: /cn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq:*
- 13: /cn2_6/ptodata/1/pubpna/US10A_PUBCOMB.seq:*
- 14: /cn2_6/ptodata/1/pubpna/US10B_PUBCOMB.seq:*
- 15: /cn2_6/ptodata/1/pubpna/US10C_PUBCOMB.seq:*
- 16: /cn2_6/ptodata/1/pubpna/US10D_PUBCOMB.seq:*
- 17: /cn2_6/ptodata/1/pubpna/US10E_PUBCOMB.seq:*
- 18: /cn2_6/ptodata/1/pubpna/US10F_PUBCOMB.seq:*
- 19: /cn2_6/ptodata/1/pubpna/US10_NEW_PUB.seq:*
- 20: /cn2_6/ptodata/1/pubpna/US11_NEW_PUB.seq:*
- 21: /cn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq:*
- 22: /cn2_6/ptodata/1/pubpna/US06_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	3484	100.0	2969	15	US-10-006-265-1
2	3451	99.1	2119	15	US-10-006-265-16
3	3451	99.1	2903	10	US-09-892-949-53
4	3451	99.1	2903	17	US-10-351-157-4
5	3451	99.1	2903	17	US-10-352-554-4
6	3451	99.1	2903	18	US-10-772-531-53
7	3441	98.8	2529	10	US-09-892-949-45
8	3441	98.8	2529	17	US-10-351-157-108
9	3441	98.8	2529	18	US-10-772-531-45
10	3435	98.6	2238	10	US-09-972-708-5
11	3435	98.6	2238	18	US-10-715-667-5
12	3435	98.6	2402	10	US-09-892-949-1
13	3435	98.6	2402	17	US-10-351-157-110
14	3435	98.6	2402	18	US-10-772-531-1
15	3435	98.6	2480	10	US-09-972-708-3
16	3435	98.6	2480	18	US-10-715-667-3
17	2850	81.8	2295	10	US-09-892-949-68
18	2850	81.8	2295	17	US-10-351-157-38
19	2850	81.8	2295	17	US-10-352-554-38
20	2850	81.8	2295	18	US-10-772-531-68
21	2810	80.7	1986	10	US-09-892-949-55
22	2810	80.7	1986	17	US-10-351-157-122
23	2810	80.7	1986	18	US-10-772-531-55
24	2779	79.8	1557	17	US-10-351-157-70
25	2779	79.8	1557	17	US-10-352-554-70
26	2758	79.2	1947	10	US-09-892-949-47
27	2758	79.2	1947	17	US-10-351-157-121
28	2758	79.2	1947	18	US-10-772-531-47
29	2758	79.2	2196	10	US-09-892-949-4
30	2758	79.2	2196	17	US-10-351-157-120
31	2758	79.2	2196	18	US-10-772-531-4
32	2606	74.8	2445	14	US-10-227-884-91
33	2606	74.8	2445	14	US-10-230-163-91
34	2606	74.8	2445	14	US-10-230-338-91
35	2606	74.8	2445	14	US-10-218-631-91
36	2606	74.8	2445	14	US-10-230-414-91
37	2606	74.8	2445	14	US-10-232-224-91
38	2606	74.8	2445	14	US-10-216-159A-91
39	2606	74.8	2445	14	US-10-218-849-91
40	2606	74.8	2445	14	US-10-227-873-91
41	2606	74.8	2445	14	US-10-227-883-91
42	2606	74.8	2445	14	US-10-219-076-91
43	2606	74.8	2445	14	US-10-230-434-91
44	2606	74.8	2445	14	US-10-219-003-91
45	2606	74.8	2445	14	US-10-219-075-91

ALIGNMENTS

RESULT 1
US-10-006-265-1

Sequence 1, Application US/1006265
Publication No. US20030125520A1

GENERAL INFORMATION:
APPLICANT: Maeda, Maatsugu
TITLE OR INVENTION: NOVEL HEMOPHILIN RECEPTOR PROTEIN, NR10
FILE REFERENCE: 06501-096001
CURRENT FILING DATE: US/10/006.265
PCT/JP00/03556
PRIOR FILING DATE: 2003-01-06
PRIOR APPLICATION NUMBER: PCT/JP00/03556
PRIOR FILING DATE: 2000-06-01
PRIOR APPLICATION NUMBER: JP 11/155797
PRIOR FILING DATE: 1999-06-02
PRIOR APPLICATION NUMBER: JP 11/217797
PRIOR FILING DATE: 1999-07-30
NUMBER OF SEQ ID NOS: 40
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 1

; LENGTH: 2969
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 ; FEATURE:
 ; NAME/KEY: CDS
 ; LOCATION: (523) ... (2478)
 ; US-10-006-265-1

Alignment Scores:

Pred. No.:	0	Length:	2969
Score:	3484.00	Matches:	652
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
	15	Gaps:	0

US-10-006-265-2 (1-652) x US-10-006-265-1 (1-2969)

QY 1 MetLysLeuSerProGlnProSerCysValAsnLeuGlyMetMetTrpThrTrpAlaLeu 20
 Db ATGAAGCTCTCCCGCCAGCTTCATGTGTAACTGGGAGATGATGACCTGGGCACTG 582
 QY 21 TrpMetLeuProSerLeuCysGlyPheSerLeuAlaAlaLeuProAlaLysProGluAsn 40
 Db TGAATGCTCCCTCAGCTGCAATTCAGCTGGCAGCTCTGCCAGCTAAGCCTGAGAAC 642
 QY 41 ILSerCysValTyrTyrTyrArgLysAsnLeuThrCysThrTrpSerProGlyLysGlu 60
 Db ATTTCCGTCTCACTACCTATAGAAAATTAACTCGCATCTTGAGCTCCAGAAAGGAA 702
 QY 61 ThrSerTyrThrGlnTyrThrValLysArgThrTyrAlaPheGlyGlyLysPheSer 80
 Db ACCAGTATATACCAGTACAGATTAAAGAACTTAAGCTTCGAGAAAACATGATTAAT 762
 QY 81 CysThrThrAsnSerSerThrSerGluAsnArgAlaSerCysSerPhePheLeuProArg 100
 Db TGTAACAACAATAGTTCTTACAAGTGAATAATCGTCTCGCTCTTTTCTTCACAGA 822
 QY 101 ILethrIleProAspAenTyrThrIleGluValGluAlaGluAsnGlyAspGlyValIle 120
 Db ATTAACATCCCAATTAATTTACATTGAGGTGGAGCTGAAAATGGAGATGGTGAAT 882
 QY 121 LysSerHisMetThrTyrTrpArgLeuGluAsnIleAlaLysThrGluProGlyLysIle 140
 Db AAATCTCATATGACATCTGAGATTAGAAACATAGCGAAACTGAACACCTTAAGATT 942
 QY 141 PheArgValLysProValLeuGlyIleLysArgMetIleGlnIleGluTrpIleLysPro 160
 Db TTCCGTGTGAACCAAGTTTGGGCAATCAACGAATGATTCAAATGTGAATGAATAAAGCT 1002
 QY 161 GluLeuAlaProValSerSerAspLeuLysTyrThrLeuArgPheArgThrValAsnSer 180
 Db GATTTGGCGCTGTTTCATCTGATTTAAATACACACTTCGATTCCAGAACAGTCAACAGT 1062
 QY 181 ThrSerTrpMetGluValAsnPheAlaLysAsnArgLysAspLysAsnGlnThrTyrAsn 200
 Db ACCAGCTGATGAGAACTCACTTCGTAAGAACCGTAAGATTAACCAACAGTCAAC 1122
 QY 201 LeuThrGlyLeuGlnProPheThrGluTyrValIleAlaLeuArgCysAlaValLysGlu 220
 Db CTACAGGGGCTGAGCCCTTTTACAGATATGTCATAGCTCTGCGATGTGGGTCACAGAG 1182
 QY 221 SerLysPheTrpSerAspTrpSerGlnGluLysMetGlyMetThrGluGluGluAlaPro 240
 Db TCAAAGTTCTGGAGTACTGAGCCCAAGAAAATGGGAATGACTGAGGAAGAGCTCCA 1242
 QY 241 CysGlyLeuGluLeuTrpArgValLysLysProAlaGluAlaAspGlyArgArgProVal 260
 Db TGTGGCTGGAACGTGTGAGAGTCTCTGAACACAGCTGAGCGGATGGAAAGAGCCAGTG 1302
 QY 261 ArgLeuLeuTrpLysLysAlaArgGlyAlaProValLeuGluLysThrLeuGlyTyrAsn 280
 Db CGGTTGTATGAGAAAGGCAAGAGAGGCCAGTCTTACAGAAAACACTTGGCTACAAAC 1362

QY 281 ILethrTyrTrpProGluSerAsnThrAsnLeuThrGluThrMetAsnThrThrAsnGln 300
 Db ATATGGTACTATCCAGAAAGCAACTAACCTCAGAGAAACATGACACTTAACCAAG 1422
 QY 301 GlnLeuGluLeuHisLeuGlyGlyLysSerPheTrpValSerMetIleSerTyrAsnSer 320
 Db CAGCTTGAACCTCATCTGGAGCGGAGACTTTTGGGTGTCTATGATTTCTTAATAATTC 1482
 QY 321 LeuGlyLysSerProValAlaThrLeuArgIleProAlaIleGlnGluLysSerPheGln 340
 Db CTGGGAATCTCCAGTGGCCACCTGAGAGATTCCAGCTATTCAAGAAAAATCATTTCCG 1542
 QY 341 CysIleGluValMetGlnAlaCysValAlaGluAspGlnLeuValValLysTrpGlnSer 360
 Db TGCATTGAGTATGAGAGCGCTGCTGTGAGACACAGCTAGTGGTGAAGTGGCAAC 1602
 QY 361 SerAlaLeuAspValAsnThrTrpMetIleGluTrpPheProAspValAspSerGluPro 380
 Db TCTGCTCTAGACGTGAACACTTGATGATGATGATTCGGAATGTGACTCAGAGCCC 1662
 QY 381 ThrThrLeuSerTrpGluSerValSerGlnAlaThrAsnTrpThrIleGlnGluAspLys 400
 Db ACCACCTTCTCGGGAATCTGTCTCAGGCCAGCAAGTGAACATCCAGCAAGATAAA 1722
 QY 401 LeuLysProPheTrpCysTyrAsnIleSerValTyrProMetLeuHisAspLysValGly 420
 Db TTAACAACCTTCTCGGTGCTATTAACATCTCTGTATCCAAATTTGATACAAAGTTGGC 1782
 QY 421 GluProTyrSerIleGlnAlaTyrAlaLysGluGlyValProSerGluGlyProGluThr 440
 Db GAGCCATATTCATCCAGCTTATGCAAGAGGCGTTCATCAGAGGCTCCTGAGACC 1842
 QY 441 LysValGluAsnIleGlyValLysThrValThrIleThrTrpLysGluIleProLysSer 460
 Db AAGGTGAACAACATTTGGCGTGAAGACGTCAAGATCACTGGAAGAAGATTCACAGACT 1902
 QY 461 GluArgLysGlyIleIleCysAsnTyrThrIlePheTyrGlnAlaGluGlyLysGly 480
 Db GAGAGAAAGGTATCATCTGCAACTACACCACTTTTACCAAGCTGAAAGTGGAAAGGA 1962
 QY 481 PheSerLysThrValAsnSerSerIleLeuGlnTyrGlyLeuGluSerLeuLysArgLys 500
 Db TTCTCCAGACAGTCAATTCAGCACTTTCAGTACGCGCTGGAGTCCCTGAAACCAAAAG 2022
 QY 501 ThrSerTrpIleValGlnValMetAlaAsnThrSerAlaGlyLysThrAsnGlyThrSer 520
 Db ACCTCTTACATTTGATGATCAAGGCAACAGCTGGGAGAACCAACGAGACACAGC 2082
 QY 521 IleAsnPheLysThrLeuSerPheSerValPheGluIleIleLeuIleThrSerLeuIle 540
 Db ATTAATTTCAAGACATTTGATCACTTCAAGTGTCTTGAGATTATCTCATTACTTCGATT 2142
 QY 541 GlyGlyGlyLeuLeuIleLeuIleIleLeuThrValAlaTyrGlyLeuLysLysProAsn 560
 Db GGTGAGGCGCTTCTTATTTCTCATTTCCGACAGTGGCATATGATGCTCAAAAAACCAAC 2202
 QY 561 LysLeuThrHisLeuCysThrProThrValProAsnProAlaGluSerSerIleAlaThr 580
 Db AATATGATCATCTGTGTGGCCACCGTTCACACCTCGTGAAGATGATTAAGCAACA 2262
 QY 581 TrpHisGlyAspAspPheLysAspLysLeuAsnLeuLysGluSerAspAspSerValAsn 600
 Db TGGCATGAGATGATTTCAAGATTAAGCTTAACCTGAAGAGATCTGATGACTCTGTGAAC 2322
 QY 601 ThrGluAspArgIleLeuLysProCysSerThrProSerAspLysLeuValIleAspLys 620
 Db ACAGAAAGACAGATCTTAACCAATGTTCCACCCCAAGTGAACAAATGGTGTGATTGACAAG 2382
 QY 621 LeuValValAsnPheGlyAsnValLeuGlnGluIlePheThrAspGluAlaArgTrpArg 640
 Db TTGGTGTGTAACCTTTGGGAATGTCTGCAAGAAATTTTCAAGATGAACCGAAGAGGAT 2442

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Qy      641 GInGluLySGlnPheArgArgGlyLySGluTrpAsp 652
Db      2443 CAGGAAAAACAATTATGAGGGGAAAAAGATGGAC 2478

RESULT 2
US-10-006-265-16
; Sequence 16, Application US/10006265
; Publication No. US20030125520A1
; GENERAL INFORMATION:
; APPLICANT: Maeda, Masatsugu
; APPLICANT: Yaguchi, No. US20030125520A1ko
; TITLE OF INVENTION: NOVEL HEMOPOIETIN RECEPTOR PROTEIN, NR10
; FILE REFERENCE: 06501-096001
; CURRENT APPLICATION NUMBER: US/10/006,265
; PRIOR FILING DATE: 2003-01-06
; PRIOR APPLICATION NUMBER: PCT/JP00/03556
; PRIOR FILING DATE: 2000-06-01
; PRIOR APPLICATION NUMBER: JP 11/155797
; PRIOR FILING DATE: 1999-06-02
; PRIOR APPLICATION NUMBER: JP 11/217797
; PRIOR FILING DATE: 1999-07-30
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 16
; LENGTH: 2119
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (11) ... (1996)
US-10-006-265-16

Alignment Scores:
Pred. No.: 0          Length: 2119
Score: 3451.00       Matches: 650
Percent Similarity: 99.85%   Conservative: 1
Best Local Similarity: 99.69%   Mismatches: 1
Query Match: 99.05%          Indels: 1
DB: 15                  Gaps: 0

US-10-006-265-2 (1-652) x US-10-006-265-16 (1-2119)
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Qy      21 TrpMetLeuProSerLeuCysLySphSerLeuAlaAlaLeuProAlaLySProGluLsn 40
Db      71 TGGATGCTCCCTCCTCCTGCAAAATTCAAGCTGGGAGCTGGCCAGCTTAAGCTGAGAAC 130
Qy      41 LLeSerCysValTyrTyrTrpArgLysAenLeuThrCysThrTrpSerProGlyLySGlu 60
Db      131 ATTCTCTGCTCTACTACTATAGGAAAAATTAACTCACTGAGATCGCAAGGAAAGGAA 190
Qy      61 ThirSerTyrThnGlnTyrThrValLysArgThrTyrAlaPheGlyGluLySHisAspAsn 80
Db      191 ACCGATTATACCCAGTACACAGTTAAGAACTTACGCTTTTGGAGAAAAACATGATATAT 250
Qy      81 CysThrThrAsnSerSerThrSerGluAsnArgAlaSerCysSerPhePheLeuProArg 100
Db      251 TGTACAACCAATAGTCTTCAAGTGAATAATCGCTGCTGCTCTTTTCTCTTCCACAGA 310
Qy      101 LLeThrLLeProAspAenTyrThrLLeGluValGluAlaGluAenGlyAspGlyValLLe 120
Db      311 ATAACGATCCAGATAATTAATACATTAGAGGTGAAGTGAATAATGGAGATGTGTATAT 370
Qy      121 LysSerHisMetThrTyrTrpArgLysGluAenLLeAlaLysThrGluProProLysLLe 140
Db      371 AAATCTCATATGACACTGAGATTAAGAACATAGGAAAACTGAACCACTTAAGATT 430
Qy      141 PheArgValLySProValLeuGlyLLeLySArgMetLLeGlnLLeGluTrpLLeLySPro 160
Db      431 TTCCGTGTGAACCAAGTTTGGGCAATCAACGAATGATTCAATTGAATGATTAAGCT 490

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Qy      161 GluLeuAlaProValSerSerAspLeuLysTyrThrLLeuArgPheArgThrValAsnSer 180
Db      491 GAGTTGGGCGCTGTTCACTGATTTAAATACACACTTCGATTCAGAGCACTCAACGT 550
Qy      181 ThrSerTrpMetGluValAsnPheAlaLysAsnArgLySAspLySAsnGlnThrTyrAsn 200
Db      551 ACCAGCTGATGAGAAAGTCAACTTCGCTTAAGAACCTTAAGATTAAGTAACCAACGATACAC 610
Qy      201 LeuThrGlyLeuGlnProPheThrGluTyrValLLeAlaLeuArgCysAlaValLySGlu 220
Db      611 CTACGGGGGCTGCAGCCCTTTTACAGAAATATGCTATAGCTCGCATGTGCCGTCAAGAG 670
Qy      221 SerLySPhetTrpSerAspTrpSerGlnGlyLysMetGlyMetThrGlnGluAlaPro 240
Db      671 TCAAGTTCTGAGTGAAGTGAAGCAAGAAAAATGGAAATGAGTGAAGAAAGAGCTCA 730
Qy      241 CysGlyLeuGlnLeuTrpArgValLeuLySProAlaGluAlaAspGlyArgArgProVal 260
Db      731 TGTGGCTGGAACCTGTGAGAGTCTCTGAACCACTGAGGGCGGATGAAAGAGCCAGTG 790
Qy      261 ArgLeuLeuTrpLySValArgGlyValaProValLeuGlnLySLeuGlyTyrAsn 280
Db      791 CGATTGTTATGAGAAAGCAAGAGAGAGCCCAAGTCTAGAGAAAAACATTGGCTACAC 850
Qy      281 LLeTrpTyrTyrProGlnLysThrAsnLeuThrGluThrMetAenThrThrAsnGln 300
Db      851 ATATGATACATACCAAGAAAGCAACACTTCAACAGAAACATGAACATCACTAACACAG 910
Qy      301 GlnLeuGluLeuHisLeuGlyGlyLysSerPheTrpValSerMetLLeSerTyrAsnSer 320
Db      911 CAGCTTGAACCTGCATCTGGAGGGGAGAGCTTTGGGTGTATGATTTCTTATATCTT 970
Qy      321 LeuGlyLySProValaLLeThrLeuArgLLeProAlaLLeGlnGlyLySLeuSerPheGln 340
Db      971 CTGGGAAAGTCTCCAGTGGCCACCTGAGATTCAGCTATTCAGAAAAATCAATTTGAG 1030
Qy      341 CysLLeGluValMetGlnAlaCysValAlaGluLysAsnGlnLeuValValLySTrpGlnSer 360
Db      1031 TGCATGTGATGATGACAGGCTGCTGTGTGAGGACCAAGCTTATGTGAATGTGCACAAAGC 1090
Qy      361 SerAlaLeuAspValaLLeThrTrpMetLLeGluTrpPheProAspValaAspSerGluPro 380
Db      1091 TCTGCTCAAGCGTGAACACTTGATGATTAAGTTTCCGATGTGAGATCAGAGGCC 1150
Qy      381 ThrThrLeuSerTrpGlnLysSerValaLLeThrAsnTrpThrLLeGlnLysAspLyS 400
Db      1151 ACCACCTTTCTCGGAATCTGTCTCAGGCCACGAACGATGACGATCCAGCAAGATTA 1210
Qy      401 LeuLySProPheTrpCysTyrAsnLLeSerValTyrProMetLeuHisAspLySValGly 420
Db      1211 TTAAACCTTTCTGTGCTATACATCTGTGTATCAATGTTGACATGAACAAAGTTGGC 1270
Qy      421 GluProTyrSerLLeGlnAlaTyrAlaLySGluGlyValaProSerGlnGlyLLeProLysSer 440
Db      1271 GAGCCATATTCATCCAGGCTTATGCCAAAGAGCGTTCCATATGAAAGGTCTGAGACC 1330
Qy      441 LysValaGluAenLLeGlyValLySThrValThrLLeThrTrpLySGluLLeProLysSer 460
Db      1331 AAGGTGAGAAACATTTGGCGTGAAGACGTCACATGATCAATGAAGAAAGATTCCCAAGAGT 1390
Qy      461 GluArgLySGlyLLeLLeCysAsnTyrThrLLePheTyrGlnAlaGluGlyLySGly 480
Db      1391 GAGAGAAAGGGTATCATCTGACATCAACATCTTTTACCAAGCTGAAGGGTGAAGAAAGGA 1450
Qy      481 PheSerLySThrValaLLeAsnSerSerLLeGlnTyrGlyLeuGlnLLeLySLeuLySArgLyS 500
Db      1451 TTCTCCAGACAGTCAATTCAGCATCTTGACATGAGCGCTCGAGTCCCTGAAACGAAG 1510
Qy      501 ThrSerTyrLLeValaGlnValaMetAlaAsnThrSerAlaGlyLLeThrAsnGlyLLeSer 520
Db      1511 ACCTCTTAACATTTGTTCAAGTCAATGATGCGCAGCCAGCTGTGGGGGAAACCAAGGGACAGC 1570

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QY 521 lLeasnPhelysThreuserPheserValphegluilelleleuileThrserleulle 540
 Db 1571 ATAAATTTCAAGACATTTGATTCAGTGCTTTGAGATTATCTCATTAATCTTCGATT 1630
 QY 541 GLYGLYGLYleuileullelleleuThValAlaTyGLYleuylsProasn 560
 Db 1631 GGTGGAGGCTCTTATTCATTATTCGACAGTGCAATGCTCTCAAAAAACCAAC 1690
 QY 561 lyeleuThrsileuCystrProthrValProasnProAlaguserSerilealatr 580
 Db 1691 AAATGACTATCTGTTTGCCACCGCTTCCACCCCTGCTGAAGATATAGCCACA 1750
 QY 581 TrpHieGLYAspAspPheylsAspLySleuasnleuylsGLuserAspAspSerValasn 600
 Db 1751 TGGCATGGAGATGATTTCAAGATTAAGCTTAACCTGAAGAGCTGATGACTCTGTAAC 1810
 QY 601 ThrGLuAspArglileuylsProCyserThrProserAspLySleuValileAspLyS 620
 Db 1811 ACAGAAAGACAGGATCTTAAACATGTTCCACCCCAAGTCAAGATGGATTCAGAAC 1870
 QY 621 leuValValasnPhelyasnValleuGluilelPheThrAspGluAlaTyThrGly 640
 Db 1871 TTGGTGGTGAACCTTGGAATGTTCTGCAGAAATTTTCACAGATGAAGCCAGAACGGGT 1930
 QY 641 GlnGluLysGlnPheArgArgLySGLuTrpAsp 652
 Db 1931 CAGGA-AAACAATTTAGAGGAGGAAAAAGATGGGAC 1965

RESULT 3

US-09-892-949-53
 ; Sequence 53, Application US/09892949
 ; Publication No. US20030096339A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Sprecher, Cindy A.
 ; APPLICANT: Premeil, Scott R.
 ; APPLICANT: Gao, Zeren
 ; APPLICANT: Whitmore, Theodore E.
 ; APPLICANT: Kuiper, Joseph L.
 ; APPLICANT: Maurer, Mark F.
 ; TITLE OF INVENTION: CYTOKINE RECEPTOR ZCYTOR17
 ; FILE REFERENCE: 00-42
 ; CURRENT APPLICATION NUMBER: US/09/892,949
 ; CURRENT FILING DATE: 2001-06-26
 ; PRIOR APPLICATION NUMBER: US 60/214,282
 ; PRIOR FILING DATE: 2000-06-26
 ; PRIOR APPLICATION NUMBER: US 60/214,955
 ; PRIOR FILING DATE: 2000-06-29
 ; PRIOR APPLICATION NUMBER: US 60/267,963
 ; PRIOR FILING DATE: 2001-08-02
 ; NUMBER OF SEQ ID NOS: 93
 ; SOFTWARE: FastSeq for Windows Version 3.0
 ; SEQ ID NO 53
 ; LENGTH: 2903
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 ; FEATURE:
 ; NAME/KEY: CDS
 ; LOCATION: (497) ... (2482)
 US-09-892-949-53

Alignment Scores:

Pred. No.: 0 Length: 2903
 Score: 3451.00 Matches: 650
 Percent Similarity: 99.85% Conservative: 1
 Best Local Similarity: 99.69% Mismatches: 1
 Query Match: 99.05% Indels: 1
 DB: 10 Gaps: 0

US-10-006-265-2 (1-652) x US-09-892-949-53 (1-2903)

QY 1 MetLysLeuSerProGlnProSerCyValAlasnleuGlyMetMetTrpThrPalaleu 20
 Db 497 ATGAAGCTCTCTCCCGACCTTCATGTGTAACTGGGAGATGATGGAACCTGGGCACTG 556

QY 21 TrpMetLeuProSerLeuCyLysPheSerLeuAlaAlaLeuProAlaLysProGluasn 40
 Db 557 TGAATGCTCCCTTCACCTCGCAAAATTCACCTCGGAGAGCTGCTCCAGCTTAAGCTAGAAC 616
 QY 41 lIeserCyValaTyTyTrpArgLysasnleuThrCyThrTrpSerProGlyLysGlu 60
 Db 617 ATTTCTGTGCTACTACTAATAGAAAAATTTAACTCGACATGGAGTCCAGAAAAAGAA 676
 QY 61 ThrSerTyThrGluTyThrValLysArgThrTrpAlaPheGlyGluLysHisAspasn 80
 Db 677 ACCAGTTATACCAGTACACAGTAAAGAACTTACGCTTTGGAGAAAAACATGATAT 736
 QY 81 CystrThrAsnSerSerThrSerGluasnArgAlaSerCySerPhePheLeuProArg 100
 Db 737 TGTAACAACCAATAGTTCTTACAGATGAAAAATCGTCTGTCTTTTCTCTCCAGAA 796
 QY 101 lIethrIleProAspAsnTyThrIleGluValGluAlaGluasnGlyAspGlyValIle 120
 Db 797 ATACAGATCCAGATTAATTAATACATTGAGTGGAAGCTGAATAATGAGATGGTAAAT 856
 QY 121 LysSerHisMetThrTyThrArgLeuGluasnIleAlaLysThrGluProProLysIle 140
 Db 857 AAATCTCATATGACATTAATGAGATTAGAACATAGCAAAACCTGAACCACTTAAGAT 916
 QY 141 PheArgValLysProValLeuGlyLysArgMetIleGlnIleGluTrpIleLysPro 160
 Db 917 TTCGGTGAAACCAAGCTTTGGGCATCAACCAATGATTCAATTAATGAATGAAGTAAAGCT 976
 QY 161 GluLeuAlaProValLysSerSerAspLeuLysTyThrLeuArgPheArgThrValAsnSer 180
 Db 977 GAGTTGGCGCCTGTTTCATCTGATTTAAATCACACCTTCGATTACAGGACACTCAACGT 1036
 QY 181 ThrSerTrpMetGluValAsnPhelAlaLysAsnArgLysAspLysAsnGlnThrTyAsn 200
 Db 1037 ACCAGCTGATGAGATCAACTTCCTGAAGAACCGTAAGATTAACCAACGTAAC 1096
 QY 201 LeuThrGlyLeuGlnProPheThrGluTyValIleAlaLeuArgCysAlaValLysGlu 220
 Db 1097 CTCACGGGCTCGACGCTTTTACAGATATGTCATAGCTCTCGCATGCTGCTCAAGAG 1156
 QY 221 SerLysPheTrpSerAspTrpSerGlnGluLysMetGlyMetThrGluGluGluAlaPro 240
 Db 1157 TCAAGTTCTGAGATGACATGAGCAACAAAAATGGGAATGATCGAGGAAGAACGCTCA 1216
 QY 241 CySGlyLeuGlnLeuTrpArgValleuLysProAlaGluAlaAspGlyArgArgProVal 260
 Db 1217 TGTGGCTGGAACTGTGAGAGTCTGAAACCAAGCTGAGGCGGATGGAAGAGCCAGTG 1276
 QY 261 ArgLeuLeuTrpLysLeuAlaArgGlyAlaProValLeuGluLysThrLeuGlyTyraen 280
 Db 1277 CGGTTCTTATGGAAGAAAGCAAGAGAGCCCAAGTCTTAGAATAAACCTTGGCTACAAAC 1336
 QY 281 lIeTrpTyTyTrpProGluSerAsnThrAsnleuThrGluThrMetAsnThrThrAsnGln 300
 Db 1337 ATATGCTACTATCCAGAAAGCAACCTAACCTCACAGAAACATGAACCTACTAACCG 1396
 QY 301 GlnLeuGluLeuHisleuGlyGlyLysSerPheTrpValSerMetLysSerTyraenSer 320
 Db 1397 CAGCTTGAACCTGATCTGGGAGCGAGAGCTTTGGGTGCTATGATTTCTTAATAATT 1456
 QY 321 LeuGlyLysSerProValAlaThrLeuArgIleProAlaIleGlnGluLysSerPheGln 340
 Db 1457 CTGGGAATCTCCAGCTGCGCAACCTGAGAGATTCACAGCATTCAGAAAAAACATTTCCG 1516
 QY 341 CySileGluValMetGlnAlaCyValAlaGluAspGlnLeuValValLysTrpGlnSer 360
 Db 1517 TGCATTTAGAGTCATGAGGCTGCGTGTGAGAGCAAGCTAGTGTGAAGTGGCAAAAGC 1576
 QY 361 SerAlaLeuAspValAsnThrTrpMetIleGluTrpPheProAspValAspSerGluPro 380
 Db 1577 TCTGCTCTGAGAGGTGAACCTTGATGATGATGATTTCCGAGATGTGACTCAGAGCCC 1636

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QY 381 ThrThrLeuSerTrpGluSerValSerGlnAlaThrAsnTrpThrIleGlnGlnAspLys 400
DB 1637 ACCACCCTTCTCGGAATCTGTGTCTCAGGCCACAACTGACGATCCAGCAAGTAA 1696
QY 401 LeuLysProPheTrpCysTyrAsnIleSerValTyrProMetLeuHisAspLysValGly 420
DB 1697 TTAACCACTTCTGGGTATTAACATCTGTGTATCAATGTTCATGATGACAAAGTTGAC 1756
QY 421 GluProTyrSerIleGlnAlaTyrAlaLysGluGlyValProSerGluGlyProGluThr 440
DB 1757 GAGCAATATTCATCCAGGCTTATGCAAGAAAGAGGGCTTCATCAAAAGTCTCTGAGAC 1816
QY 441 LysValGluAsnIleGlyValLysThrValThrIleThrTrpLysGluIleProLysSer 460
DB 1817 AAGGTGGAACATTCGCGCTGAAAGCGTCACGATCACTGAAAGAGATCCCAAGACT 1876
QY 461 GluArgLysGlyIleIleCysAsnTyrThrIlePheTyrGlnAlaGluGlyGlyGly 480
DB 1877 GAGAGAAAGGTATCATCTGCAACTCACCATCTTTTACCAAGCTGAAGTGGAAGAA 1936
QY 481 PheSerLysThrValAsnSerSerIleLeuGlnTyrGlyLeuGluSerLeuLysArgLys 500
DB 1937 TTCTCCAAACAGTCATTCAGCATCTTGACAGTACGGCTGAGTCCCTGAAACGAAAG 1996
QY 501 ThrSerTyrIleValGlnValMetAlaAsnThrSerAlaGlyGlyThrAsnGlyThrSer 520
DB 1997 ACCTCTTACATTTGTCAGTCTACGGCACACACAGTCTGGGGGAAACCAACGGAGCAC 2056
QY 521 IleAsnPheLysThrLeuSerPheSerValPheGluIleIleLeuIleThrSerLeuIle 540
DB 2057 ATAAATTCACAGACATGTGCTAGTGTCTTGAGATTATCTCTAATCTCTGAT 2116
QY 541 GlyGlyGlyLeuLeuIleLeuIleIleLeuThrValAlaTyrGlyLeuLysLysProAsn 560
DB 2117 GGTGAGGCGCTTATTCATTCATTCCTGACAGTGGCATATGCTCTCAAAACCCAAC 2176
QY 561 LysLeuThrHisIleLeuCysTrpProThrValProAsnProAlaGluSerSerIleAlaThr 580
DB 2177 AATGATCTCATCTGTGTGGCCACCGTCCCAACCTGCTGAAAGTATGATGACCA 2236
QY 581 TrpHisGlyAspAspPheLysAspLysLeuAsnLeuLysGluSerAspAspSerValAsn 600
DB 2237 TGGCATGGAGATGATTCACAGATTAAGCTAAACCTGAAGAGTCTGATCCTGTGAAC 2296
QY 601 ThrGluAspArgIleLeuLysProCysSerThrProSerAspLysLeuValIleAspLys 620
DB 2297 ACAGAAAGCAGGATCTTAAACCATGTTCCACCCAGTGAACAACTGGTGTGATGACAA 2356
QY 621 LeuValIleAsnPheGlyAsnValIleGlnGluIlePheThrAspGluAlaArgThrGly 640
DB 2357 TTGGTGTGAACTTTGGGAATGTTCTGCAAGAAATTTTCAACAGATGAACCAAGCGGT 2416
QY 641 GlnGluLysGlnPheArgArgGlyLysGluTrpAsp 652
DB 2417 CAGGA-AAACAATTTAGGAGGGGAAAGAAATGGAC 2451

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; FILE REFERENCE: 02-02
; CURRENT APPLICATION NUMBER: US/10/351,157
; PRIOR FILING DATE: 2003-01-21
; PRIOR APPLICATION NUMBER: US 60/435,361
; PRIOR FILING DATE: 2002-12-19
; PRIOR APPLICATION NUMBER: US 60/389,108
; PRIOR FILING DATE: 2002-06-14
; PRIOR APPLICATION NUMBER: US 60/350,325
; PRIOR FILING DATE: 2002-01-18
; NUMBER OF SEQ ID NOS: 183
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 2903
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (497)...(2482)
US-10-351-157-4

Alignment Scores:
Pred. No.: 0 Length: 2903
Score: 3451.00 Matches: 650
Percent Similarity: 99.85% Conservative: 1
Best Local Similarity: 99.69% Mismatches: 1
Query Match: 99.05% Indels: 1
DB: 17 Gaps: 0

US-10-006-265-2 (1-652) x US-10-351-157-4 (1-2903)
QY 1 MetLysLeuSerProGlnProSerCysValAsnLeuGlyMetMetTrpThrTrpAlaLeu 20
DB 497 ATGAAGCTCTCTCCCAAGCTTTCATGTGTAACTGGGGAATGATGAACCTGGGCACTG 556
QY 21 TrpMetLeuProSerLeuCysLysPheSerLeuAlaLeuProAlaLysProGluAsn 40
DB 557 TGGAGTCCCTTCACTCTGCAAAATTCAGCTGGGAGCTGCCAGCTAAAGCTGAGAAC 616
QY 41 IleSerCysValIleTyrTyrArgLysAsnLeuThrCysThrTrpSerProGlyLysGlu 60
DB 617 ATTTCTGTGTCTACTACTATAGGAAATTTAACTGTCACCTGGAGTCCAGAAAGAA 676
QY 61 ThrSerTyrTrpGlnIleThrValLysArgThrTyrAlaPheGlyLysLysAspAsn 80
DB 677 ACCAGTTATACCAGTACACAGTTAAGAACTTACGTTTGAAGAAACATGATATAT 736
QY 81 CysThrThrAsnSerSerThrSerGluAsnArgLaseCysSerPhePheLeuProArg 100
DB 737 TGTACAAACCAATAGTCTACAAAGTGAATGTGTCTCTCTTTTCTCTCCAAAG 796
QY 101 IleThrIleProAspAsnTyrThrIleGluValAlaGluAsnGlyAspGlyValIle 120
DB 797 ATTAAGATCCAGATTAATTATACCATGAGGTGAAGCTGAATAATGAGATGTAATT 856
QY 121 LysSerHisMetTrpTyrTrpArgLeuGluAsnIleAlaLysThrGluProProLysIle 140
DB 857 AAATCTCATATGACATCTGAGATTTAGAGAACTAGAGAAACCTGAACCACTTAAGATT 916
QY 141 PheArgValLysProValIleGluIleLysArgMetIleGlnIleGluTrpIleLysPro 160
DB 917 TTCCGTGTGAACCAAGTTTGGGCACTCAAGAGATGATTCAAATTGAATGATTAAGCT 976
QY 161 GluLeuAlaProValIleSerSerAspLeuLysTyrThrLeuArgPheArgThrValAsnSer 180
DB 977 GAGTTGGCGCTGTTTCATCTGATTTAAATACACACTCGATTCAAGACAGTCAACAGT 1036
QY 181 ThrSerTrpMetGluValAsnPheAlaLysAsnArgLysAspLysAsnGlnThrThrAsn 200
DB 1037 ACCAGCTGGATGAAGTCAACTTGTGTAAGAACGTAAGGATTAACCAACCTACAC 1096
QY 201 LeuThrGlyLeuGlnProPheThrGluTyrValIleAlaLeuArgCysAlaValLysGlu 220
DB 1097 CTCACGGGGCGTCAAGCTTTTACGAATATGTCTACTGCGATGTGCGGTACAGAG 1156

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QY 221 SerIysPheTrpSerAspTrpSerGlnGluYsMeGlyMetThrGlnGlnGlnAlaPro 240
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QY 241 CysGlyLeuGlnLeuTrpArgValLeuLysProAlaGlnAlaAspGlyArgArgProVal 260
Db 1217 TGTGGCTGTGAACGTGGAGAGTCTGGAAACAGCTGAGGCGGATGGAAAGAGCCAGAGT 1276
QY 261 ArgLeuLeuTrpLysLysAlaArgGlyAlaProValLeuGlnLysTrpLeuGlnYTrpAsn 280
Db 1277 CGGTGTATTGAGAAAGAGCAAGAGAGGCCCTGCTTACAGAAACACTTGCTGCTACAC 1336
QY 281 IleTrpYTrpProGlnSerAsnTrpAsnLeuThrGlnThrMetAsnThrThrAsnGln 300
Db 1337 ATATGGTACTATCCAGAAAGCAACACTAACCTCAGAAACCAATGAACTTAACCCAG 1396
QY 301 GlnLeuGlnLeuHisLeuGlnGlyGlnSerPheTrpValSerMetIleSerYTrpAsnSer 320
Db 1397 CAGCTTGAACCTGATCTGGAGAGCGAGAGCTTTGGGTGTCTATGATTTCTTATTAATTC 1456
QY 321 LeuGlyLysSerProValAlaThrLeuArgIleProAlaIleGlnGlnLysSerPheGln 340
Db 1457 CTGGGAAAGTCTCAGTGGCCAGCCAGGAAATTCAGCTATTCAGAAATAATCATTTCCAG 1516
QY 341 CysIleGlnValMetGlnAlaCysValAlaGlnAspGlnLeuValValLysTrpGlnSer 360
Db 1517 TGCATTGAGGTCAATGACAGCGCTCGCTTGTGAGAGCACAGCTAATGAGTGGCAAGC 1576
QY 361 SerAlaLeuAspValAlaThrTrpMetIleGlnTrpPheProAspValAspSerGlnPro 380
Db 1577 TCTGCTCTAGACCTGAAACCTTGATGATGATGATGATGATGATGATGATGATGATGAT 1636
QY 381 ThrThrLeuSerTrpGlnSerValSerGlnAlaThrAsnTrpThrIleGlnGlnAspLys 400
Db 1637 ACCACCTTCTCTGGGAAATGTGTCTCAGGCCACAGAACTGGACGATCCAGCAAGATAA 1696
QY 401 LeuLysPhePheTrpCysYTrpAsnIleSerValYTrpMetLeuHisAspLysValGly 420
Db 1697 TTAAACCTTCTGTGGTCTATTAACATCTGTGTATCAATGTTGATGACAAAGTTGGC 1756
QY 421 GluProTrpSerIleGlnAlaYTrpAlaLysGlnGlyValProSerGlnGlyProGlnThr 440
Db 1757 GAGCCATATTCATCCATCCAGGCTTATGCCAAAGAGGCTTCCATCAGAGGCTCTGAGACC 1816
QY 441 LysValGlnAsnIleGlyValLysThrValThrIleThrTrpLysGlnIleProLysSer 460
Db 1817 AAGGTGAGAACATTTGGCGTGAAGAGGTCACATTCATGAAAGAGATTTCCAAAGAGT 1876
QY 461 GluArgLysGlyIleIleCysAsnYTrpIlePheTrpGlnAlaGlnGlyGlyLysGly 480
Db 1877 GAGAGAAAGGATCATCTGCACTACACATCTTTTACCAAGCTGAGAGTGAAGAAAGAG 1936
QY 481 PheSerLysThrValLysSerSerIleLeuGlnYTrpGlyLeuGlnSerLeuLysArgLys 500
Db 1937 TTCTCCAAAGCACTCATCTGACATCTTGACATAGCGGCTTGAGAGTCCCTGAAACCAAG 1996
QY 501 ThrSerTrpIleValGlnValMetAlaAsnThrSerAlaGlyGlyThrArgGlyTrpSer 520
Db 1997 ACCTTCTTACCTTTTCAAGTCAAGGCAAGCAAGAGCTGAGGAGAAACCAAGGAGACAGC 2056
QY 521 IleAsnPheLysThrLeuSerPheSerValPheGlnIleIleLeuIleThrSerLeuIle 540
Db 2057 ATAAATTTCAAGCAATGTCATTCAAGTCTTTGAGATTAATCTCAATTAATTTCTGATT 2116
QY 541 GlyGlyGlyLeuLeuIleLeuIleIleLeuThrValAlaYTrpGlyLeuLysLysProAsn 560
Db 2117 GGTGGAGGCGCTTCTTATCTCATTAATCTGACAGTGGCATATGCTCTCAAAAAACCAAC 2176
QY 561 LysLeuThrHisLeuCysTrpProThrValProAsnProAlaGlnSerSerIleAlaThr 580
Db 2177 AATTTACTCATCTGTGTGTGGCCCAACCGTTCCCAACCTGTGTAAGATGATAGCAACA 2236

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QY 581 TrpHisGlyAspAspPheLysAspLysLeuAsnLeuLysGlnSerAspAspSerValAsn 600
Db 2237 TGGCATGAGAGATGATTTCAAGGATTAAGCTAAACCTGAAGAGTGTGATGATCTGTGAAC 2296
QY 601 ThrGlnAspArgIleLeuLysProCysSerThrProSerAspLysLeuValIleAspLys 620
Db 2297 ACAGAAAGACAGGATCTTAAACCATGTTCCACCCCAAGCAAGTGTGTGATGACAAAG 2356
QY 621 LeuValAlaAsnPheGlyAsnValLeuGlnGlnIlePheThrAspGlnAlaArgTrpGly 640
Db 2357 TTGGTGTGTAACCTTTGGGAAATGTTCTGCAAGAAATTTTCAAGATCAACCAAGCGGT 2416
QY 641 GlnGlnLysGlnPheArgArgGlyLysGlnTrpAsp 652
Db 2417 CAGGA-AAACAAATTAAGAGGGAAGAAATGGGAC 2451

RESULT 5
US-10-352-554-4
/ Sequence 4, Application US/10352554
/ Publication No. US20030224487A1
/ GENERAL INFORMATION:
/ APPLICANT: Sprecher, Cindy A.
/ APPLICANT: Kuilber, Joseph L.
/ APPLICANT: Dasovich, Maria M.
/ APPLICANT: Grant, Francis J.
/ APPLICANT: Hammond, Angela K.
/ APPLICANT: Novak, Julia E.
/ APPLICANT: Grose, Jane A.
/ APPLICANT: Dillon, Stacey R.
/ TITLE OF INVENTION: NOVEL CYTOKINE ZCYTOR17 LIGAND
/ FILE REFERENCE: 02-01
/ CURRENT APPLICATION NUMBER: US/10/352,554
/ PRIOR FILING DATE: 2003-01-21
/ PRIOR APPLICATION NUMBER: US 60/350,325
/ PRIOR FILING DATE: 2002-01-18
/ PRIOR APPLICATION NUMBER: US 60/375,323
/ PRIOR FILING DATE: 2002-04-25
/ PRIOR APPLICATION NUMBER: US 60/435,315
/ PRIOR FILING DATE: 2002-12-19
/ NUMBER OF SEQ ID NOS: 168
/ SOFTWARE: FastSeq for Windows Version 3.0
/ SEQ ID NO 4
/ LENGTH: 2903
/ TYPE: DNA
/ ORGANISM: Homo sapiens
/ FEATURE:
/ NAME/KEY: CDS
/ LOCATION: (497) ... (2482)
/ US-10-352-554-4

Alignment Scores:
Pred. No.: 0 Length: 2903
Score: 3451.00 Matches: 650
Percent Similarity: 99.85% Conservative: 1
Best Local Similarity: 99.69% Mismatches: 1
Query Match: 99.05% Indels: 1
DB: 17 Gaps: 0

US-10-006-265-2 (1-652) x US-10-352-554-4 (1-2903)
QY 1 MetLysLeuSerProGlnProSerCysValAsnLeuGlyMetTrpThrTrpAlaLeu 20
Db 497 ATGAAGCTCTCTCCCAAGCTTCATGTTGTTAACTGGGGATGATGAGACTGGGACACTG 556
QY 21 TrpMetLeuProSerLeuLysPheSerLeuAlaAlaLeuProAlaLysProGlnAsn 40
Db 557 TGGATGCTCTCCCTTCACTCGAAATTCAGCTGGAGGCTCTGCAAGCTTAAGCTTGAAGAC 616
QY 41 IleSerCysValYTrpYTrpYTrpYTrpYTrpYTrpYTrpYTrpYTrpYTrpYTrpYTrp 60
Db 617 ATTTCTGTGTCTACTACTATGAGAAATTTAACTGCACTTGGAGTCCAGGAAAGAA 676
QY 61 ThrSerYTrpGlnYTrpValLysArgThrYTrpAlaPheGlyGlyLysHisAspAsn 80

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Db 677 ACCAGTATACCAAGTACAGAGTAAAGAACTTACGCTTTGGAGAAAACATGATAT 736
Qy 81 CysThrThrAsnSerSerThSerGluAsnArgAlaSerCysSerPhePheLeuProArg 100
Db 737 TGTACAAACCAATAGTCTTACAAAGTAAATCGTCTGCTCTTTTCTTTTCTTCCCAAGA 796
Qy 101 IleThrIleProAspAsnThrThrIleGluValGluAlaGluAsnGluValIle 120
Db 797 ATAAAGATCCAGATTAATTAATACATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 856
Qy 121 LysSerHisMetThrTyrTrpArgLeuGluAsnIleAlaLysThrGluProGlyIle 140
Db 857 AAATCTCATATGACATCTGAGGAGATTAGAGAACATAGGAGAAACAGAACCTTAAGATT 916
Qy 141 PheArgValLysProValLeuGluLysLysArgMetIleGlnIleGluTrpIleLysPro 160
Db 917 TTCCGTGTGAAACCGTGTGGGCATCAACCAATGATTCAAATGGAATGGATTAAGCCT 976
Qy 161 GluLeuAlaProValSerSerAspLeuLysTyrThrLeuArgPheArgThrValAsnSer 180
Db 977 GAGTTGGCGCTGTTTCACTGATTTAAATACACACTTCGATTCAGAGACAGTCAACAGT 1036
Qy 181 ThrSerTrpMetGluValAsnPheAlaLysAsnArgLysAspLysAsnGlnThrTyrAsn 200
Db 1037 ACCAGCTGAGTGAAGTCACTGCTGCTAAGAACCTTAAGATTAAGAACCAACGTAACAC 1096
Qy 201 LeuThrGlyLeuGlnProPheThrGluTyrValIleAlaLysArgCysAlaValLysGlu 220
Db 1097 CTCACGGGGCTGACGCTTTTACAGAAATATGTCATAGCTCTGCGATGTGGCTCAAGAG 1156
Qy 221 SerLysPheTrpSerAspTrpSerGlnLysMetGlyMetThrGluGluGluAlaPro 240
Db 1157 TCAAGGTTCTGAGAGTGAAGCCAGAGAAAAGGAGAAATGAGTGAAGAGAGAGCTCA 1216
Qy 241 CysGlyLeuGluLeuTrpArgValLeuLysProAlaGluAlaAspGlyArgArgProVal 260
Db 1217 TGTGGCCTGGAAGTGTGAGAGTCTCTGAACCAAGTGAAGCGAGTGAAGAGGCAAGT 1276
Qy 261 ArgLeuLeuTrpLysLysAlaArgGlyValAProValLeuGluLysThrLeuGlyTyrAsn 280
Db 1277 CGGTGTATGGAAGAGCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1336
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Db 1337 ATATGATCTATCCAGAAAGAACACTAACCTCAAGAAACAAATGAACATCACTAACAG 1396
Qy 301 GlnLeuGluLeuHisLeuGlyGlyLysSerPheTrpValSerMetIleSerTyrAsnSer 320
Db 1397 CAGCTTGAACCTGCATCTGGAGAGGCGAGAGCTTTGGGTGTCTATGATTTCTTATATCT 1456
Qy 321 LeuGlyLysSerProValAlaThrLeuArgIleProAlaIleGlnLysSerPheGln 340
Db 1457 CTGGGAAGTCTCCAGTGGCCACCTGAGGATTCAGCTATTCAGAAATAATCATTTTCAAG 1516
Qy 341 CysIleGluValMetGlnAlaCysValAlaGluAspGlnLeuValValLysTrpGlnSer 360
Db 1517 TGCATGTAGGTCTAGCAGCGCTGCTTCTGAGGACCGAGTGAAGTGAAGGGAAGC 1576
Qy 361 SerAlaLeuAspValAsnThrTrpMetIleGluTrpPheProAspValAspSerGluPro 380
Db 1577 TCTCTCTAGACGTAACACTTGGATGATTAATGCTTTCCGATGTGATCTCAGAGGCC 1636
Qy 381 ThrThrLeuSerTrpGluSerValSerGlnAlaThrAsnTrpThrIleGlnGlnAspLys 400
Db 1637 ACCACCCCTTCTCTGGGATCTGTGTCTCAGGCGACAGACTGAGACATCCACAGATTA 1696
Qy 401 LeuLysProPheTrpCysTyrAsnIleSerValTyrProMetLeuHisAspLysValGly 420
Db 1697 TTAAACCTTTCTGTCTATTAACATCTCTGTGATTCCAAGTGTGACAGAAAGTGGC 1756
Qy 421 GluProTyrSerIleGlnAlaTyrAlaLysGluGlyValProSerGluGlyProGluThr 440

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Db 1757 GAGCCATATTCATCCAGGCTTATGCCAAAGAGCGTTCATCAGAGTCTGAGACC 1816
Qy 441 LysValGluAsnIleGlyValLysThrValThrIleThrTrpLysGluIleProLysSer 460
Db 1817 AAGGTGAGAACATTGGCGTGAAGACGCTACGATCAATGAGAAAGATTCACCAAGGT 1876
Qy 461 GluArgLysGlyIleIleCysAsnTyrThrIlePheTyrGlnAlaGluGlyValLysGly 480
Db 1877 GAGAGAAAGGTTATCATCTGACATCAACCATCTTTTACCAAGCTGAAGGTGGAAGAA 1936
Qy 481 PheSerLysThrValAsnSerSerIleLeuGlnTyrGlyLeuGluSerLeuLysArgLys 500
Db 1937 TTCTCAAGACAGTCAATTCAGCATCTTGAGATCGGCTGAGAGTCCCTGAAACGAAG 1996
Qy 501 ThrSerTyrIleValGlnValMetAlaAsnThrSerAlaGlyTyrThrAsnGlyThrSer 520
Db 1997 ACCCTTCAATGTTGATGAGTATGAGCCAGCACAGTGTGGGGAACCAAGGAGCCAGC 2056
Qy 521 IleAsnPheLysThrLysSerPheSerValPheGluIleIleLeuIleThrSerLeuIle 540
Db 2057 ATAAATTTCAAGACATTTCTCATTCAGTGTCTTGAATATACCTCATTAATCTCTGATT 2116
Qy 541 GlyGlyLeuLeuLeuIleIleLeuThrValAlaTyrGlyLeuLysLysProAsn 560
Db 2117 GGTGAGGCTTCTTATTTCTCATTCCTGACAGTGGCATGTGCTCAAAAAACCCAAC 2176
Qy 561 LysLeuThrHisLeuCysTrpProThrValProAsnProAlaGluSerSerIleAlaThr 580
Db 2177 AAATGACTCATCTGTGTGGCCACCGCTTCCCAACCTGCTGAAGTGAATGATGACACA 2236
Qy 581 TrpHisGlyAspAspPheLysAspLysLeuAsnLeuLysGluSerAspAspSerValAsn 600
Db 2237 TGGCATGAGATGATTTTCAGAGATTAAGCTTAACCTGAAGAGTCTGATCTGTGAGC 2296
Qy 601 ThrGluAspArgIleLeuLysProCysSerThrProSerAspLysLeuValIleAspLys 620
Db 2297 ACAGAAAGCAGAGATCTTAAACCATGTTCCACCCCGAGTCAAGATGTGATGACAAAG 2356
Qy 621 LeuValValAsnPheGlyAsnValLeuGlnGluIlePheThrAspGluAlaArgThrGly 640
Db 2357 TTGGTGTGAACTTTGGAAAGTGTCTCAAGAAATTTTTCACAGATGAAGCCAGAACGGT 2416
Qy 641 GlnGluLysGlnPheArgArgGlyLysGluTrpAsp 652
Db 2417 CAGCA-AAACATTTAGAGGAGGGAAGAAATGAGAC 2451

RESULT 6
US-10-772-531-53
; Sequence 53, Application US/10772531
; Publication NO. US20040142422A1
; GENERAL INFORMATION:
; APPLICANT: Sprecher, Cindy A.
; APPLICANT: Presnell, Scott R.
; APPLICANT: Gao, Zeren
; APPLICANT: Whitmore, Theodore E.
; APPLICANT: Kuiper, Joseph L.
; APPLICANT: Maurer, Mark F.
; TITLE OF INVENTION: CYTOKINE RECEPTOR ZCYTOR17
; FILE REFERENCE: 00-42
; CURRENT APPLICATION NUMBER: US/10/772,531
; CURRENT FILING DATE: 2004-02-05
; PRIOR APPLICATION NUMBER: US/09/892,949
; PRIOR FILING DATE: 2001-06-26
; PRIOR APPLICATION NUMBER: US 60/214,282
; PRIOR FILING DATE: 2000-06-26
; PRIOR APPLICATION NUMBER: US 60/214,955
; PRIOR FILING DATE: 2000-06-29
; PRIOR APPLICATION NUMBER: US 60/267,963
; PRIOR FILING DATE: 2001-08-02
; NUMBER OF SEQ ID NOS: 93
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 53
; LENGTH: 2903

```



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; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (497)...(2482)
; US-10-772-531-53

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Alignment Scores:

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Pred. No.: 0
Score: 3451.00
Percent Similarity: 99.85%
Best Local Similarity: 99.69%
Query Match: 99.05%
DB: 18

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Length: 2903
Matches: 650
Conservative: 1
Mismatches: 1
Indels: 1
Gaps: 0

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US-10-006-265-2 (1-652) x US-10-772-531-53 (1-2903)

```

QY 1 MetLysLeuSerProGlnProSerCysValAsnLeuGlyWetMetTrpThrTrpAlaLeu 20
DB 497 ATGAAGCTCTCTCCAGCCTTCATGTGTTAACTGGGGATGATGTGAGACTGGGACCTG 556
QY 21 TrpMetLeuProSerLeuCysLysPheSerLeuAlaLeuProAlaLysProGlnLys 40
DB 557 TGGATGCTCCCTCCTCAGCTGCAAAATTCAGCTGGCAGCTCTGCACCTAAAGCTGAGAAC 616
QY 41 LLeSerCysValTyTrpTyTrpArgLysAsnLeuThrCysThrTrpSerProGlyLysGlu 60
DB 617 ATTTCTGTGTCTACTACTATAGAAAATTAACTGACCTTGGAGCTCCAGGAAAGGAA 676
QY 61 ThrSerTyTrpGlnTyTrpValLysArgThrTyTrpAlaPheGlyGluLysHisAspAsn 80
DB 677 ACCAGTTAATACCCAGTACACAGTTAAGAACTTAAGCTTTGGAGAAAACATGATTAAT 736
QY 81 CysThrThrAsnSerSerThrSerGluAsnArgAlaSerCysSerPhePheLeuProArg 100
DB 737 TGTACACCAACAAATGTTCTCAAGTGAATAATCGTCTTCCTTTTCCCTTCCCAAG 796
QY 101 LLeThrLLeProAspAsnTyTrpThrLLeGluValAlaGluLysAsnGlyAspGlyValLLe 120
DB 797 ATACACATCCCAATATATATACATTGAGGTGGAAGCTGAAAATGAGATGAGTGTATAT 856
QY 121 LysSerHisMetThrTyTrpArgLeuGluAsnLLeAlaLysThrGluProProLysLLe 140
DB 857 AAATCTCATATGACATACATGAGATTAGAAACATGACGAAACCTGAACCACTTAAGATT 916
QY 141 PheArgValLysProAlaLeuGlyLLeLysArgMetLLeGlnLLeGluTrpLLeLysPro 160
DB 917 TTCGGTGAACCAAGTTTGGGCATCAACGAATGATTCAAAATTGATGATTAAGCCT 976
QY 161 GluLeuAlaProValSerSerAspLeuLysTyTrpThrLeuArgPheArgThrValAsnSer 180
DB 977 GAGTGGCCGCTTTTCATCTGATTTAAATACACACTTCGATTCAGACACAGCAACAGT 1036
QY 181 ThrSerTrpMetGluValAsnPheAlaLysAsnArgLysAspLysAsnGlnThrTyTrpAsn 200
DB 1037 ACCAGCTGAGTGAAGTCAACTTCGCTAAGAACCGTAAGATTAATAAACCAACGTAAC 1096
QY 201 LeuThrGlyLeuGlnProPheThrGluTrpValLLeAlaLeuArgCysAlaValLysGlu 220
DB 1097 CTCACGGGGCTGAGCTTTTACAGATATGTCATAGCTCTGCAAGTGGCGCAAGAG 1156
QY 221 SerLysPheTrpSerAspTrpSerGlnGluLysMetGlyWetThrGluGluGluAlaPro 240
DB 1157 TCAAAGTTCGAGAGTACCTGAGCCCAAGAAAATGGGAATGACTGAGGAAGAAAGCTCCA 1216
QY 241 CysGlyLeuGlnLeuTrpArgValLLeuLysProAlaGluAlaAspGlyArgArgProVal 260
DB 1217 TGTGGCTGGAACCTGTGAGAGAGTCTGTAACACAGCTGAGGCGGATGGAAGAGCCAGTG 1276
QY 261 ArgLeuLeuTrpLysLysAlaArgGlyAlaProValLeuGluLysThrLeuGlyTyTrpAsn 280
DB 1277 CGGTTGTATGAGAAAGGCAAGAGAGGCCCTCCTAGAGAAAACCTTGGCTACAAAC 1336

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QY 281 LLeTrpTyTrpProGluSerAsnThrAsnLeuThrGluThrMetAsnThrThrAsnGln 300
DB 1337 ATATGCTACTATCCAGAAAGCAACTAATCTCACAGAAACATGAACACTACTAACAG 1396
QY 301 GlnLeuGlnLeuHisLeuGlyGlyLysSerPheTrpValSerMetLLeSerTyTrpAsnSer 320
DB 1397 CAGCTTGAACCTCATCTGGGAGGCGAGACCTTTGGGTGCTATGATTTCTTAATAATTTCT 1456
QY 321 LeuGlyLysSerProValAlaThrLeuArgLLeProAlaLLeGlnGluLysSerPheGln 340
DB 1457 CTTGGGAAGTCTCCAGAGGCCACCTCGAGATTTCCAGCTATTCAGAAAAATCATTTCCAG 1516
QY 341 CysLLeGluValMetGlnAlaCysValAlaGluAspGlnLeuValLysTyTrpGlnSer 360
DB 1517 TGCATTGAGGTATGAGGCGTGGCTGTGAGGACCAAGCTAGTGGTGAAGTGGCAAGC 1576
QY 361 SerAlaLeuAspValAsnThrTrpMetLLeGluTrpPheProAspValLysSerGluPro 380
DB 1577 TCTGCTCTAGAGGTGAACCTTGATGATGATGATGATTCGGAATGTGAGCTCAGAGCCC 1636
QY 381 ThrThrLeuSerTrpGluSerValSerGlnAlaThrAsnTrpThrLLeGlnLysAspLys 400
DB 1637 ACCACCTTCTCCGGAATCTGTGCTCAGGCCACGAACTGAACTGACGCAAGATTA 1696
QY 401 LeuLysProPheTrpCysTyTrpAsnLLeSerValTyTrpMetLeuHisAspLysValGly 420
DB 1697 TTAAACCTTCTGGGTGATTAACATCTGTGATACCAATGTTCATGATGATCAAGAGTTGSC 1756
QY 421 GluProTyTrpSerLLeGlnAlaTyTrpAlaLysGluGlyValProSerGluGlyTrpThr 440
DB 1757 GAGCATATTCATCCAGCTCAGGCTTATGCAAGAGGCGTTCATCGAAGGCTCCTGAGACC 1816
QY 441 LysValAlaAsnLLeGlyValLysThrValThrLLeThrTyTrpLysGluLLeProLysSer 460
DB 1817 AAGGTGGAACAATTGGCTGTAAGACGTCACAGATCACAGAAAGATTTCCAAAGAT 1876
QY 461 GluArgLysGlyLLeLLeCysAsnTyTrpLLePheTyTrpGlnAlaGluGlyLysGly 480
DB 1877 GAGAGAAAGGTATATCATCTGCAACATACACATCTTTTCAAGCTGAAGTGAAGAAAGGA 1936
QY 481 PheSerLysThrValAsnSerSerLLeLeuGlnTyTrpGlyLeuGluSerLeuLysArgLys 500
DB 1937 TTCTCCAGACAGTCAATTCAGCATCTTGACATGAGCTGAGAGCTCTGAAACCAAG 1996
QY 501 ThrSerTyTrpLLeValGlnValMetAlaAsnThrSerAlaGlyGlyThrAsnGlyThrSer 520
DB 1997 ACCTCTTACATTTGTCAGGTATGCTGACACAGTGGCGGAGAACCAAGGACCAAG 2056
QY 521 LLeAsnPheLysThrLeuSerPheSerValPheGluLLeLLeuLLeThrSerLeuLLe 540
DB 2057 ATTAATTTCAAGACATTTGTCATTCAGTGTCTTGAAGATTATCCTATTACTTCTGAT 2116
QY 541 GlyGlyGlyLeuLeuLLeLLeLLeLLeLLeLLeLLeLLeLLeLLeLLeLLeLLeLLeLLe 560
DB 2117 GGTGAGGCGCTTATTTCTCATTTCTGACAGTGGCATATGCTCTCAAAAAACCAAC 2176
QY 561 LysLeuThrHisLeuCysTrpProThrValProAsnProAlaGluSerSerLLeAlaThr 580
DB 2177 AATATGACTCATCTGTGTGGCCACCGTTCCCAACCTGCTGAAAGTATGATAGCAACA 2236
QY 581 TrpHisGlyAspAspPheLysAspLysLeuAsnLeuLysGluLysAspAspSerValAsn 600
DB 2237 TGGCAGTGAAGATTTTCAAGATTAAGCTTAACCTGAAGAGATGATGATCACTGTGAAC 2296
QY 601 ThrGluAspArgLLeLLeLysProCysSerThrProSerAspLysLeuValLLeAspLys 620
DB 2297 ACAGAAAGACAGATCTTAATAACATGTTCCACCCAGAGCAAGTAAGTGTGATTTGCAAG 2356
QY 621 LeuValValAsnPheGlyAsnValLeuGlnGluLLePheThrAspGlnAlaArgThrGly 640
DB 2357 TTGGTGTGAACCTTGGGATGTCTGCAAGAAATTTTACAGATGAAGCCAGAACGGGT 2416
QY 641 GlnGluLysGlnPheArgArgLysGluTrpAsp 652

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Db      2417 CAGCA-AAACAAATTAGAGGGGAAAAAGAAATGGGAC 2451
RESULT 7
US-09-892-949-45
; Sequence 45, Application US/09892949
; Publication No. US20030096339A1
; GENERAL INFORMATION:
; APPLICANT: Sprecher, Cindy A.
; APPLICANT: Premeil, Scott R.
; APPLICANT: Gao, Zeren
; APPLICANT: Whitmore, Theodore E.
; APPLICANT: Kuitjper, Joseph L.
; APPLICANT: Maurer, Mark F.
; TITLE OF INVENTION: CYTOKINE RECEPTOR ZCYTOR17
; FILE REFERENCE: 00-42
; CURRENT APPLICATION NUMBER: US/09/892,949
; CURRENT FILING DATE: 2001-06-26
; PRIOR APPLICATION NUMBER: US 60/214,282
; PRIOR FILING DATE: 2000-06-26
; PRIOR APPLICATION NUMBER: US 60/214,955
; PRIOR FILING DATE: 2000-06-29
; PRIOR APPLICATION NUMBER: US 60/267,963
; PRIOR FILING DATE: 2001-08-02
; NUMBER OF SEQ ID NOS: 93
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 45
; LENGTH: 2529
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (162)...(2108)
; US-09-892-949-45

Alignment Scores:
Pred. No.: 0          Length: 2529
Score: 3441.00       Matches: 648
Percent Similarity: 99.85%
Best Local Similarity: 99.69%
Query Match: 98.77%   Mismatches: 1
                Indels: 1
                Gaps: 0

US-10-006-265-2 (1-652) x US-09-892-949-45 (1-2529)
QY      3 LeuserProgluInProSerCyValaIenleuGlyMetMetTrpThrTyrAlaIeuTrpMet 22
Db      129 CTCTCTCCCAAGCCTTCATGTGTAACTGGGGAGATGTGGACCTGGGCACTGTGATG 188
QY      23 LeuProSerleuCyValaIenleuGlyMetMetTrpThrTyrAlaIeuTrpMet 42
Db      189 CTCTCTCCCAAGCCTTCATGTGTAACTGGGGAGATGTGGACCTGGGCACTGTGATG 248
QY      43 CyValaIenleuGlyMetMetTrpThrTyrAlaIeuTrpMet 62
Db      249 TGTGTCTACTACTATAGAAAAATTTAACTGCACTTGGAGTCCGAGAAAGAAACCACT 308
QY      63 TyrThrGlnTyrThrValaIenleuGlyMetMetTrpThrTyrAlaIeuTrpMet 82
Db      309 TATACCCAGTACACAGTTAAGAACTTACGCTTTGGAGAAAAATGATTAATTGTACA 368
QY      83 ThrIenSerSerThrSerGluAsnArgAlaSerCySerSerPhePheLeuProArgLeuThr 102
Db      369 ACCAAATAGTTCTACAAAGTAAATGCTGCTTCTTTCTTTCTTTCTTTCTTTCTTTCT 428
QY      103 IleProAsnArgTyrThrIleGluValaIenleuGlyMetMetTrpThrTyrAlaIeuTrpMet 122
Db      429 ATCCCAAGTAATTAACCACTTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 488
QY      123 HisMetThrTyrTrpArgLeuGluAsnIleAlaIeuTrpThrTyrAlaIeuTrpMet 142
Db      489 CATATGACATACGTGAGATTAAGAAACATAGGAAACATGAAACCACTTAAGATTTCCGT 548

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QY      143 ValIysProValaIenleuGlyIleuYsaArgMetIleGlnIleGluTrpIleValaIenleu 162
Db      549 GTGAACCAAGTTTGGGATCAAAAGCAATGATTTCAATTTGAATGATTAAGCTGAGTTG 608
QY      163 AlaProValaIenleuGlyMetMetTrpThrTyrAlaIeuTrpMet 182
Db      609 GCGCTGTTTCTATCTGATTTAAATTAACACACTGATTCAGAGACAGTCAACAGTCAAGC 668
QY      183 TrpMetGluValaIenleuGlyMetMetTrpThrTyrAlaIeuTrpMet 202
Db      669 TGGATGAAGTCAACTTGTGTAAGAACCTTAAGATTAAGAACCTTAAGAACCTTAAGAAC 728
QY      203 GlyLeuGlnProPheThrGluTyrValaIleAlaIeuArgGlyValaIleValaIeuGlySer 222
Db      729 GGGCTGCAAGCTTTTACGAATATGTCTACTGCTTGCATGTGCGGTCAAGAGTCAAG 788
QY      223 PheTrpSerAspTrpSerGlnIleuYsaArgMetIleGlnIleGluTrpIleValaIenleu 242
Db      789 TTCTGAGTGACTGGAGCCAAAGAAATGGGAATGACTGAGAAAGACCTCATGTGCG 848
QY      243 LeuGluLeuTrpArgValaIenleuGlyMetMetTrpThrTyrAlaIeuTrpMet 262
Db      849 CTGGAACGTGGAGAGTCTGTAACCAAGTGAAGGAGTGAAGAGGAGTGAAGAGGAGTGAAG 908
QY      263 LeuTrpIysValaIenleuGlyValaIleProValaIenleuGlySerThrLeuGlyTyrAsnIleTrp 282
Db      909 TTATGAAAGAAAGCAAGAGAGCCCAAGTCTTAAGAAACCACTTGGTCAACATATAG 968
QY      283 TyrTrpProgluSerAsnThrAsnleuThrGluThrMetAsnThrThrAsnGlnIleu 302
Db      969 TACTATCCAGAAACCAACACTCACTCAACAAACAAATGAAACACTCACTCACTCACTCACT 1028
QY      303 GluLeuHisleuGlyGlyLeuSerPheTrpValaIenleuGlySerThrAsnleuGly 322
Db      1029 GAACGTGACATCTGGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1088
QY      323 LysSerProValaIenleuGlyIleProValaIenleuGlySerPheGlyCysIle 342
Db      1089 AAGTCTCCAGTGGCCACCTGAGAGATTCACACTTTCAGAAATTCATTTCAAGTGCATT 1148
QY      343 GluValaIenleuGlyValaIenleuGlyValaIenleuGlyValaIenleuGlyValaIenleu 362
Db      1149 GAGGCAATGCAAGGCTGGTGTGTAAGAGCAGCAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 1208
QY      363 LeuAspValaIenleuTrpMetIleGluTrpPheProAspValaIenleuGlyProThr 382
Db      1209 CTAAACGTAACACCTGATGATTAAGATTTGCTTCCGATGAGGAGTCAAGCCCAAGCACC 1268
QY      383 LeuSerTrpGluSerValaIenleuGlyValaIenleuGlyValaIenleuGlyValaIenleu 402
Db      1269 CTTCCTGAGATCTGTCTCAAGCCCAAGATGAGCAGATCCAGCAAGATTAATAA 1328
QY      403 ProPheTrpCyTrpAsnIleSerValaIenleuGlySerPheMetIleAspValaIenleuGly 422
Db      1329 CTTTCTGAGTCAATCACTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1388
QY      423 TyrSerIleGlnAlaIenleuGlyValaIenleuGlyValaIenleuGlyValaIenleuGly 442
Db      1389 TATTCATCCAGGCTTATGCAAGAAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1448
QY      443 GluAsnIleGlyValaIenleuGlyValaIenleuGlyValaIenleuGlyValaIenleuGly 462
Db      1449 GAGAAACATGGCGTGAAGAGGAGTCAACATCACTGAAGAAAGATTTCCCAAGAGTGAAGAG 1508
QY      463 LysGlyIleIleCysAsnArgTyrThrIlePheTyrGlnAlaIenleuGlyValaIenleuGly 482
Db      1509 AAGGATTAATCTGCACTCACTCACTCACTCACTCACTCACTCACTCACTCACTCACTCACT 1568
QY      483 LysThrValaIenleuGlyValaIenleuGlyValaIenleuGlyValaIenleuGlyValaIenleu 502
Db      1569 AAGACATCAATTCACATCTTGCATGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 1628
QY      503 TyrIleValaIenleuGlyValaIenleuGlyValaIenleuGlyValaIenleuGlyValaIenleu 522

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Db      1629 TACATTGTCAGTCAATGACACACACAGTGTGGGGGAACCAACGGACACGACATTAAT 1688
Qy      523  PhelyThreuserPheSerValPheGluIleIleuIleThreSerIleGlyGly 542
Db      1689 TTCAAGACATGTCATTCACATGTCCTTGAGATTATCTCTCAATTCCTCTGATTTGGTGA 1748
Qy      543  GlYleuIleuIleuIleIleuThrValAlaTyrglyeulysylsProAnlySleu 562
Db      1749 GGCCTTCTTATTCCTATTCCTGACAGTGGCATATGCTCAAAAAACCAACCAATTC 1808
Qy      563  ThriSleuCystrpProthrValProAnpProAlaGluSerIleAlaThrTrpHis 582
Db      1809 ACTCATCTGTGTGGCCACCGTCCCAACCTGTGAAAGTAGTATGACCATGGCAT 1868
Qy      583  GlYAspAspPheIysAspIysSleuAnleuIleGluSerAspAspSerValAnThrGlu 602
Db      1869 GGAGATGATTCAAGAGTAAGCTAAACCTGAAGAGTGTGATGACTTGAAACACAGAA 1928
Qy      603  AspArgIleuIysProCySerThrProSerAspIysleuValIleAspIysleuVal 622
Db      1929 GACAGATCTTAAACATATTCACCCCAAGCAAGTTGGTGTGCAAGTTGGTG 1988
Qy      623  ValAspPheGlyAsnValIleuGlnGluIlePheThrAspGluIleArgThrIleGlnGlu 642
Db      1989 GTGAACCTTGGGATGTTCTGCAAGAAATTTTCACAGATGAACCGAAGCGGTCAAGA- 2047
Qy      643  LysGlnPheArgArgGlyIysGluTrpAsp 652
Db      2048 AAACAATTGAGAGGAGGAGGAGGAGGAC 2077

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RESULT 8

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US-10-351-157-108
; Sequence 108, Application US/10351157
; Publication No. US0030215838A1
; GENERAL INFORMATION:
; APPLICANT: Sprecher, Cindy A.
; APPLICANT: Gao, Zeren
; APPLICANT: Kuiper, Joseph L.
; APPLICANT: Dasovich, Maria M.
; APPLICANT: Grant, Francis J.
; APPLICANT: Presnell, Scott R.
; APPLICANT: Whitmore, Theodore E.
; APPLICANT: Hammond, Angela K.
; APPLICANT: NO. US20030215838A1ak, Julia E.
; APPLICANT: Gross, Jane A.
; APPLICANT: Dillon, Stacey R.
; TITLE OF INVENTION: CYTOKINE RECEPTOR ZCYTOR17 MULTIMERS
; FILE REFERENCE: 02-02
; CURRENT APPLICATION NUMBER: US/10/351,157
; PRIOR FILING DATE: 2003-01-21
; PRIOR APPLICATION NUMBER: US 60/435,361
; PRIOR FILING DATE: 2002-12-19
; PRIOR APPLICATION NUMBER: US 60/389,108
; PRIOR FILING DATE: 2002-06-14
; PRIOR APPLICATION NUMBER: US 60/350,325
; PRIOR FILING DATE: 2002-01-18
; NUMBER OF SEQ ID NOS: 183
; SOFTWARE: PaacSeq for Windows Version 4.0
; SEQ ID NO 108
; LENGTH: 2529
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (162)...(2108)
US-10-351-157-108

```

Alignment Scores:

```

Pred. No.: 0
Score: 3441.00
Percent Similarity: 99.85%
Best Local Similarity: 99.69%

```

```

Length: 2529
Matches: 648
Conservative: 1
Mismatch: 1

```

```

Query Match: 98.77% Indels: 1
DB: 17 Gaps: 0
US-10-006-265-2 (1-652) x US-10-351-157-108 (1-2529)
Qy      3  LeuSerProGlnProSerCysValAsnIleuGlyMetMetTrpThrAlaLeuTrpMet 22
Db      129  CTCTCTCCCAACCTTCAATGTTAACTGGGAGATGATGTGACCTGGGACCTGTGGAG 188
Qy      23  LeuProSerLeuCylyAspPheSerIleuAlaIleuProAlaIysProGluAnIleSer 42
Db      189  CTCCTCTCACTGCAAAATTCAGCTGCGAGCTCTGCAAGCTGAGCTGAGAACATTTCC 248
Qy      43  CysValTyTrpTyArgIysAsnIleuThrcysThrTrpSerProGlyIysGluThrSer 62
Db      249  TGTGTCTACTATATGAGAAAATTTAACTTCACCTGAGTCCAGGAAAGGAAACCACT 308
Qy      63  TyrThrGlnTyThrValIysArgThrTyraIaPheGlyGluIysHisAspAnCyThr 82
Db      309  TATACCACTACACAGTTAAAGAACTTACGCTTTTGGAGAAAACATGATTAATTGTACA 368
Qy      83  ThrAsnSerSerThrSerGluAsnArgIleSerCysSerPhePheLeuProArgIleThr 102
Db      369  ACCAATAGTTTCAACAAGTAAATCGTGTGCTCTTTTCTTCCACAGAAATTAAG 428
Qy      103  IleProAspAsnTyThrIleGluValGluIleGluAsnGlyAspGlyValIleYsSer 122
Db      429  ATCCCAAGATTAATTAATCACTGAGGTGAGAGCTGAAATGAGAGATGTCTAATTAATCT 488
Qy      123  HisMetThrTyTrpArgIleuGluAnIleAlaIysThrGluProProIysIlePheArg 142
Db      489  CATATGACATCTGAGATTAAGAACTAGCAAGGAAACCTGAACCACTTAAGATTTTCCCT 548
Qy      143  ValIysProValIleuGlyIleYsArgMetIleGlnIleGluTrpIleYsProGluLeu 162
Db      549  GTGAACCAAGTTTGGGCAATCAACGATGATTCAAATTTGAATGATTAAGCTTGAGTTG 608
Qy      163  AlaProIysSerSerAspLeuIysTyThrLeuArgPheArgThrValAsnSerThrSer 182
Db      609  GGGCTGTTTCAATCTGATTTAAATATACACATTCGATTAAGCAAGTCAACAGTACCAAC 668
Qy      183  TrpMetGluValAsnPheAlaYsAsnArgIysAspIysAsnGlnThrTyThrAsnLeuThr 202
Db      669  TCGATGAGAGTCAACTCTCTTAAGAACCTTAAGAGATTAAGAACCAACCTTAACCACTC 728
Qy      203  GlYleuGlnProPheThrGlnTyThrValIleAlaIleuArgCysAlaValIysGluSerIys 222
Db      729  GGGCTGCAAGCTTTTACAGAAATATGTCATAGCTCTGCGATGTGCGGTCAAGAGTCAAG 788
Qy      223  PheTrpSerAspTrpSerGlnIlyIysMetGlyMetThrGluGluGluIleProCysGly 242
Db      789  TTCTGAGAGTCTGAGAGCCCAAGAAAATGGGAATGACATGAGGAAGAACTCATGTGTC 848
Qy      243  LeuGluLeuTyArgValIleuIysProAlaGluIleAspGlyArgArgProValArgLeu 262
Db      849  CTGGAACCTGTGAGAGTCTCTGAACCAAGCTGAGGCGGAGTGAAGAGGCACTGCGCTTG 908
Qy      263  LeuTrpIysValAlaArgIleValProValIleuGluIysThrIleuGlyTyThrAnIleTrp 282
Db      909  TTATGGAAGAGCAAGAGAGAGCCCAAGTCTTAGAGAAAACCTTGCTACAAACATATGG 968
Qy      283  TyrTyProGluSerAsnThrAsnIleuThrcysThrMetLeuAsnThrThrAsnGlnIleu 302
Db      969  TACTATCCAGAAAGCAACCTAACTCACAGAAACATGAACATCACTAACAGCAGCTT 1028
Qy      303  GluLeuHisLeuGlyIleGluSerPheTrpValSerMetIleSerTyTrpAsnSerLeuGly 322
Db      1029  GAACTGCACTGGGAGGCGAGAGCTTTTGGGTGTCTATGATTTCTTAATTTCTCTTGGG 1088
Qy      323  LysSerProValAlaThrLeuArgIleProAlaIleGlnIlyIysSerPheGlnCysIle 342
Db      1089  AAGTCTCCAGTGCCACCTCGAGAGATCCAGCTATTTCAAGAAAATCAATTTCAAGTCATT 1148

```

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Qy 343 GUVAlmeGlnAlaCyEValAlaGlnuApGlnLeuValValLeuTrpGlnSerSerAla 362
Db 1149 GAGGTCATGCGAGCCCTGCTTCTCTAGAGACAGCTAGTGTGTAAAGTGGCAAGCTCTGCT 1208
Qy 363 LeuApValAsnThrTrpMetIleGluTrpPheProAspValAspSerGluProThrThr 382
Db 1209 CTAGACGTGAACACTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1268
Qy 383 LeuSerTrpGlnSerValSerGlnAlaThrAsnTrpThrIleGlnGlnAspValLeuVal 402
Db 1269 CTTCCTGGAATCTGTCTCTCAAGGCGACGAACTGACGATCCACAGATTAATTAATAA 1328
Qy 403 ProPheTrpCyETrpAsnIleSerValTyrProMetLeuHisAspValValGluPro 422
Db 1329 CCTTCCTGCTGCTATACATCTCTGTGTATCCAACTGTGATGACAAAGTTGGCAGCCA 1388
Qy 423 TyrSerIleGlnAlaTyrAlaValGlnGluValProSerGluGluProGluThrVal 442
Db 1389 TATTCATCCAGGCTTATGCGAAAGAGCGCTTCATCGAAGGCTCTGAGCCAAAGTG 1448
Qy 443 GlnuAsnIleGlyValLeuThrValThrIleThrTrpGluIleProLysSerGluArg 462
Db 1449 GAGAACATTTGGCGTGAACAGCGTCAAGATCAATGAAAGATTTCCAAAGATGAGAGA 1508
Qy 463 LysGlyIleIleCyEAsnTrpThrIlePheTrpGlnAlaGluGlyValGlyLysGlyPheSer 482
Db 1509 AAGGTCATCATCTGCACTACCACTCTTTTTCACAACTGAAAGTGGAAAGATTTCTCC 1568
Qy 483 LysThrValAsnSerSerIleLeuGlnTyrGlyLeuGlnSerIleLysArgLysThrSer 502
Db 1569 AAGACAGTCAATTCAGCATCTTGCAAGTACGCGCTCGAGTCCCTGAAAGAAAGCCCTCT 1628
Qy 503 TyrIleValGlnValMetAlaAsnThrSerAlaGlyIleThrAsnGlyThrSerIleAsn 522
Db 1629 TACATTTGTCAGGTCATGCGCACGAGTGTGGGAGAACCAACGAGCAAGCATTAAT 1688
Qy 523 PheLysThrLeuSerPheSerValPheGluIleIleLeuIleThrSerLeuIleGlyGly 542
Db 1689 TTCAGACATTTGCTCATGATGCTTTAGATTAATCTCATTAATCTCTGATTTGCTGGA 1748
Qy 543 GlyLeuLeuIleLeuIleIleLeuThrValAlaTyrGlyLeuValLysProAsnLysLeu 562
Db 1749 GGCCTTCTTATTCATTAATCTGACAGTGGCATTTGCTCAAAAACCCAAACAATTTG 1808
Qy 563 ThrIleLeuCyETrpProThrValProAsnProAlaGlnSerSerIleAlaThrTrpHis 582
Db 1809 ACTCATCTGTGTGGCCACCGTTCCCAACCTGCTGAAAGTATGATGCAATGGCAT 1868
Qy 583 GlyAspAspPheLysAspValLeuAsnLeuLysGlnuSerAspAspSerValAsnThrGlu 602
Db 1869 GGAAGTATTTCAAGGATTAAGTAACTGAAAGGATGATGATGATGATGATGATGATGAT 1928
Qy 603 AspArgIleLeuLysProCyEserThrProSerAspValLeuValIleAspLysLeuVal 622
Db 1929 GACAGGATCTTAAACATGTTTCCACCCCGAGTGCAGAGTTGTCATGACAAAGTTGGTG 1988
Qy 623 ValAsnPheGlyAsnValLeuGlnGluIlePheThrAspGluAlaArgThrGlyGlnGlu 642
Db 1989 GTGAACCTTTGGGAATGTTCTCAAGAAATTTTTCACATGAAAGCAAGAACGGTCCAGA- 2047
Qy 643 LysGlnPheArgGlyValGlyGluTrpAsp 652
Db 2048 AAACAATTTAGAGAGGGGAAAGAAATGGGAC 2077

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; APPLICANT: Kuiper, Joseph L.
; APPLICANT: Maurer, Mark F.
; TITLE OF INVENTION: CYTOKINE RECEPTOR ZCYTOR17
; FILE REFERENCE: 00-42
; CURRENT APPLICATION NUMBER: US/10/772,531
; PRIOR FILING DATE: 2004-02-05
; PRIOR APPLICATION NUMBER: US/09/892,949
; PRIOR FILING DATE: 2001-06-26
; PRIOR APPLICATION NUMBER: US 60/214,282
; PRIOR FILING DATE: 2000-06-26
; PRIOR APPLICATION NUMBER: US 60/214,955
; PRIOR FILING DATE: 2000-06-29
; PRIOR APPLICATION NUMBER: US 60/267,963
; PRIOR FILING DATE: 2001-08-02
; NUMBER OF SEQ ID NOS: 93
; SOFTWARE: FASTSEQ for Windows Version 3.0
; SEQ ID NO 45
; LENGTH: 2529
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (162)...(2108)
US-10-772-531-45
Alignment Scores:
Pred. No.: 0 Length: 2529
Score: 3441.00 Matches: 648
Percent Similarity: 99.85% Conservative: 1
Best Local Similarity: 99.69% Mismatches: 1
Query Match: 98.77% Indels: 1
DB: 18 Gaps: 0
US-10-006-265-2 (1-652) x US-10-772-531-45 (1-2529)
Qy 3 LeuSerProGlnProSerCyEValAsnLeuGlyMetMetTrpThrTrpAlaLeuTrpMet 22
Db 129 CTCCTCCCGAGCTTCAATGATGTTTACCTGGGATGATGATGATGATGATGATGATGATG 188
Qy 23 LeuProSerLeuCyLysPheSerLeuAlaLeuProAlaLysProGluAsnIleSer 42
Db 189 CTCCTCCAGCTCTCAAAATTCAGCTGGAGCTCTGACAGCTAAGCTGAGAAACATTTCC 248
Qy 43 CysValTyrTyrTyrArgLysAsnLeuThrCyEThrTrpSerProGlyLysGluThrSer 62
Db 249 TGTGTCACTACATTAAGAAATTTTAACTGCACTTGAGTCCAGAAAGAAACCAAGT 308
Qy 63 TyrThrGlnTyrThrValLysArgThrTyrAlaPheGlyGluLysHisAspAsnCyEThr 82
Db 309 TATACCCAGTACACAGTTAAAGAACTTACGCTTTTGGAGAAACATGATTAATGATCA 368
Qy 83 ThrAsnSerThrSerGluAsnArgAlaSerCyEserPhePheLeuProArgIleThr 102
Db 369 ACCAATAGTTCTACAGTGAATCGTGGCTTCTTTTCTTTCCCTTCCAAAGATTAACG 428
Qy 103 IleProAspAsnTyrThrIleGluValGluAlaGlnuAsnGlyAspGlyValIleLysSer 122
Db 429 ATCCCAATTAATTAACATTAAGTGAAGCTGAAATGAGATGATGATTAATTAATCT 488
Qy 123 HisMetThrTyrTrpArgGluAsnIleAlaLysThrGluProProLysIlePheArg 142
Db 489 CATATGACATCTGAGATTAAGAACTTAAGCAATGCAAACTGAAACCACTTAAGATTTCCGT 548
Qy 143 ValLysProValLeuGlyIleLysArgMetIleGlnIleGluTrpIleLysProGluLeu 162
Db 549 GTGAACACAGTTTGGCATCAACGAAATGATTAATGATGATGATGATGATGATGATGATG 608
Qy 163 AlaProValSerSerAspLeuLysTyrThrLeuArgPheArgThrValAsnSerThrSer 182
Db 609 GCGCCTTTTCATCTGATTTAAATATACACTTCGATTCAGGACAGCAACAGTACAGC 668
Qy 183 TrpMetGluValAsnPheAlaLysAsnArgLysAspLysAsnGlnThrTyrAsnLeuThr 202

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RESULT 9

US-10-772-531-45

; Sequence 45, Application US/10772531

; Publication No. US20040142422A1

; GENERAL INFORMATION:

; APPLICANT: Sprecher, Cindy A.

; APPLICANT: Presnell, Scott R.

; APPLICANT: Geo. Zeren

; APPLICANT: Whitmore, Theodore E.

Db 669 TGGATGAGTCACTTCGCTTAAGAACCGTAAGATTAACCAACGTAACAACCTCAG 728
Qy 203 GATLeuGlnProPheThrGluTyrValIleAlaLeuArgCysAlaValLysGluSerLys 222
Db 729 GGAGCTCAGGCTTTTACAGAAATGTCATAGCTGTGAGTGTGGTCAAGAGGTCAAG 788
Qy 223 PheTyrSerAspTyrPheSerGlnGlyLysMetGlyMetThrGluGluAlaProCysGly 242
Db 789 TTCGTGAGTGACTGGAGCCAAAGAAAAATGGAAATGCTGAGAGAAAGAGCTCATGTGG 848
Qy 243 LeuGluLeuTyrArgValLeuLysProAlaGluAlaAspGlyArgArgProValArgLeu 262
Db 849 CTGGAACTGGAGAGATCTCGAAACCAAGCTGAGCGGATGGAAGAAAGCGCAGTGTG 908
Qy 263 LeuTyrLysLysAlaArgGlyAlaProValLeuGluLysThrLeuGlyTyrAsnIleTyr 282
Db 909 TTTTGAAGAGAGCAAGAGAGGCCCAAGTCTTAGAGAAACACTGTGCTAACACATATGG 968
Qy 283 TTTTyrProGluSerAsnThrAsnLeuThrGluThrMetAsnThrThrAsnGlnGlnLeu 302
Db 969 TACTATCCAGAAAGCAACACTAACCTCAGAAACATGAACACTACTAACCGACGCTT 1028
Qy 303 GlnLeuHisLeuGlyGlyGluSerPheTyrPvalSerMetLysSerTyrAsnSerLeuGly 322
Db 1029 GAACCTCATCTGGAGAGCGAGACCTTTGGTGTCTATGATTTCTTAATATCTCTTGGG 1088
Qy 323 LysSerProValAlaThrLeuArgIleProAlaIleGlnGluLysSerPheGlnCysIle 342
Db 1089 AAGTCTCCAGATGGCCACCTGAGAGATTCAGCTATTCAGAAAAATCATTTCACTGCTAT 1148
Qy 343 GluValMetGlnAlaCysValAlaGluAspGlnLeuValLysTyrPginSerSerAla 362
Db 1149 GAGGTATGAGGCGCTGCGTGTCTGAGGACCACTAGTGTGAAGTGGCAAACTCTGTGT 1208
Qy 363 LeuAspValAsnThrTyrMetIleGluTyrPheProAspValLysSerGluProThrThr 382
Db 1209 CTAGAGCTGAAACCTTGATGATTTGAATGTTTCCGATGTGACCTCAGACCCACACACC 1268
Qy 383 LeuSerTyrGluSerValSerGlnAlaThrAsnTyrThrIleGlnGlnAspLysLeuLys 402
Db 1269 CTTTCTGGGAATCTGTCTCAGGCCACGACCTGACGATCCAGCAAGATTAATTAATA 1328
Qy 403 ProPheTyrCysTyrAsnLysSerValTyrProMetLeuHisAspLysValGlyGluPro 422
Db 1329 CTTTCTGGGATATTAACATCTGTGTATCCAAATGTGATGACAAAGTGGCGAGCCA 1388
Qy 423 TyrSerIleGlnAlaTyrAlaLysGluGlyValProSerGluGlyProGluThrLysVal 442
Db 1389 TATTTTCATCCAGGCTTATGCAAAAGAGCGTTCATCAGAAAGTCTCTGAGACCAAGGTG 1448
Qy 443 GluAsnIleGlyValLysThrValThrIleThrTyrLysGluIleProLysSerGluArg 462
Db 1449 GAGAACTTTGGCTGAAGACGTCACGATCACAAGAAAGATTTCCCAAGATGAGAGA 1508
Qy 463 LysGlyIleIleCysAsnTyrThrIlePheTyrGlnAlaGluGlyLysGlyPheSer 482
Db 1509 AAGGATATATCTGCAACTACACACATCTTTACCAAGCTGAAGTGGAAAAAGATTCTCC 1568
Qy 483 LysThrValAsnSerSerIleLeuGlnTyrGlyLeuGluSerLeuLysArgLysThrSer 502
Db 1569 AAGACAGTCAATTCAGCATCTTGACGTACGGCTTGAGATCCCTGAAACCAAAAGACCTCT 1628
Qy 503 TyrIleValGlnAlaMetAlaAsnThrSerAlaGlyGlyThrAsnGlyThrSerIleAsn 522
Db 1629 TATATGTTCAAGTCAATGCGCACACAGTGTGGGGGAAACCAAGGACACACATTAAT 1688
Qy 523 PheLysThrLeuSerPheSerValPheGluIleIleLeuIleThrSerLeuIleGlyGly 542
Db 1689 TTCAAGGCATGTGCATTCAGTGTCTTGAGATTAATCTCTTAATCTCTCGATTGGTGA 1748
Qy 543 GlyLeuLeuIleLeuIleIleLeuThrValAlaTyrGlyLeuLysLysProAsnLysLeu 562
Db 1749 GGCTCTTATTTCTATTCATTCAGACAGTGGCATATGTTCTCAAAAAACCAACAATTTG 1808

Qy 563 ThrHisLeuCysTyrProThrValProAsnProAlaGluSerSerIleAlaThrTyrHis 582
Db 1809 ACTCATCTGTCTGTGGCCCACTTCCCAACCTGTGTAAGATTAAGCCACATGGCAT 1868
Qy 583 GlyAspAspPheLysAspLysLeuAsnLeuLysGluSerAspAspSerValAsnThrGlu 602
Db 1869 GGAGATGATTTCAAGATTAAGTAAACCTGAAGGAGTGTGATGACTGTGTGAACACAGA 1928
Qy 603 AspArgIleLeuLysProCysSerThrProSerAspLysLeuValIleAspLysLeuVal 622
Db 1929 GACAGATCTTAAACCATGTTCCACCCCACTGACAAAGTTGATGACAAAGTTGGTG 1988
Qy 623 ValAsnPheGlyAsnValLeuGlnGluIlePheThrAspGluAlaArgThrGlyGlnGlu 642
Db 1989 GTGAACCTTGGGAAAGTTCTTGCAAGAAATTTTCAACGATGAAGAACCAAGCGGTACGA 2047
Qy 643 LysGlnPheArgArgGlyLysGluTyrAsp 652
Db 2048 AAACAATTTAGAGGGGAAAGAAATGGGAC 2077

RESULT 10
US-09-972-708-5
; Sequence 5, Application US/09972708
; Publication No. US20030059871A1
; GENERAL INFORMATION:
; APPLICANT: Immunex Corporation
; APPLICANT: Cosman, David J.
; APPLICANT: Mosley, Bruce A.
; APPLICANT: Bird, Timothy A.
; APPLICANT: DuBoise, Robert F.
; APPLICANT: Wiley, Steven R.
; TITLE OF INVENTION: HEMATOPOIETIN RECEPTORS HPRL AND HPR2
; FILE NUMBER: 3160-B
; CURRENT APPLICATION NUMBER: US/09/972,708
; CURRENT FILING DATE: 2001-10-05
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 5
; LENGTH: 2238
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-972-708-5

Alignment Scores:
Pred. No.: 0 Length: 2238
Score: 3435.00 Matches: 647
Percent Similarity: 99.69% Conservative: 2
Beet Local Similarity: 99.39% Mismatches: 2
Query Match: 98.59% Indels: 1
DB: 10 Gaps: 0

US-10-006-265-2 (1-652) x US-09-972-708-5 (1-2238)

Qy 1 MetLysLeuSerProGlnProSerCysValAsnLeuGlyMetMetTyrThrTyrAlaLeu 20
Db 1 AAGAAGCTCTCTCCCAAGCTTCATGTGTAACTGGGAGATGATGGAGCTGGGACATG 60
Qy 21 TyrMetLeuProSerLeuCysLysPheSerLeuAlaAlaLeuProAlaLysProGluAsn 40
Db 61 TGGATGCTCCCTTCACTCGCAAAATTCAGCCCTGGAGAGCTCTCCAGCTAAAGCTTGAAGAC 120
Qy 41 HisSerCysValTyrTyrTyrArgLysAsnLeuThrCysThrTyrSerProGlyLysGlu 60
Db 121 ATTTCTGTGTACTACTATAGAAAAATTTAAACCTGACATGGAGTCCAGAGAAAGGAA 180
Qy 61 ThrSerTyrThrGlnTyrThrValLysArgThrTyrAlaPheGlyGlyLysHisAspAsn 80
Db 181 ACCAGTTAAACCAAGTACACATTAAGAGAACTTAAGCTTTTGAAGAAAAACATGATAAT 240
Qy 81 CysThrThrAsnSerSerThrSerGluAsnArgAlaSerCysSerPhePheLeuProArg 100
Db 241 TGTACAAACAATAGTTCTCAAGTGAATAATCGTGTCTGTCTTTTTCCTTCCAAAGA 300

QY 11ethrileproaspasentyrthrilegluvalagluasngluasgluvalle 120
 Db ATAAAGATCCAGATTAATATACCATTTAGGTGAAGCTGAAAATGGAATGATGTAAAT 360
 QY 121 lysSerHisMetThrTyrTrpArgLeuGluAenilealalyThrGluProProlysile 140
 Db AAATCTCATATGACATACCTAGAGATTAGAGAACATAGCAAAACCTGAACCTAAGATT 420
 QY 141 pheArgValLysProvalleuglyilelysarMetileglnileglnitripilelyspro 160
 Db TTCCCTGTGTAACCAAGTTTGGGCATCAAAACGAATGATTCAATGGAATGAATGAAGCCT 480
 QY 161 gluLeuAlaprovalSerSerAspLeuLysTyrThrLeuArgPheArgThrValanser 180
 Db GAGTTGGGCGCTGTTCATCTGATTTAAATACACCTTCGATTCAGACAGCTCAACACT 540
 QY 181 ThrSerTrpMetGluValAsnPheAlalyAsnArgLysAspLysAsnGlnThrTyrAsn 200
 Db ACCACCTGGATGGAAAGTCAACTTCCTTAAGAACCGTAAGATTAACCAACCTAACAC 600
 QY 201 LeuThrGlyLeuGlnProPheThrGluTyrValilealaleuArgCysAlavalysglu 220
 Db CTCACGGGGCTGCACACCTTTTACAGAAATATGTCATAGCTCTGCATGTCCGGTCAAGGAG 660
 QY 221 SerLysPheTrpSerAspTrpSerGlnGluLysMetGlyMetThrGluGlnGluAlapro 240
 Db TCAAAAGTTCTGAGAGTGAAGCTGAGCCAGAAAATGGGAATATCGAGAGAAACCTCCA 720
 QY 241 CysGlyLeuGluLeuTrpArgValleuLysProAlagluAlaAspGlyYArgArgProval 260
 Db TGTGGCTTGGAAGTGTGAGAGCTCTGAACCACTGAGGCGGATGGAAAGAGCCAGTGT 780
 QY 261 ArgLeuLeuTrpLysLysAlaArgLysAlaprovalleuGlnLysThrleuGlyTyrAsn 280
 Db CGGTGTATGAGAAAGAGCAAGAGAGAGCCAGCTCTAGAGAAAACCTGGCTACAAAC 840
 QY 281 IletppTyrTyrProGluSerSerAsnThrAsnLeuThrGluThrMetAsnThrThrAsnGln 300
 Db ATATGGTACTATCCAGAAAGCAACCTAACCTCAAGAAAACATGAACCTACTAACAG 900
 QY 301 GlnLeuGluLeuHisLeuGlyGlyLysSerPheTrpValSerMetLysSerTyrAsnSer 320
 Db CAGCTTGAAGTGCATCTGGAGAGCCAGAGCTTTTGGGTGTCTATATATTTCTTATATCT 960
 QY 321 LeuGlyLysSerProValAlaThrLeuArgLysProAlaleglnLysSerPheGln 340
 Db CTGGGAAGTCTCCAGTGGCCACCTGAGGATTCAGGATTCAGAAAATCATTTGAG 1020
 QY 341 CysileglnValMetGlnAlaCysAlaAlagluAspGlnLeuValLysTrpLysSer 360
 Db TGCATTTGAGGTCTATCAGAGCCCTGCTCTGAGGACCAAGCTAGTGTGAAGGGCAAGC 1080
 QY 361 SerAlaLeuAspValAsnThrTrpMetileglnitripheProAspValAspSerGluPro 380
 Db CCTGCTTACAGCTGAACCTTGATGATGATGATGATTTCCGAGTGTGACCTCAAGCCC 1140
 QY 381 ThrThrLeuSerTrpGluSerValSerGlnAlaThrAsnTrpThrileglnAlaAspLys 400
 Db AACACCTTTCTCTGGGAATCTGTCTCAGGCCAGCAAGACTGGACATCCAGAAACATAAA 1200
 QY 401 LeuLysPhePheTrpCysTyrAsnLysSerValTyrPheMetLeuHisAspLysValGly 420
 Db TTTAAACCTTTCTGTGTCTATTAACATCTCTGTGTATCCAAATGTTCTCAAGACAAATTTGGC 1260
 QY 421 GluProTyrSerileglnAlaTyrAlalyGluGlyValProSerGluGlyProGluThr 440
 Db GAGCATATTTCCATCCAGCTTATTCCTCAAAAGAGCGTTCTCATCGAAAGCTCTGAGACC 1320
 QY 441 LysValGluAsnileglnValLysThrValThrileThrTrpLysGluileProLysSer 460
 Db AAGGTGAGAAACATTTGGCGTGAAGACGGTCAAGATCAATGGAAAGAGATTTCCCAAGAGT 1380

QY 461 GluArgLysGlyileileCysAsnTyrThrilePheTyrGlnAlagluGlyLysGly 480
 Db GAGAGAAAGGATATATCTGACATACCACTTTTACCAAGCTGAAGGTGGAAGAGA 1440
 QY 481 PheSerLysThrValAsnSerSerileuGlnTyrGlyLeuGlnSerleuLysArgLys 500
 Db TTCTCCAGACAGCTCAATTCAGCATCTTGAGTACGGCCCTGAGACTCCCTGAACGAAAG 1500
 QY 501 ThrSerTyrileValGlnValMetAlaAsnThrSerAlaglyLysThrAsnGlyThrSer 520
 Db ACCCTTCAATGTTCTGAGTCATGGCCAGCACAGTGTGGGGGAACGACGGGACAGC 1560
 QY 521 IleAsnPheLysThrLeuSerPheSerValPheGlnileileleuileThrSerLeuile 540
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 QY 541 GlyLysGlyLeuLeuileleuileleuThrValAlaTyrGlyLysLysLysProAsn 560
 Db GTGGAGGCTTCTTATCTCATTAATCTGACAGTGGCATATGGTCTCAAAAACCCAAAC 1680
 QY 561 LysLeuThrHisLeuCysTrpProThrValProAsnProAlagluSerSerileAlaThr 580
 Db AAATGACTCATCTGTGTGGCCCAACCGTTCCCAACCTGTGAAAGATGATAGCCACA 1740
 QY 581 TrpHisGlyAspAspPheLysAspLysLeuAsnLeuLysGluSerAspAspSerValAsn 600
 Db TGGATGAGATGATTTTAAGATTAAGCTTAACCTGAAGAGTCTGATGACTCTGTGAAAC 1800
 QY 601 ThrGluAspArgLysLeuLysProCysSerThrProSerAspLysLeuValileAspLys 620
 Db ACAAGAGCAAGATCTTAAACCATGTTCCACCCCACTGACAAAGTTGTGATGACAAAG 1860
 QY 621 LeuValValAsnPheGlyAsnValleuGlnGluilePheThrAspGluAlaArgThrGly 640
 Db TTGGTGTGAATCTTGGGAATGTTCTGCAGAAAATTTTCAAGATGAAGCCAGAACGGGT 1920
 QY 641 GlnGluLysGlnPheArgArgLysGluTrp 651
 Db 1921 CAGGA-AAACAATTTAGAGGGGGAAGAAATGG 1952

RESULT 11
 US-10-715-667-5
 ; Sequence 5, Application US/10715667
 ; Publication No. US20040152161A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Immunex Corporation
 ; APPLICANT: Cosman, David J.
 ; APPLICANT: Mosley, Bruce A.
 ; APPLICANT: Bird, Timothy A.
 ; APPLICANT: Dubose, Robert F.
 ; TITLE OF INVENTION: HEMATOPOIETIN RECEPTORS HPR1 AND HPR2
 ; FILE REFERENCE: 3160-B
 ; CURRENT APPLICATION NUMBER: US/10/715,667
 ; PRIOR FILING DATE: 2003-11-14
 ; PRIOR APPLICATION NUMBER: US/09/972,708
 ; NUMBER OF SEQ ID NOS: 29
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO 5
 ; LENGTH: 2238
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 US-10-715-667-5

Alignment Scores:
 Pred. No.: 0 Length: 2238
 Score: 3435.00 Matches: 647
 Percent Similarity: 99.69% Conservative: 2
 Best Local Similarity: 99.39% Mismatches: 2
 Query Match: 98.59% Indels: 1
 DB: 18 Gaps: 0

US-10-006-265-2 (1-652) x US-10-715-667-5 (1-2238)

QY 1 MetLysLeuSerProGlnProSerCysValAsnLeuGlyMetMetTrpThrTrpAlaLeu 20
 Db 1 ATGAACTCTCTCCAGACCTTCACTGTTTAACTTGGGATGATGAGACCTGGGACCTG 60
 QY 21 TrpMetLeuProSerLeuCysLysPheSerLeuAlaAlaLeuProAlaLysProGluAsn 40
 Db 61 TGGATGCTCCCTTCACTGTCGAAATTCAGCTGCGAGCTTGCAGCTAAGCTCGAAGAC 120
 QY 41 1LeSerCysValTrpTrpTrpArglyAsnLeuThrCysThrTrpSerProGlyLysGlu 60
 Db 121 ATTTCTGTGTCTACACTATAGAAAAATTAACTGCACTTGGAGTCCAGAAAAAGGAA 180
 QY 61 ThrSerTrpThrGlnTrpThrValLysArgThrTrpAlaPheGlyGlyLysHisAspAsn 80
 Db 181 ACCAGTTATACCCAGTACAGACAGTTAAGAGAACTTACGCTTTTGGAGAAAAACATGATAT 240
 QY 81 CysThrThrAsnSerSerThrSerGluAsnArgAlaSerCysSerPhePheLeuProArg 100
 Db 241 TGTACAAACCAATAGTTCTACAGATGAAATCGTGTGCTCGTCTTTTCCCTTCCAAAG 300
 QY 101 1LeThr1LeProAspSerTrpThr1LeGluValGluAlaGluAsnGlyAspGlyVal1Le 120
 Db 301 ATACACATCCCAATATATATACCATTTGAGTGAAGCTGAAAAATGGAGATGGTGTAAAT 360
 QY 121 LysSerHisMetThrTrpTrpArgLeuGluAsn1LeAlaLysThrGluProProLys1Le 140
 Db 361 AAATCTCATATGACATCTGAGATTTAGAGACATACGAAAACTGAAACCACTTAAGATT 420
 QY 141 PheArgValLysProValLeuGlyLysArgMet1LeGln1LeGluTrp1LeLysPro 160
 Db 421 TTCGGTGTGAAACCAAGTTTGGGCATCAACGAATGATTCAAAATTTGATGAATGAAGCCT 480
 QY 161 GluLeuAlaProValSerSerAspLeuLysTrpThrLeuArgPheArgThrValAsnSer 180
 Db 481 GAGTTGGCGCTTTTCATCTGATTTAAATAACACCTTGATTTCCAGGAAGCAACAGT 540
 QY 181 ThrSerTrpMetGluValAsnPheAlaLysAsnArgLysAspLysAsnGlnTrpTrpAsn 200
 Db 541 ACCAGCTGATGAGATGACATTCCTGCTAAGAACCGTAAAGATTAACCAACCAAGCTACAC 600
 QY 201 LeuThrGlyLeuGlnProPheThrGluTrpVal1LeAlaLeuArgCysAlaValLysGlu 220
 Db 601 CTCACGGGGCTGCAGCTTTTACAGAAATATGTCATAGCTCTGCGAGTGGCGTCAAGAG 660
 QY 221 SerLysPheTrpSerAspTrpSerGlnGluLysMetGlyMetThrGluGluGluAlaPro 240
 Db 661 TCAAACTTCTGAGGTGACTGAGACCAAGAAAAATGGGAATGACTGGAAGAAAGCTCCA 720
 QY 241 CysGlyLeuGlnLeuTrpArgVal1LeuLysProAlaGluAlaAspGlyArgArgProVal 260
 Db 721 TGTGGCTGGAACCTGTGAGAGATCTGTAAACAGCTGAGCGAGTGAAGAAAGGCCAGTG 780
 QY 261 ArgLeuLeuTrpLysLysAlaArgGlyAlaProValLeuGluLysThrLeuGlyTrpAsn 280
 Db 781 CGGTTGTTATGAGAAAGCAAGAGAGGCCCACTAGTCTTACAGAAAAACACTTGGCTCAAC 840
 QY 281 1LeTrpTrpTrpProGluSerAsnThrAsnLeuThrGluThrMetAsnThrThrAsnGln 300
 Db 841 ATATGTACTATCCAGAAACCAACACTAACCTCACAGAAAACAATGAACACTTACTAACAG 900
 QY 301 GluLeuGluLeuHisLeuGlyLysGlyLysSerPheTrpValSerMet1LeSerTrpAsnSer 320
 Db 901 CAGCTTGAATCTGATCTGGAGAGCGAGAGCTTTTGGGTGTCTATGATTTCTTTAATTTCT 960
 QY 321 LeuGlyLysSerProValAlaThrLeuArg1LeProAla1LeGlnGluLysSerPheGln 340
 Db 961 CTGGAGAACTCCAGAGGCCCACTGAGATTCCAGCTATTCAGAAAAAATCATTTTCAG 1020
 QY 341 Cys1LeGluValMetGlnAlaCysValAlaGluAspGlnLeuValValLysTrpGlnSer 360
 Db 1021 TGCATTGAGGTGATGAGGCTGCGTTGCTGAGAGACCAAGCTAATGTGTGAAGTGGCAAGC 1080

QY 361 SerAlaLeuAspValAsnThrTrpMet1LeGluTrpPheProAspValAspSerGluPro 380
 Db 1081 CCTGCTCTAGAGCTGAGACCTTGGATGATGATGATTTCCGAGATGAGCTCAAGGCC 1140
 QY 381 ThrThrLeuSerTrpGluSerValSerGlnAlaThrAsnTrpThr1LeGlnGluLysLys 400
 Db 1141 ACCACCTTCTCCGGGAATCTGTGTCTCAGGCGACAGAACCTGAGCATCCAGCAAGTAA 1200
 QY 401 LeuLysProPheTrpCysTrpAsn1LeSerVal1TrpProMetLeuHisAspLysValGly 420
 Db 1201 TTAAACCTTCTCGGCTCTATACATCTGTGTATCCATGTTGCATACAAAGTTGGC 1260
 QY 421 GluProTrpSer1LeGlnAlaTrpAlaLysGluGlyValProSerGluGlyProGluThr 440
 Db 1261 GAGCATATTCATCCAGCTTATGCAAAAGAGGCTTCATCAGAAAGCTCTGAGACC 1320
 QY 441 LysValGluAsn1LeGlyValLysThrVal1Thr1LeThrTrpLysGlu1LeProLysSer 460
 Db 1321 AAGGTGAGAACATTTGGCTGAAAGCGGTACAGATCACATGAAAGAGATTCCTCAAGAT 1380
 QY 461 GluArgLysGly1LeLeCysAsnTrpThr1LePheTrpGlnAlaGluGlyLysGly 480
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 QY 481 PheSerLysThrValAsnSerSer1LeLeuGlnTrpGlyLeuGluSerLeuLysArgLys 500
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 QY 501 ThrSerTrp1LeValGlnValMetAlaAsnThrSerAlaGlyGlyThrAsnGlyThrSer 520
 Db 1501 ACCCTTTCATATTGTTCACTGATGCGACACAGCGTGGGGAACCAAGCGGACCAAC 1560
 QY 521 1LeAsnPheLysThrLeuSerPheSerVal1PheGlu1LeLeu1LeThrSerLeu1Le 540
 Db 1561 ATTAATTTCAAGACATGTCATTCAGTTCAGTCTTTGAGATTATCTCTAATCTTCTGATT 1620
 QY 541 GlyGlyGlyLeuLeu1LeLeu1Le1LeLeuThrValAlaTrpGlyLeuLysLysProAsn 560
 Db 1621 GGTGAGAGGCTCTTATTTCTCATTTTCCGACAGTGGCATATGCTCAAAAAACCAAC 1680
 QY 561 LysLeuThrHisLeuCysTrpProThrValProAsnProAlaGluSerSer1LeAlaThr 580
 Db 1681 AAATTGACTCATCTGTGTGGGCCACCGTCCCAACCTGCTGAAGATGTATGACACA 1740
 QY 581 TrpHisGlyAspAspPheLysAspLysLeuAsnLeuLysGluSerAspAspSerValAsn 600
 Db 1741 TGGCATGAGATGATTTCAAGATTAAGCTTAACCTGAAAGAGTCTGATGACTGTGAAC 1800
 QY 601 ThrGluAspArg1LeLeuLysProCysSerThrProSerAspLysLeuVal1LeAspLys 620
 Db 1801 ACAGAAAGACAGATCTTAAACATATGTTCCACCCCAAGAGACAAAGTTGGATGACAAAG 1860
 QY 621 LeuValAlaAsnPheGlyAsnValLeuGlnGlu1LePheThrAspGluAlaArgThrGly 640
 Db 1861 TTGGTGTGTAACTTTGGGAATGTCTGCAAGAAATTTTACAGATGAAACCAAGAGGAT 1920
 QY 641 GlnGluLysGlnPheArgArgGlyLysGluTrp 651
 Db 1921 CAGGA-AAACAAATTTAGAGGGGAGAAAGATGG 1952

RESULT 12
 US-09-892-949-1
 ; Sequence 1, Application US/09892949
 ; Publication No. US20030096339A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Sprecher, Cindy A.
 ; APPLICANT: Presnell, Scott R.
 ; APPLICANT: Gao, Zeren
 ; APPLICANT: Whitmore, Theodore E.
 ; APPLICANT: Kujiper, Joseph L.
 ; APPLICANT: Maurer, Mark F.
 ; TITLE OF INVENTION: CYTOKINE RECEPTOR ZCYTOR17

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: FILE REFERENCE: 00-42
: CURRENT APPLICATION NUMBER: US/09/892,949
: CURRENT FILING DATE: 2001-06-26
: PRIOR APPLICATION NUMBER: US 60/214,282
: PRIOR FILING DATE: 2000-06-26
: PRIOR APPLICATION NUMBER: US 60/214,955
: PRIOR FILING DATE: 2000-06-29
: PRIOR APPLICATION NUMBER: US 60/267,963
: PRIOR FILING DATE: 2001-08-02
: NUMBER OF SEQ ID NOS: 93
: SOFTWARE: FastSeq for Windows Version 3.0
: SEQ ID NO 1
: LENGTH: 2402
: TYPE: DNA
: ORGANISM: Homo sapiens
: FEATURE:
: NAME/KEY: CDS
: LOCATION: (171)...(2366)
: US-09-892-949-1

Alignment Scores:
Pred. No.: 0 Length: 2402
Score: 3435.00 Matches: 647
Percent Similarity: 99.85% Conservative: 1
Best Local Similarity: 99.69% Mismatches: 1
Query Match: 98.59% Indels: 1
DB: 10 Gaps: 0

US-10-006-265-2 (1-652) x US-09-892-949-1 (1-2402)
QY 3 LeuSerProGlnProSerCysValAsnLeuGlyMetThrTrpAlaLeuTrpMet 22
Db 138 CTCCTCCCGACCTTCATGTGTAACTGGGGAAGATGTGACCTGGGCACTGGATG 197
QY 23 LeuProSerLeuGlyPheSerLeuAlaLeuProAlaLeuProGlnAsnLleSer 42
Db 198 CTCCTCCCGACCTTCATGTGTAACTGGGGAAGATGTGACCTGGGCACTGGATG 257
QY 43 CysValTrpTrpTrpTrpTrpTrpTrpTrpTrpTrpTrpTrpTrpTrpTrp 62
Db 258 TGTGTCTAATCTAATGAGAAATTTTAACTGCACTTGAAGTCCAGAAAGAAACCA 317
QY 63 TyrThrGlnTrpTrpValLeuArgThrTyrAlaPheGlyGluValAspAsnCysThr 82
Db 318 TATACCCAGTACACGTTAAGAACTTAACGCTTTGAGAAATAACATGATTTGACA 377
QY 83 ThrAsnSerSerThrSerGluAsnArgLaseCysSerPheLeuProArgLleThr 102
Db 378 ACCAATAGTCTTACAGTGAATGATGCTGCTCTTTTCTTCCAAAGATAACG 437
QY 103 IleProAspAsnTrpThrIleGluValGluValAspGlyAspGlyValIleLeuSer 122
Db 438 ATCCAGATTAATTAATCAATGAGGTGAGACCTGAAATGAGATGATTAATTAAT 497
QY 123 HisMetThrTrpTrpArgLeuGluAsnIleAlaLeuSerGluProProValIlePheArg 142
Db 498 CATATGACATCTGAGATTAGAGAACATACGAAACCTGAACCACTTAAGATTTCC 557
QY 143 ValLeuProValLeuGlyIleLeuArgMetIleGlnIleGluTrpIleLeuProGluLeu 162
Db 558 GTGAACCAAGTTTGGGCATCAACGATGATTTCAATGATGATTAAGCTGAGTTG 617
QY 163 AlaProValSerSerAspLeuLysTrpTrpLeuArgPheArgThrValAsnSerThrSer 182
Db 618 GCGGCTTTTCATCTGATTTAAATACACACTTCATTCAGACAGTCAACAGTACAGC 677
QY 183 TrpMetGluValAsnPheAlaLeuAsnArgLysAspLysAsnGlnThrTyrAsnLeuThr 202
Db 678 TGGATGAGATCAACTTCCTTAAGAACCTTAAGATTAAGAACCTTAAGAACCTTA 737
QY 203 GlyLeuGlnProPheThrGluTrpValIleAlaLeuArgCysAlaValLeuGluSerLys 222
Db 738 GGGGTGACGCTTTTACAGATATGTATCTAGCTGCGATGTGGGTCAAGAGATCAAG 797

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QY 223 PheTrpSerAspTrpSerGlnGluValMetGlyMetThrGluGluAlaProCysGly 242
Db 798 TTCTGAGTACTGGAGCCAGAAATAATGGGAATGACTGAGAGAAAGCTTCATGTGC 857
QY 243 LeuGluLeuTrpArgValLeuLeuProAlaGluAlaAspGlyArgArgProValArgLeu 262
Db 858 CTGGAACGTGTGAGAGTCTTGAACCACTGAGGGGATGGAAGAAAGCCAGTGGGTTG 917
QY 263 LeuTrpLysValAlaArgGlyAlaProValLeuGluLysTrpLeuGlyTyrAsnLleTrp 282
Db 918 TTATGAGAAAGGAGGAGGAGCCCACTCTAAGAAACCACTTGGCTTACAACTATGG 977
QY 283 TyrTrpProGlnSerAsnThrAsnLeuThrGluThrMetAsnTrpThrAsnGlnLeu 302
Db 978 TACTATCCAGAAAGCACTTAACCTCACAAGAAACATGAACACTTACCAAGCAGCTT 1037
QY 303 GluLeuHisLeuGlyGlyGlySerPheTrpValSerMetLleSerTyrAsnSerLeuGly 322
Db 1038 GAACGCACTGGGAGGAGGAGGAGCTTTGGGTGTCTATGATTTCTTAATTTCTTTGG 1097
QY 323 LysSerProValAlaThrLeuArgLleProAlaIleGlnGluLysSerPheGlnCysIle 342
Db 1098 AAGTCTCCAGTGGCCACCTGAGGATTCACATATTCAAGAAATACTTTCAGTGCAAT 1157
QY 343 GluValMetGlnAlaCysValAlaGluAspGlnLeuValLysTrpGlnSerSerAla 362
Db 1158 GAGGTGATGACAGGCTGGTGTGTGAGGACCAAGCTAGTGTGAAGTGGCAAGCTTCT 1217
QY 363 LeuAspValAsnThrTrpMetIleGluTrpPheProAspValAspSerGluProThrThr 382
Db 1218 CTAGACGTAACACTTGGATGATTAATGATTTCCGATGTGAGCTCAGAACCCACCAAC 1277
QY 383 LeuSerTrpGlnSerValSerGlnAlaThrAsnTrpThrIleGlnGlnAspLysLeuLys 402
Db 1278 CTTTCTCGGGAATCTGTGTCTCAGGCCACGAATCGACATCCAGCAAGATAATTAATA 1337
QY 403 ProPheTrpCysTyrAsnLleSerValTyrProMetLeuHisAspLysValGlyGluPro 422
Db 1338 CTTTCTCGGGAATCTGTGTCTCAGGCCACGAATCGACATCCAGCAAGATAATTAATA 1397
QY 423 TyrSerIleGlnAlaTyrAlaLeuGlyGlyValProSerGluGlyProGluThrLysVal 442
Db 1398 TATTCATCCAGGCTTATGCAAGAAAGCCTTCATCAGAAAGTCTCGAACAAGTGG 1457
QY 443 GluAsnIleGlyValLysThrValThrIleThrTrpLysGluIleProLysSerGluArg 462
Db 1458 GAGAACTTGGCGTGAAGACGATCAGCATCAATGAAAGATTTCCCAAGAGTGAAGA 1517
QY 463 LysGlyLleIleCysAsnTrpThrIlePheTrpGlnAlaGluGlyGlyLysGlyPheSer 482
Db 1518 AAGGTATCACTCACTCACTCACTTTTAACTCACTCACTCACTCACTCACTCACT 1577
QY 483 LysThrValAsnSerSerIleLeuGlnTyrGlyLeuGlnSerLeuLysArgLysThrSer 502
Db 1578 AAGCACTCAATTCAGCATTTTCAAGTACGCTTGAAGTCTCTGAAGCAAGAACTCT 1637
QY 503 TyrIleValGlnValMetAlaAsnThrSerAlaGlyGlyThrAsnGlyThrSerIleAsn 522
Db 1638 TACATTTGTCAGTCAATGAGCAGACACAGTCTGGGGAACCAACGGGACCATTAAT 1697
QY 523 PheLysThrLeuSerPheSerValPheGluLleIleLeuLleThrSerLeuIleGlyGly 542
Db 1698 TTCAAGACATTTGATTCAGTGTCTTGAAGTATTCCTCATTAATCTTCTGATTTGG 1757
QY 543 GlyLeuLeuIleLeuIleIleLeuThrValAlaTyrGlyLeuLysLysProAsnLysLeu 562
Db 1758 GGCCTTTTATTTCTATTAATCTTCACTGACAGTGCATATGCTTCAAAAAACCAATTTG 1817
QY 563 ThrHisLeuCysTrpProThrValProAsnProAlaGlnSerSerIleAlaThrTrpHis 582
Db 1818 ACTCATCTGTGTGGCCACCGTTCACCACTGCTGAAGATGATATAGCACATGTCAT 1877

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QY      583 GLYAspAspPheLysAspLysLeuAsnLeuLysGluSerAspAspSerValAsnThrGlu 602
Db      1878 GGAGATCATTTCAAGATTAAGCTAAACCTGAAGAGATCTGATCCTGTGGACACAGAA 1937
QY      603 AspariIleLeuLysProCysSerThrProSerAspLysLeuValIleAspLysLeuVal 622
Db      1938 GACAGATCTTAAACCAATGTTCCACCCACAGACAAAGTGTGATTGCAAGTTGGTG 1997
QY      623 ValAsnPheGluValenValleuGlnGluIlePheThrAspGluIleAspThrGlnGlu 642
Db      1998 GTAACTTTGGGAATGTTCTGCAGAAATTTTACAGATGAACCCAGACGGGTCAAGA- 2056
QY      643 LysGlnPheArgArgGlyLysGluTrp 651
Db      2057 AACCAATTAGAGAGGGGAAAAAGATGG 2083

RESULT 13
US-10-351-157-110
; Sequence 110, Application US/10351157
; Publication No. US20030215838A1
; GENERAL INFORMATION:
; APPLICANT: Sprecher, Cindy A.
; APPLICANT: Gao, Zeren
; APPLICANT: Kujiper, Joseph L.
; APPLICANT: Dasovich, Maria M.
; APPLICANT: Grant, Francis J.
; APPLICANT: Presnell, Scott R.
; APPLICANT: Whitmore, Theodore E.
; APPLICANT: Hammond, Angela K.
; APPLICANT: No. US20030215838A1ak, Julia E.
; APPLICANT: Gross, Jane A.
; APPLICANT: Dillon, Stacey R.
; TITLE OF INVENTION: CYTOKINE RECEPTOR ZCYTOR17 MULTIMERS
; FILE REFERENCE: 02-02
; CURRENT APPLICATION NUMBER: US/10/351,157
; CURRENT FILING DATE: 2003-01-21
; PRIOR APPLICATION NUMBER: US 60/435,361
; PRIOR FILING DATE: 2002-12-19
; PRIOR APPLICATION NUMBER: US 60/389,108
; PRIOR FILING DATE: 2002-06-14
; PRIOR APPLICATION NUMBER: US 60/350,325
; PRIOR FILING DATE: 2002-01-18
; NUMBER OF SEQ ID NOS: 183
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 110
; LENGTH: 2402
; TYPE: DNA
; ORGANISM: Homo sapiens
; NAME/KEY: CDS
; LOCATION: (171)...(2366)
US-10-351-157-110

Alignment Scores:
Pred. No.: 0          Length: 2402
Score: 3435.00       Matches: 647
Percent Similarity: 99.85%    Conservative: 1
Best Local Similarity: 99.69%  Mismatches: 1
Query Match: 98.59%          Indels: 1
DB: 17                Gaps: 0

US-10-006-265-2 (1-652) x US-10-351-157-110 (1-2402)
QY      3 LeuSerProGlnProSerCysValAsnLeuGlyMetMetTrpThrTrpAlaLeuTrpMet 22
Db      138 CTCTCTCCCAAGCTTCATATGTTAACTGGGATGATGTGGACCTGGGACCTGTGATG 197
QY      23 LeuProSerLeuLysLysPheSerLeuAlaLeuProAlaLysProGluAsnIleSer 42
Db      198 CTCCTCATCTTCGAAATTCAGCCCTGGACGCTCTGCACTTAAGCTTGAAACATTTCC 257
QY      43 CysValIleTrpTrpArgLysAsnLeuThrCysThrTrpSerProGlyLysGluThrSer 62

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Db      258 TGTGTCTACTACTATAGAAAAATTTAACTGCACCTGGAGTCCAGAAAAAGAAACGACT 317
QY      63 TyrThrGlnTyrThrValLysArgThrTyrAlaPheGlyGlyValHisAspAsnCysThr 82
Db      318 TATACCACTACACACTTAAGAGAACTTACGCTTTGGAGAAAAACATATATCTTACA 377
QY      83 ThrAsnSerSerThrSerGluAsnArgAlaSerCysSerPhePheLeuProArgIleThr 102
Db      378 AACATATAGTTCTACAAAGTAAATCGTCTGTGCTCTTTTCTCTTCCAGAAATTAAG 437
QY      103 IleProAspAsnTyrThrIleGluValGluIleAsnGlyAspGlyValIleLysSer 122
Db      438 ATCCCAAGTAATATATACATTAAGAGTGAAGCTGAAAAAGAGATGTATTAATATCT 497
QY      123 HisMetThrTyrTrpArgLeuGluAsnIleAlaLysThrGluProProHisIlePheArg 142
Db      498 CATATACATCTGAGATTAAGAACATAGCAAAACCTGAACCACTTAAGATTTCCGT 557
QY      143 ValLysProValLeuGlyLysArgMetIleGlnIleGluTrpIleLysProGluLeu 162
Db      558 GTGAACCAAGTTTGGGATCAACAGATGATCAAAATTAAGATTAAGCTGAGTTG 617
QY      163 AlaProValSerSerAspLeuLysTyrThrLeuArgPheArgThrValAsnSerThrSer 182
Db      618 GGCCCTGTTTCATCTGATTTAAATACACACTTCGATTAAGACACTCAACAGTACCAC 677
QY      183 TrpMetGluValAsnPheAlaLysAsnArgLysAspLysAsnGlnThrTyrAsnLeuThr 202
Db      678 TGATGAAATCAACTTCCTTAAGAACCTTAAGATTAAGAACCAACCTTAACCTCAAG 737
QY      203 GlyLeuGlnProPheThrGluTyrValIleAlaLeuArgCysAlaValLysGluSerLys 222
Db      738 GGCTCAGACCTTTTACAGAAATATGCTAGCTCTCCAGTGGCGGTCAAGAGTCAAG 797
QY      223 PheTrpSerAspTrpSerGlnGlyLysMetGlyMetThrGluGlnGluAlaProCysGly 242
Db      798 TTCTGAGAGTCTGAGCGCAAGAAAAATGGAAATCAGCAGAGAAACCTCATGTGC 857
QY      243 LeuGluLeuTrpArgValLeuLysProAlaGluAlaAspGlyArgArgProValArgLeu 262
Db      858 CTGAACTGTGAGAGTCTTGAACCACTGAGCGGATGGAAGAGCCAGTCCGCTTG 917
QY      263 LeuTrpLysLeuAlaArgGlyAlaProValLeuGluLysThrLeuGlyTyrAsnIleTrp 282
Db      918 TATAGAAAGAGCAAGAGAGAGCCAGTCTTAAGAAAAACCTTGCTACCAATATGG 977
QY      283 TyrTyrProGluSerAsnThrAsnLeuThrGluThrMetAsnThrThrAsnGlnLeu 302
Db      978 TACTATCCAGAAAGCAACCTAACTCACAGAAACATGAACATTAACCGACGAGCTT 1037
QY      303 GluLeuHisLeuGlyGlyGluSerPheTrpValSerMetIleSerTyrAsnSerLeuGly 322
Db      1038 GACCTGATCTGGAGAGCAAGACCTTTTGGGTGTCTATGATTTCTTAATATCTCTTGG 1097
QY      323 LysSerProValAlaThrLeuArgIleProAlaIleGlnGluLysSerPheGlnCysIle 342
Db      1098 AAGTCCCAAGTGGCCACCTCGAGATTCAGGATTCAGAAAAAAATCTTCACTGATTC 1157
QY      343 GluValMetGlnAlaCysValAlaGluAspGlnLeuValValLysTrpGlnSerSerAla 362
Db      1158 GAGGTATCAGAGCCCTGCGTGTCTGAGGACCAAGCTAGTGTAAGTGGCAAGCTGTGCT 1217
QY      363 LeuAspValAsnThrTrpMetIleGluTrpPheProAspValAspSerGluProThrThr 382
Db      1218 CTAGACGTGAACCTTGATGATGATGATTTCCGATGTGACTCAAGGCCACACACC 1277
QY      383 LeuSerTrpGluSerValSerGlnAlaThrAsnTrpThrIleGlnGlnAspLysLeuLys 402
Db      1278 CTTTCTGGGAATCTGTGCTCAGGCCAGCAAGCTGAGCATCAGCAAGATTAATTAATA 1337
QY      403 ProPheTrpCysTyrAsnIleSerValTyrProMetLeuHisAspLysValGlyGluPro 422
Db      1338 CTTTCTGTGTGCTATTAACATCTCTGTGATCCAAATGTGCATGACAAAGTGGCGAGCCA 1397

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QY	423	LYRSERILEGINALSTRVALAVESGLUGLYVALPROSERGLUGLYPROGLIUTHRYSLV	442
DB	1398	TATTCATCTCAGGCTTATGCCAAAGAGGCGTTCCATCCAGAAAGCTCTGAGACCAAGG	145
QY	443	GLUAEINILEGLYVALLYETHRVATHRILETHTRPLYSGLUILEPROLYSERGLUATG	462
DB	1458	GAGAACATTTGGCGTGAAGCGGTCCAGATCAGATGAAAGAAATTTCCCAAGATGAGAGA	151
QY	463	LYSGIYLIELLECYASNTYRTHRIIEPETHYRGINALGLUGLYLYSGLYPHESE	482
DB	1518	AAGGATATCATCTGCACATCACATCTTTTCAAGAGTGAAAGGTGAAAGAAAGATTCTCC	157
QY	483	LYSTHVALAENSSERILEUGINTRYGLYUAGUSERLEULYBARGLYETHRSE	502
DB	1578	AAGACAGTCATTTCCAGCATCTTGAGTAGAGGCGCTGAGATCCTTGAAAGAAAGACCTCT	163
QY	503	TYRIIEVALGINVALMETALAEANTHRSERIALGLYLYTHIRASNGLYTHSERILEAN	522
DB	1638	TACATTTGTCAGGTGATGCGCCAGACACAGTCTGGGGGAGAACACGGGACAGCATTAAT	169
QY	523	PHELYSTRLEUSERPHESEVALPHEGLUIELLEULEUIERTH-SERLEUIELGLYGLY	542
DB	1698	TTCAAGACATTTGTCATTCAGTGTCTTGTGAGATTATCCATTAATCTTCTGATTTGGTGA	175
QY	543	GLYLEULEUIELLEUIELLEULEUTHVALAATYRGLYLEULYLYBPROBANTYSLEU	562
DB	1758	GACCTTCTTATTTCTATTAATCTTGACAGTGGGATATGGCTCAAAAACCAACCAAAATTG	181
QY	563	THRIASLEUCYSTRPROTHRVATPROANPROALAGUSERSERILEATHTRPHIS	582
DB	1818	ACTCATCTGTGTGGCCACCGTTCACAACTGCTGAAGTAAGTATAGCCACATGGCAT	187
QY	583	GLYASBAPPHIELYASPLYSLEUBANLEULYSGLYUSERASBPASERVALANTHRGLU	602
DB	1878	GGAGATGATTTCCAAAGATAGCTAAACCTGMAAGGATCTGAGATCTCTGTGAACACAGAA	193
QY	603	ASPAAGLILEULYBPROCYSESETHRPROSEASPLYSLEVALILASPLYSLEVALI	622
DB	1938	GACAGGATCTTAAACCATTTTCCACCCCACTGACAGATGGTATATGACAAATTTGGTG	199
QY	623	VALANPHEGLYASNVALLLEUGINLUILEPETHRASPGLUALAARGTHRGLYNGINLU	642
DB	1998	GTGAACCTTTGGGAATGTTCTGCAAGAAATTTTTCACAGATGAAGCCAGAACGGGTCAAGA-	205
QY	643	LYEGINPHEATGARGGLYLYSGLUITTP	651
DB	2057	AAACATTTTAGAGAGGGAAGAAATG	2083
RESULT 14			
US-10-772-531-1			
Sequence 1, Application US/10772531			
Publication No. US20040142422A1			
GENERAL INFORMATION:			
APPLICANT: Sprecher, Cindy A.			
APPLICANT: Preenell, Scott R.			
APPLICANT: Gao, Zeren			
APPLICANT: Whitmore, Theodore E.			
APPLICANT: Kuljper, Joseph L.			
APPLICANT: Maurer, Mark F.			
TITLE OF INVENTION: CYTOKINE RECEPTOR ZCYTOR17			
FILE REFERENCE: 00-42			
CURRENT APPLICATION NUMBER: US/10/772,531			
CURRENT FILING DATE: 2004-02-05			
PRIOR APPLICATION NUMBER: US/09/892,949			
PRIOR FILING DATE: 2001-06-26			
PRIOR APPLICATION NUMBER: US 60/214,282			
PRIOR FILING DATE: 2000-06-26			
PRIOR APPLICATION NUMBER: US 60/214,955			
PRIOR FILING DATE: 2000-06-29			
PRIOR APPLICATION NUMBER: US 60/267,963			
PRIOR FILING DATE: 2001-08-02			
NUMBER OF SEQ ID NOS: 93			

/ SOFTWARE:FastSeq for Windows Version 3.0									
/ SEQ ID NO 1									
/ LENGTH: 2402.									
/ TYPE: DNA									
/ ORGANISM: Homo sapiens									
/ FEATURE:									
/ NAME/KEY: CDS									
/ LOCATION: (171) ... (2366)									
US-10-772-531-1									
Alignment Scores:									
Pred. No.:		0	Length:	2402					
Score:		3435.00	Matches:	647					
Percent Similarity:		99.85%	Conservative:	1					
Best Local Similarity:		99.69%	Mismatch:	1					
Query Match:		98.59%	Indels:	1					
DB:		18	Gaps:	0					
US-10-006-265-2 (1-652) x US-10-772-531-1 (1-2402)									
QY	3	LeuSerProGlnProSerCyValAlaLeuGlyMetThrTrpAlaLeuTrpMet	22						
DB	138	CTCTCTCCCAAGCTTCATGTGTAACTGGGGATGATGTGGACCTGGGCACTGGATG	197						
QY	23	LeuProSerLeuCyValyPheSerLeuAlaAlaLeuProAlaValyProGluAsnIleSer	42						
DB	198	CTCCCTCACTCGCAAAATTCAGCCCTGGAGCTTCCAGCTTAACCTCGAACAATTTCC	257						
QY	43	CysValTyrTyrTyrArgLysAsnLeuThrCysThrTrpSerProGluLysGluThrSer	62						
DB	258	TGTGTCTACTACTATGAAAAATTTTAACTCTCACTTGGATGTCGAGAAAGAAACCACT	317						
QY	63	TyrThrGlnTyrThrValLysArgThrTyrAlaPheGlyLysLysAspAsnCysThr	82						
DB	318	TATACCAAGTACACAGTTAAGAACTTACGCTTTGGAGAAAAACATGATATTGTACA	377						
QY	83	ThrAsnSerSerThrSerGluAsnArgAlaSerCysSerPhePheLeuProArgIleThr	102						
DB	378	ACCAATGTTCTCAAGTAAAAATCGTGTCTCTTTTTCCTTCCCAAGAAATACG	437						
QY	103	IleProAspSerThrThrIleGluValGluAlaGluAsnGlyAspGluValIleValSer	122						
DB	438	ATCCCAATATATATACCATGAGGGAGGTGAAAAATGGAGATGGTATATTAAATCT	497						
QY	123	HisMetThrTyrTrpArgLeuGluAsnIleAlaLysThrGluProPheValIlePheArg	142						
DB	498	CATATGACATACGTGGAGATTAGAGAACATACGAAACATGAACCACTTAAGATTTTCGT	557						
QY	143	ValIysProValLeuGlyIleLysArgMetIleGlnIleGluTrpIleLysProGluLeu	162						
DB	558	GTTGAACACGTTTGGGCGATCAACAGATGATTCAAATTGAATGATTAAGCTCGAAGTTGG	617						
QY	163	AlaProValSerSerAspLeuLysTyrThrLeuArgPheArgThrValAsnSerThrSer	182						
DB	618	GCGCTGTTTCATCTGATTTAAAAATACACACTTCATTCAGAGACGTCAACAGTACACAGC	677						
QY	183	TrpMetGluValAsnPheAlaLysAsnArgLysAspLysAsnGlnThrTyrAsnLeuThr	202						
DB	678	TGAGTGAAGTCAACTTCGCTTAAGAACCGTAAAGATATAAAACCAAGCTACAACTCAAG	737						
QY	203	GlyLeuGlnProPheThrGluTyrValIleAlaLeuArgCysAlaValLysGluSerLys	222						
DB	738	GGGCTGAGCTTTTACAGAAATATGTCAATAGCTTCGCAATGTGGCGTCAAGAGATCAAG	797						
QY	223	PheTrpSerAspTrpSerGlnGluLysMetGlyMetThrGluGlnGluAlaProCysGly	242						
DB	798	TTCTGAGAGTACGTGGAGCCAAAAAAATGGGATGATGTGGAGAAAGACTCCCATGTGGC	857						
QY	243	LeuGluLeuTrpArgValLysLysProAlaGluAlaAspGlyArgGlyAspProValArgLeu	262						
DB	858	CTGAACCTGTGGAGATCTCTGAACCACTGAGGGCGAGTGAAGAAAGGCCAGTGGCGGTG	917						
QY	263	LeuTrpLysLysValaArgLysAlaProValLeuGlnLysThrLeuGlyTyrAsnIleTrp	282						

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Db      918 TTATGAGAGAGGCAAGAGAGCCCAAGTCTAGAGAAACCTGGCTACACATATGG
Qy      283 TTTTyrProGluSerAsnThrAsnLeuThrGluThrMetAsnThrThrAsnGlnGlnLeu
Db      978 TACTATCCAGAAAGCAACATACTACAGAAACATGAACATACTAACTTACAGCAGCTT
Qy      303 GluLeuHisLeuGlyGlyGluSerPheTrpValSerMetCileSerTyrAsnSerLeuGly
Db      1038 GAATCTCATCTGGAGAGCCGAGACCTTTGGGTCTATGATTTCTTAATATCTCTTGGG
Qy      323 LysSerProValAlaThrLeuArgGleProAlaIleGlnGluYserPheGlnCysIle
Db      1098 AAGCTCCAGTGGCCACCCCTGAGAGATTCCAGTATTCAGAAAAATCATTTTCAGTCATT
Qy      343 GluValMetGlnAlaCysValAlaGluAspGlnLeuValValYserTrpGlnSerSerAla
Db      1158 GAGGTCAATGAGGCGCTGGCTGTGAGGACACCTAGTGGTGAAGTGGCAAAAGCTCTGCT
Qy      363 LeuAspValAsnThrTrpMetCileGluTrpPheProAspValAspSerGluProThrThr
Db      1218 CTAGACCTGAACCTTGAGATTTGAATGTTCCGGATGTGACTCAGAGCCACACCACC
Qy      383 LeuSerTrpGluSerValSerGlnAlaThrAsnTrpThrIleGlnGlnAspYsLeuYs
Db      1278 CTTTCCGGAATCTGTGCTCAGGCCACGAACTGAGCATCCAGCAAGATAATTAA
Qy      403 ProPheTrpCysTrpAsnIleSerValTyrProMetLeuHisAspYsValGlyGluPro
Db      1338 CTTTCTGGTGGATTAACATCTCTGTATCCAAATGTGATACAAAGTGGCGAGCCA
Qy      423 TyrSerIleGlnAlaTyrAlaYsGluGlyValProSerGluGlyProGluThrIleVal
Db      1398 TATTCATCCAGCTTATGCCAAAGAGGCTTCCATCAGAAAGTCTTGAGACCAAGGTG
Qy      443 GluAsnIleGlyValIleYsThrValThrIleThrTrpYsGlnIleProYsSerGluArg
Db      1458 GAGAAATCTGGCTGAAGACGCTCAGCATCAGTGAAGAAAGATGCCCAAGATGAGAGA
Qy      463 LysGlyIleIleCysAsnTyrThrIlePheTyrGlnAlaGlnGlyIleYsGlyPheSer
Db      1518 AAGGGATCATCTGCAACATACCATCTTTTACCAGCTGAAGGTGAAGAAAGATCTCC
Qy      483 LysThrValAsnSerSerIleLeuGlnTyrGlyLeuGluSerLeuYsArgIleYsThrSer
Db      1578 AAGACGCTCAATTCAGCACTTCGCACTAGCGCTGGAAGTCCCTGAACCAAAAGACCTCT
Qy      503 TyrIleValGlnValMetAlaAsnThrSerAlaGlyGlyThrAsnGlyThrSerIleAsn
Db      1638 TACATGTTCAGGTATGCGCACACACAGTGTGGGGAGCAACAGGAGCACACATTAAT
Qy      523 PheLysThrLeuSerPheSerValPheGlnIleIleLeuIleThrSerLeuIleGlyGly
Db      1698 TTCAAGCATATGTCATTCAGTGTCTTGAAGATTACCTCAATCTCTGATGGTGGGA
Qy      543 GlyLeuLeuIleLeuIleIleLeuThrValAlaTyrGlyLeuYsYsProAsnYsLeu
Db      1758 GGGCTTCTTATTTCTCATTAATCCGACAGTGGCATATGCTCTCAAAAAACCAAAATTTG
Qy      563 ThrHisLeuCysTrpProThrValProAsnProAlaGluSerSerIleAlaThrTrpHis
Db      1818 ACTCATCTGTGTGGCCACCGTCCCAACCTGTGTAAGTAGTATAGCACATGGCAT
Qy      583 GlyAspAspPheYsAspYsLeuAsnLeuLeuGluSerAspAspSerValAsnThrGlu
Db      1878 GAGATGATTTCAAGATTAAGCTAAACCTGAAGAGCTGATGATCTCTGGAACACAGAA
Qy      603 AspArgIleLeuYsProCysSerThrProSerAspYsLeuValIleAspYsLeuVal
Db      1938 GACAGATCTTAAACCATATTTCCACCCCAAGTACAGATTGGTGAATGCAAGTTGGTG
Qy      623 ValAsnPheGlyAsnValLeuGlnGluIlePheThrAspGluAlaArgThrGlnGlu

```

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Db      1998 GTGAACCTTGGGAATGTTCTGCAAGAAATTTTTCACAGATGAAGCCAGAAAGGCTCAGGA
Qy      643 LysGlnPheArgArgGlyYsGluTrp
Db      2057 AAACAAATTTTGAAGGGGAAAGAAATGG
Qy      651
Db      2083

RESULT 15
US-09-972-708-3
; Sequence 3, Application US/09972708
; Publication No. US20030059871A1
; GENERAL INFORMATION:
; APPLICANT: Immunex Corporation
; APPLICANT: Cosman, David J.
; APPLICANT: Mosley, Bruce A.
; APPLICANT: Bird, Timothy A.
; APPLICANT: Dubose, Robert F.
; APPLICANT: Wiley, Steven R.
; TITLE OF INVENTION: HEMATOPOIETIN RECEPTORS HPRI AND HPR2
; FILE REFERENCE: 3160-B
; CURRENT APPLICATION NUMBER: US/09/972,708
; CURRENT FILING DATE: 2001-10-05
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3
; LENGTH: 2480
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-972-708-3

Alignment Scores:
Pred. No.: 0 Length: 2480
Score: 3435.00 Matches: 647
Percent Similarity: 99.69% Conservative: 2
Best Local Similarity: 99.39% Mismatches: 2
Query Match: 98.59% Indels: 1
DB: Gaps: 0

US-10-006-265-2 (1-652) x US-09-972-708-3 (1-2480)
Qy      1 MetLysLeuSerProGlnProSerCysValAsnLeuGlyMetMetTrpThrTrpAlaLeu
Db      132 ATGAAGCTCTCTCCAGGCTTCATGTGTAACTGGGGATATGTGGACCTGGGCACTG
Qy      21 TrpMetLeuProSerLeuCysLysPheSerLeuAlaAlaLeuProAlaYsProGluAsn
Db      192 TGGATCTCTCTTCACTCTGCAAAATTCAGCTGGAGAGCTCTGCCAGTAAAGCTGAAGAC
Qy      41 IleSerCysValTyrTyrTyrArgYsAsnLeuThrCysThrTrpSerProGlyYsGlu
Db      252 ATTTCTGTGTCTACTACTATAGAAATTTAACTGCACCTTGGAGTCCAGGAAAGGAA
Qy      61 ThrSerTyrThrGlnTyrThrValIleYsArgThrTyrAlaPheGlyGluYsHisAspAsn
Db      312 ACCAGTTAAACCCAGATACAGTAAAGAGAACTTACGCTTTTGGAGAAAAACATGATTAAT
Qy      81 CysThrThrAsnSerSerThrSerGluAsnArgAlaSerCysSerPhePheLeuProArg
Db      372 TGTACAAACCAATAGTTCTTCAAGTGAATTCGTGCTCTCTTTTCTCTTCCACAAGA
Qy      101 IleThrIleProAspAsnTyrThrIleGluValGluAlaGluAsnGlyAspGlyValIle
Db      432 ATPAAGATCCCAAGATTAATATACCAATGAGTGAAGAGCTGAAGAAATGAGATGATTAAT
Qy      121 LysSerHisMetThrTyrTrpArgLeuGluAsnIleAlaYsThrGluProProYsIle
Db      492 AAATTCATATGACATACATACGAGATTAGAGAAACATAGCAAAACCTGAACACCTTAAGATT
Qy      141 PheArgValYsProValLeuGlyIleYsArgMetIleGlnIleGluTrpIleYsPro
Db      552 TTCCGTTGAACCAAGTTTGGCATCAACCAATGATTTCAATTCATTAATGATTAAGCCT
Qy      161 GluLeuAlaProValSerSerAspLeuYsTyrThrLeuArgPheArgThrValAsnSer

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Db 612 GAGTGGCCGCTTTCATCTGATTTAAATACACACTTCGATCAGGACAGTCAACAGT 671
 Qy 181 ThSertPmetGluValAsnPhenAlaIysAsnArgIleAspIleValAsnGlnThrTyrAsn 200
 Db 672 ACCAGCTGGAGGAGGAGTCAACTTCGTAAAGAACCTTAAGATAAACCAACCGTACAC 731
 Qy 201 LeuThrGlyLeuGlnProPheThrGlnTyrValIleAlaLeuArgCysAlaValIleGlu 220
 Db 732 CTCACGGGGCTGCACCCCTTTTACAGAAATATGTCATAGCTCTGCGATGTGGGTACAGAG 791
 Qy 221 SerIysPheTyrSerAspTyrPserGlnIleIysMetGlyMetThrGluGluGluAlaPro 240
 Db 792 TCAAGTTCTGGAGAGCTGGAGCCAGAAAAAATGGAAATGACTGAGGAAGAAAGCTCCA 851
 Qy 241 CysGlyLeuGluLeuTTPArgValIleuIysProAlaGluAlaAspGlyArgArgProVal 260
 Db 852 TGTGGCTGGAAAGCTGGAGAGTCTGAAACCAAGCTGAGGCGGAGGAGGAAGAGGCAATG 911
 Qy 261 ArgLeuLeuTTPlysIleValArgGlyAlaProValIleuGluIysThrLeuGlyTyrAsn 280
 Db 912 CGGTGTTATGAAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 971
 Qy 281 IleTyrTyrTyrProGluSerAsnThrAsnLeuThrArgIleThrMetAsnThrThrAsnGln 300
 Db 972 ATATGTAATCTACGAAAGCAACCTAACCTCACAGAAACATGAACTACTAACCAAG 1031
 Qy 301 GlnLeuGluLeuHleuGlyGlyGluSerPheTyrPvalSerMetIleSerTyrAsnSer 320
 Db 1032 CAGCTTGAACTGCACTGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1091
 Qy 321 LeuGlyIysSerProValAlaThrIleuArgIleProAlaIleGlnIleIysSerPheGln 340
 Db 1092 CTGAGAGAGTTCCTCAGTGGCCACCTCGAGATTCAGCTATTCAGAAATAATCATTTTCA 1151
 Qy 341 CysIleGluValMetGlnAlaCysValAlaGluAspGlnLeuValIleTyrPqlnSer 360
 Db 1152 TGCATTGAGGTGATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1211
 Qy 361 SerIleuAspValAsnThrTTPMetIleGluTTPheProAspValAspSerGluPro 380
 Db 1212 CTGTCTTACGACGTGAACACTGTGATGATTAATGTGTTCCGAGTGTGACTCAGAGCCC 1271
 Qy 381 ThrThrIleuSerTTPGluSerValSerGlnAlaThrAsnTTPThrIleGlnIleAspIys 400
 Db 1272 ACCACCTTCTCTGAGATCTGTCTCAGGCCACAGAACTGAGCATCAGCAAGATTA 1331
 Qy 401 LeuIysProPheTyrPylAsnIleSerValTyrProMetLeuHleuAspIysValGly 420
 Db 1332 TTTAAACCTTCTGTGTCTATTAATCTCTGTATCCATGTTGATGACAAAGTTGGC 1391
 Qy 421 GluProTyrSerIleGlnAlaTyrAlaIysGluGlyValProSerGluGlyProGluThr 440
 Db 1392 GAGCATATTCATCCAGGCTTAATGCCAAGAGAGGCGTTCCATCAGAAAGTCTGAGACC 1451
 Qy 441 LysValGluAsnIleGlyValIleValThrValThrIleThrTTPlysGluIleProIysSer 460
 Db 1452 AAGGTGAGAACATTTGGCGTGAAGCGGTCAAGATCACATGAAAGAGATTTCCCAAGAGT 1511
 Qy 461 GluArgIysGlyIleIleCysAsnTyrThrIlePheTyrGlnAlaGluGlyGlyIle 480
 Db 1512 GAGAGAAAGGATATCATCTGCACTACACCATCTTTTACCAAGCTGAAGGTGAAGAAAGA 1571
 Qy 481 PheSerIysThrValAsnSerSerIleuGlnTyrGlyLeuGluSerLeuIysArgIys 500
 Db 1572 TTTCTCAAGACATCAATTCAGCATCTTGACATACGCGCTGAGATCCCTGAAAAGAAAG 1631
 Qy 501 ThrSerTyrIleValGlnValIleMetAlaAsnThrSerAlaGlyIleValAsnGlyThrSer 520
 Db 1632 ACCTCTTACATTTGTCAGGTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1691
 Qy 521 IleAsnPheIysThrLeuSerPheSerValPheGluIleIleuIleThrSerLeuIle 540
 Db 1692 ATAAATTTCAAGACATTTGTCTATTCAGTGTCTTTGAGATTATCTCATTAATCTCTGATT 1751

Qy 541 GlyGlyGlyLeuLeuIleLeuIleIleuThrValAlaTyrGlyLeuIysIysProAsn 560
 Db 1752 GGTGAGGCTTCTTATTTCTATTAATCTGACAGGAGCATATGCTCAAAAACCCCAAC 1811
 Qy 561 LysLeuThrIleLeuCysTyrProThrValProAsnProAlaGluSerSerIleAlaThr 580
 Db 1812 AAATTTGACTCATCTGTGTGTGAGGCCACCGTTCCAACCTGCTGAAGATGATAGCCACA 1871
 Qy 581 TrpHisGlyAspAspPheIysAspIysLeuAsnLeuIysGluSerAspAspSerValAsn 600
 Db 1872 TGGCATGAGATGATTTCAAGATTAAGCTAAACCTGAAGAGTGTGATGACTCTGTGAAC 1931
 Qy 601 ThrGluAspArgIleLeuIysProCysSerThrProSerAspIysLeuValIleAspIys 620
 Db 1932 ACAGAAAGCAGAACTTAAACCAATGTTCCACCCCGAGTGCACAGTGTGATGACAAAG 1991
 Qy 621 LeuValValAsnPheGlyAsnValLeuGlnIlePheThrAspGluAlaArgThrGly 640
 Db 1992 TTGGTGGTGAATCTTGGGAATGTTCTGCAAGAAATTTTCAAGATGAAGCCAGAACGGGT 2051
 Qy 641 GlnIleIysGlnPheArgArgGlyIysGluTyr 651
 Db 2052 CAGGA-AAACATTTAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2083

Search completed: February 23, 2005, 20:17:05
 Job time : 1084.05 secs

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GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Run on: February 23, 2005, 08:54:07, Search time 5993.32 Seconds
(without alignments)
1140.927 Million cell updates/sec

Title: US-10-006-265-2

Perfect score: 3484
Sequence: 1 MKLSPQPCVNLGMMTWAL.....FTDEARTQEQKFRGKEMD 652

Scoring table:

BLOSUM62
Xgapop 10.0, Xgapext 0.5
Ygapop 10.0, Ygapext 0.5
Fgapop 6.0, Fgapext 7.0
Delop 6.0, Delext 7.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Command line parameters:

-MODEL=frame+g2n.model -DEV=xlh
-Q=/cgn2.1/USPRO.spool/US10006265/runat.18022005.094658.22193/app.query.fasta_1.2069
-DB=BS1 -QFMT=fastcap -SUFFIX=rest -MINMATCH=0.1 -LOOPEXT=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=1 -MATRIX=biosum62 -TRANS=human40.cdi -LIST=45
-DOCLIGN=200 -THR_SCORE=DCT -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTMT=ptco -NORM=ext -HEAPSIZ=500 -MINLEN=0 -MAXLEN=200000000
-USER=US10006265 @CGN_1_1_7723 @runat.18022005.094658.22193 -NCPU=6 -ICPU=3
-NO MMAP -LARGQUERY -NEG_SCORES=0 -WAIT -DSPELCK=100 -LONGLOG
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -Fgapop=6
-Fgapext=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

EST:
1: gb_est1:
2: gb_est2:
3: gb_hic:
4: gb_est3:
5: gb_est4:
6: gb_est5:
7: gb_est6:
8: gb_gsa1:
9: gb_gsa2:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	709.5	20.4	2232	3	AK030512 Mus muscu
2	655.5	18.8	5264	3	BC071555 Homo sapi
3	647.5	18.6	3055	3	AY110138 Rattus no
4	526	15.1	663	2	BB617934 BB617934
5	470.5	13.5	653	5	BU455838 BU455838
6	468.5	13.4	637	7	CF174021 CF174021
7	464.5	13.3	2804	3	AK089305 Mus muscu
8	459.5	13.2	2592	9	AY412152 Homo sapi
9	423.5	12.2	2792	3	BC040954 Homo sapi

10	397	11.4	651	7	CF915066
11	395.5	11.4	2535	9	AY412154 Mus muscu
12	389	11.2	1931	3	CR610771 full-leng
13	355	10.2	1512	3	BC020454 Mus muscu
14	347	10.0	592	6	CA561173 K0283D09-CA560924 K0279C07-BU271003 603508092
15	342	9.8	479	6	CA560924 K0279C07-BU271003 603508092
16	326	9.4	821	5	BU460273
17	325.5	9.3	851	5	BU460273
18	320.5	9.2	825	6	CB518939
19	320.5	9.2	2591	9	AY412153 Pan trogl
20	315.5	9.1	776	7	CF747542
21	306	8.8	715	7	CK634184
22	305.5	8.8	1131	5	BX380515 BX380515 BX380515
23	304	8.7	1659	3	CR611411 full-leng
24	302	8.7	546	6	CA535774
25	297	8.5	553	6	CA559989
26	296.5	8.5	763	5	BU288431 603607401
27	294.5	8.5	628	6	CB427282
28	294	8.4	697	7	CN529323
29	291	8.4	459	8	A0022781
30	291	8.4	642	6	CB512958
31	286	8.2	751	5	BQ770280
32	286	8.2	1097	5	BX359249
33	283	8.1	1577	3	CR612729 full-leng
34	282	8.1	761	5	BU460413
35	279	8.0	669	5	BU322304
36	278	8.0	721	7	CN454854
37	277	8.0	709	5	BQ185371
38	275.5	7.9	612	9	AG138991 Pan trogl
39	275.5	7.9	1073	5	BX382126 BX382126
40	270	7.7	518	6	CA561193 K0283F09-CA559290 K0256G09-CD350375
41	270	7.7	523	6	CD350375
42	270	7.7	698	6	CF780723
43	268.5	7.7	887	4	BC921322
44	268	7.7	587	7	BC921322
45	266.5	7.6	699	6	CB168262

ALIGNMENTS

RESULT 1	AK030512	2232 bp	mus musculus adult male pituitary gland cDNA, RIKEN full-length enriched library, clone:530424C19 product:hypothetical protein, full insert sequence.
ACCESSION	AK030512	1	GI:26326508
VERSION	AK030512.1		
KEYWORDS	HTC, CAP trapper.		
SOURCE	Mus musculus (house mouse)		
ORGANISM	Mus musculus		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.		
AUTHORS	Carninci, P. and Hayashizaki, Y.		
TITLE	High-efficiency full-length cDNA cloning		
JOURNALS	Meth. Enzymol. 303, 19-44 (1999)		
MEDLINE	99279253		
PUBMED	10349636		
REFERENCE	2		
AUTHORS	Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Kono, H., Okazaki, Y., Muramatsu, M., and Hayashizaki, Y.		
TITLE	Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes		
JOURNALS	Genome Res. 10 (10), 1617-1630 (2000)		
MEDLINE	20499374		
PUBMED	11042159		
REFERENCE	3		
AUTHORS	Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P., Kono, H., Akiyama, J., Nishi, K., Kitesu, T., Tashiro, H., Itoh, M., Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A., Yamamoto, R., Matsunoto, H., Sakaguchi, S., Ikegami, T., Kaishiwagi, K., Fujiwaka, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Wataniki, M.,		

TITLE
Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsunura, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y.
RIKEN Integrated sequence analysis (RISA) system-384-format sequencing pipeline with 384 multiplexed sequence

JOURNAL
Genome Res. 10 (11), 1757-1771 (2000)

MEDLINE
20530913

REFERENCE
PUBMED
11076861

TITLE
The RIKEN Genome Exploration Research Group Phase II Team and the FANTOM Consortium.
Functional annotation of a full-length mouse cDNA collection
Nature 409, 685-690 (2001)

JOURNAL
Nature 420, 563-573 (2002)

REFERENCE
PUBMED
12022222

TITLE
The FANTOM Consortium and the RIKEN Genome Exploration Research Group Phase I & II Team.
Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs
Nature 420, 563-573 (2002)

JOURNAL
Nature 420, 563-573 (2002)

REFERENCE
PUBMED
12022222

TITLE
Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail: genome-res@gscc.riken.jp, URL: http://genome.gsc.riken.jp/, Tel: 81-45-503-9222, Fax: 81-45-503-9216)

JOURNAL
Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail: genome-res@gscc.riken.jp, URL: http://genome.gsc.riken.jp/, Tel: 81-45-503-9222, Fax: 81-45-503-9216)

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TITLE
Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail: genome-res@gscc.riken.jp, URL: http://genome.gsc.riken.jp/, Tel: 81-45-503-9222, Fax: 81-45-503-9216)

JOURNAL
Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail: genome-res@gscc.riken.jp, URL: http://genome.gsc.riken.jp/, Tel: 81-45-503-9222, Fax: 81-45-503-9216)

TITLE
Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail: genome-res@gscc.riken.jp, URL: http://genome.gsc.riken.jp/, Tel: 81-45-503-9222, Fax: 81-45-503-9216)

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TITLE
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Alignment Scores:
Pred. No.: 1,156-64
Score: 709.50
Percent Similarity: 79.81%
Best Local Similarity: 67.79%
Query Match: 20.36%
DB: 3
Gaps: 2

US-10-006-265-2 (1-652) x AK030512 (1-2232)

QY	434	ProsergluylprogluThrValGluAenlleGlyVallyThrValThrleThr	453
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QY	454	TrpLysGluIleProLysSerGluArgLysGlyIleleCysAsnThrThrlePheTyr	473
DB	272	TGGAGGAGATTCTTAAGGTCTTGAATGATGATTTATCAATTAACCTGATTTTC	331
QY	474	GlnAlaGluIleGlyLysGlyPheSerIleThrValAsnSerSerleuGlnTyrGly	493
DB	332	CAAGGTGAAGGTGAAGAAAGAACTCTCAAGACTGTTAACTTCATGCGCTGAGTGC	391
QY	494	LeuGluSerleuLysArgLysThrSerTyrIleValGlnValMetAlaAsnThrSerAla	513
DB	392	CTGGAGTCTCTCAACGAGGACCTCTTAATCTGTTGGTATGCGCAGCAGAGCT	451
QY	514	GlyGlyThrAsnGlyThrSerleuAsnPhenylThrLeuSerPheSerValPheGluIle	533
DB	452	GAGAGTCAACGAGGTGAGATTAATCTCAAGACTTCTCAATCATGCTGTTGAAAT	511
QY	534	IleleuIleThrSerleuIleGlyGlyLeuLeuIleleuIleThrValAla	553
DB	512	GTCCTTCTCAACCTCTTAATGAGAGGCTTCTTCTTCTTCAATCAACGAGT	571
QY	554	TyrGlyLeuLysLysProAsnLysleuThrIleLysCysTrpProThrValProAsnPro	573
DB	572	TTTGCTTCAAGGACCAACCGGTGACTCCCTGCTGCTGATGTTCCCAACCT	631
QY	574	AlaGluSerSerleuAlaThrThrPheIleGlyAspAspPheLysAspLysLeuAsnLys	593
DB	632	GCTGAAGAGTATTGATCCATGCTCGAGATGTTTCAAG---AAGTCAATATGAA	688
QY	594	GluSerAspAspSerValAsnThrGluAspArgIleLeuLysProCysSerThrProSer	613
DB	689	GAGACTGGAACCTCTGCGGACACAGAGCGTCTTCAACATGTCCTCCGCTCCGCG	748
QY	614	AspLysLeuValIleAspLysLeuValAlaAsnPheGlyAsnValLeuGlnIlePhe	633
DB	749	GAT-----CTCATTTGACAAAGCTGTAAGAACTTTGAGAAATTTCTGGAATTTTG	802
QY	634	ThrAspGluAlaArgThrGlyGln	641
DB	803	ACAGAGAGAGCTGGAAGGCTCAG	826
RESULT 2	BC071555	5264 bp	mRNA linear
LOCUS	BC071555	5264 bp	5264 bp
DEFINITION	BC071555.1	GI:47938807	containing frame-shift
ACCESSION	BC071555		
VERSION	BC071555.1		
KEYWORDS	HTC		
SOURCE	Homo sapiens (human)		
ORGANISM	Homo sapiens		
REFERENCE	Strausberg, R.L., Feigold, E.A., Grouse, L.H., Derge, J.G., Klausner, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D., Altschul, S.F., Zeeberg, B., Buetow, K.H., Schefer, C.F., Bhat, N.K., Hopkins, R.F., Jordan, H., Moore, T., Wax, S.I., Wang, J., Hsieh, F., Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L., Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L.,		

ORIGIN


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Db      1664 CCTGAATCCATAAAGCATATCACTTAAACAAGCTTCACCTTCAAGGACCTACTGTTCCG 1723
Qy      442 ValGluAsnIleGlyValIleThrValThIleThrTrpIleProIleProIleSerGlu 461
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Qy      462 ArgIleGlyIleIleCysAsnIleThrIlePheThrGlnIleGluGlyIleGlySerGlyPhe 481
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Qy      482 SerIleThrValAsnSerSerIleLeuGlnIleThrGlyLeuGluSerIleuIleSarGlyThr 501
Db      1843 GCTGTAAGTGGATTCCTTCCACACAGATATATACATTGCTCTTGAAGTACGACACA 1902
Qy      502 SerThrIleValGlnIleMetAlaAsnThrSerAlaGlyIleThrAsnGlyThrSerIle 521
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Qy      522 AsnPheIleThrLeuSerPheSerValPheGluIleIleLeuIleThrSerIleuIleGly 541
Db      1963 ACTTTTACATACCCCAAGTTTGCCTCAAGAGAAATTTGAGCCATATGCTGCTGTTTC 2022
Qy      542 GlyGlyLeuLeuIleLeuIleIleLeuThrValAlaIleThrGlyLeuGlySerProAsnIle 561
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Qy      562 LeuThrIleIleuIleSerProThrValProAsnProAlaGluSerIleIleIleThrTrp 581
Db      2083 ATTAATAAACACATCTGGCTTAATGTTCCAGATCTTCAAAAGATCATATATGCTCCAGTGG 2142
Qy      582 -----HIGlyAspAspPheIleAspIleu----- 590
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Qy      590 ----- 590
Db      2203 AATTTCATGATGTAAGTGTGTGAAATGAAACAATGACAAAGACCTTTTCCAGAA 2262
Qy      591 AsnLeuIleGluSerAsp-----AspSerValAsnThrGlu 602
Db      2263 GATCTGAATCATTTGACCTGTTCAAAAAGAAAAAATTATATCTGAA 2310

RESULT 3
LOCUS      AY310138              3055 bp      mRNA      linear      HTC      07-JUL-2003
DEFINITION Rattus norvegicus Acl1055 mRNA, complete cds.
ACCESSION  AY310138
VERSION     AY310138.1  GI:32264598
KEYWORDS   HTC.
SOURCE      Rattus norvegicus (Norway rat)
ORGANISM   Rattus norvegicus
REFERENCE  1 (bases 1 to 3055)
AUTHORS    Xu,C.S., Li,W.Q., Li,Y.C., Han,H.P., Wang,G.P., Chai,L.Q.,
            Yuan,J.Y., Yang,K.J., Yan,H.M., Chang,C.F., Zhao,L.F., Ma,H.,
            Wang,L., Wang,S.F., Shi,J.B., Rahman,S., Wang,Q.N. and Zhang,J.B.
            Liver regeneration after PH
            Unpublished
TITLE      2 (bases 1 to 3055)
JOURNAL    Xu,C.S., Li,W.Q., Li,Y.C., Han,H.P., Wang,G.P., Chai,L.Q.,
            Yuan,J.Y., Yang,K.J., Yan,H.M., Chang,C.F., Zhao,L.F., Ma,H.,
            Wang,L., Wang,S.F., Shi,J.B., Rahman,S., Wang,Q.N. and Zhang,J.B.
            Direct Submision
            Submitted (29-MAY-2003) Henan Bioengineering Key Lab, Henan Normal
            University, No. 148 Jianshe Road, Xinxiang City, Henan 453002, P.R.
            China
FEATURES
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ORIGIN
Alignment Scores:
Pred. No.:      9,53e-58      Length:      3055
Score:          647.50      Matches:      185
Percent Similarity: 45.64%      Conservative: 108
Best Local Similarity: 28.82%      Mismatches:  276
Query Match:    18,58%      Indels:       74
DB:              3          Gaps:          22

US-10-006-265-2 (1-652) x AY310138 (1-3055)
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Db      362 CAGATATATCTTCAAAATTTGAGTTGATTCGATGAGGGAAGAACATGCTGTTCCAG 421
Qy      55 TrpSerProGlyIleGluIleThrSerIle---ThrGlnIleThrValIleAsnArgThrIleVal 73
Db      422 TGGGACCCAGGAAGGAGACATATCCTTGAACAAACTACATTGAAATGTCAGAGTGGCA 481
Qy      74 PheGlyGluIlePheIleAspAsnIleThrIleAsnSerSerIleSerGluAsnArgAlaSer 93
Db      482 ---ACAGAGAAAGTTCCTGATTTGCGAACAAAGCATGACGACGAC-----TTC 526
Qy      94 CysSerPhe---PheLeuProAlaGlyIleThrIleProAspAsnIleThrIleGluValGlu 112
Db      527 TGCATATGGGCTATATCCCCCATCTATTTTGTG-----AACATGAGAGTCTGGGTGGAG 580
Qy      113 AlaGluAsnGlyIleAspIleValIleIleIleIleIleIleIleIleIleIleIleIle 132
Db      581 GCGGAGAAATGCCCTTGGGAATGCTCTCCAGAGCCATCAATTTTGAACCCCGGATGAATA 640
Qy      133 AlaIleThrGluProProIlePheAlaGlyIleIleProValIleGluIleIleIleIleIle 152
Db      641 GTGAAGCCAGGCCCACTCATATTTGTCAGACCACTCAGAAAGAAATTAATCCAGTATA 700
Qy      153 IleGlnIleGluThrIleIleIleIleIleIleIleIleIleIleIleIleIleIleIle 172
Db      701 TTAAATCTGATGATGGTCAATTCAGGTTTGGACAGATTTTAAG---CTGAAGTGGGAC 757
Qy      173 LeuArgPheArgThrValAsnSerThrSerIleThrMetGluValAlaAsnPheAlaIleAsnArg 192
Db      758 ATCCATATATAGGACCAAAATGCTCAACTTGATTCAGTCCCTCTT---GAAATTAACA 814
Qy      193 LysAspIleAsnGlnIleThrIleAsnLeuThrGlyIleGluIleProPheThrGluIleValIle 212
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Qy	213	AlaLeuAaGcySaAlaValLygIuser-----LysPheMetSerAspTrpSerGlnIu	230
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Qy	231	LywMetGlyMetThrGluGluGluIuaIaProCys---GlyLeuGluLeuTrpArgValIeu	249
Db	932	GGAGCGGGGACCAATATGAAGACAGACCATCCAAAGCGCCAAAGTTTCTGGTAAAGGA	991
Qy	250	LywProAlaGluAlaAspGlyAArgArgProValAlaGluLeuTrpLysLysAlaArgGly	269
Db	992	AATGCMAACCATCCACAGAGATATGGCTGTGCACGGCTCATATGGAAGCATTTGCCCTT	1053
Qy	270	AlaProValLeuGluIuLysThrLeuGlyLysTrpAsnIleIleTrpLysTrpGluSerAsnThr	289
Db	1052	TCTGAAGCCATGGGAAGATCTTGGAATTATGAAGGTCTTAAKACAGTCCAAAGTCAGTT	1111
Qy	290	AsnLeuThrArgLysThrMetAsnThrThrAsnGlnIleuGluLeuAsnIleuGlyGlu	309
Db	1112	TCGGAAATCTACACAGTTAAACGGCAC-----GAGTTGATAGTAAACCTCASCATTAAC	1166
Qy	310	SerPheTrpValSerMetIleSerLysTrpAsnSerLeuGlyLysSerProValAlaThrIleu	329
Db	1166	CGTATGTAGCGGCTCTCTAGCACAGAAATGTGTGCGAGATCTCCCTGCACACGTCCTC	1222
Qy	330	ArgIleProAlaIleGlnGluLysSerPheGlnCysIleGluValMetGlnAlaCysVal	349
Db	1226	ACCATCCCGGCGTCCCACTTCAA-----GTGGATCTTAAAGCATTTCCA	1276
Qy	350	AlaGluAspGlnLeuValValLysTrpGlnSerAlaLeuAspValAsnThrTrpMet	369
Db	1271	AAAGTAAACCTGCCTCTGGGTAAAGAGACACCGCCATCTAAACCTGTAAACAAATACATA	1333
Qy	370	IleGluTrpPheProAspValAspSerGluProThrThrLeuSerTrpGluSerValSer	389
Db	1331	CTAAGTGTGTGTGTCTGTACAGAACTCACCCCTGCATCCAGACTGGCAGCAAGAAAT	1393
Qy	390	GlnAlaThrAsnTrpThrIleGlnGlnAspLysLeuLysProPheTrpCysTrpAsnIle	409
Db	1391	GGCACTGTGAATCGGACCCACTTAAAGAGAACCTTACGTAGAGACAAATGCTATGTGATC	1450
Qy	410	SerValTrpProMetLeuAsnAspLysValGlyLysProLysTrpIleGlnAlaTrpAla	429
Db	1451	ACAGTAACCCCAAGTGTCTTCCCGGTGGCGCTGGAAAGCCCTGAGTCCATAGAAGCGTAATC	1510
Qy	430	LywGluGlyValProSerGluGlyProGluThrLysValGluAsnIleGlyValLysThr	449
Db	1511	AAACAGACAGCTCCTTTAAAGAGACCGACTGTGGCAAAAGAAAGGAGGAAAAATGA	1576
Qy	450	ValThrIleThrTrpLysGluIleProLysSerGluAspGlyIleLeuCysAsnTrp	469
Db	1571	GCTGTCTTAAAGTGGGACCATCTTCCTTGATGTCCGAACGGAATTCATTAGAAATCAC	1630
Qy	470	ThrIlePheTrpGlnAlaGluGlyLysGlyPheSerLysThrValAsnSerSerIle	489
Db	1631	TCCATATCTTATAGAACACAGTGTGGAAAAAGAAATGTTGCGCTGTGATCTTCTTCA	1699
Qy	490	LeuGlnTrpGlyLeuGlnSerLeuLysArgLysThrSerLysIleValGlnValMetAla	509
Db	1691	ACAAATATCACACTGTCTCTTTGAGTGCATACATGACATGATGCATGCACATGGCACCA	1750
Qy	510	AsnThrSerAlaGlyGlyLysThrAsnGlyThrSerIleAsnPheLysThrLeuSerPheSer	529
Db	1751	TACACAGAAAGGAGGAGATGGCGCGGAATTCACCTTTTAAACAACCTAAAGTTGGT	1810
Qy	530	ValPheGluIleIleLeuIleThrSerLeuIleGlyGlyLysLeuIleIleLeuIleIle	549
Db	1811	GAA-----TCGTCGTGTGGCGGCTCGGCGCTCATAGCATGCGCGCTA	1855
Qy	550	-----LeuThrValAlaTrpGlyLeuLysLysPro	559
Db	1853	AACCTTGGCTACAGACAGACGATCATTTGATGAATGCTGTACCAATTAATAAAA---1909	

OY		560	AshnlyseuthrHshleucyTrrProthrvalProanPfoalaglseSerllela	579	
Dd	1910	-----CACATC--TggCGAATGfCCAGATCCTTTCAAAAGCATATGTGC		1954	
OY		580	ThrtTp-----HisglYAspApPhelysAsPlysleu-----	590	
Dd	1955	CAGTGTCACCTCAOACCCCCCAAGGACAATTATACTCCAAGAATCAGATGTACTCA		2011	
OY		591	AsnleulysgIuseRasPaspSer---ValasnThrngluAspaAgilleuleulyProcys	609	
Dd	2015	GATGCCAATTTCACTGACGTAAGCGTTGTGGAAATAGAACGAACAACMAAAAGCCTTGT		2074	
OY		610	SerthrProserAspPlysleuValIIleAspPlysleuValValasnPhcglyAsnValIueu	629	
Dd	2075	----CCAGATGACCTGAAAATCCTTGACCCT-----GTT		2103	
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OY		650	GlutrTp	651	
Dd	2137	CAGTGG	2142		
RESULT 4					
LOCUS	Bb617934				
DEFINITION	Bb617934 RIKEN full-length enriched, adult male pituitary gland Mus musculus cDNA clone 530424C19 5', mRNA sequence.				
ACCESSION	Bb617934				
VERSION	Bb617934.1				
KEYWORDS	EST.				
SOURCE	Mus musculus (house mouse)				
ORGANISM	Eukaryotes; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.				
REFERENCE	1 (bases 1 to 663)				
AUTHORS	Hara,A., Hiramoto,K., Hori,F., Ishii,Y., Ito,M., Kawai,J., Arai,A., Okazaki,T., Carninci,P., Fukuda,S., Furuno,M., Hanagaki,T., Ono,M., Okada,M., Koya,S., Macumaya,T., Miyazaki,A., Nomura,K., Ohno,M., Okazaki,Y., Okido,T., Saito,R., Sakai,C., Sakai,K., Sano,H., Sasaki,D., Shibata,K., Shinagawa,A., Shiraki,T., Sugabe,Y., Suzuki,H., Tagami,M., Tagawa,A., Takahashi,F., Takeda,Y., Tanaka,T., Toyota,T., Muramatsu,M. and Hayashizaki,Y.				
TITLE	RIKEN Mouse ESTs (Arakawa,T., et al. 2001)				
JOURNAL	Unpublished (2001)				
COMMENT	Contact: Yoshihide Hayashizaki Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), Yokohama Institute The Institute of Physical and Chemical Research (RIKEN) 1-7-22 Suehiro-cho, Teurumi-Ku, Yokohama, Kanagawa 230-0045, Japan Tel.: 81-45-503-9222 Fax: 81-45-503-9216 Email: genome-res@gsc.riken.jp, URL:http://genome.gsc.riken.jp/ Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Hayashizaki,Y., Ichih.M., Konno.H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y. Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes. Genome Res. 10 (10), 1617-1630 (2000) wagi,K., Fujisake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Matsuhki,M., Yoneda,Y., Ishikawa,T., Oawa,K., Tanaka,T., Matsura,S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y. RIKEN integrated sequence analysis (RISA) system-184-format sequencing pipeline with 384 multiceptillary sequencer. Genome Res. 10 (11), 1757-1771 (2000) Konno,H., Fukuishi,Y., Shibata,K., Itoh,M., Carninci,P., Sugahara,Y. and Hayashizaki,Y. Computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001) Yamanaka,I., Kiyosawa,H., Kondo,S., Saito,T., Shinagawa,A., Atzawa,K., Fukuda,S., Hara,A., Itoh,M., Kawai,J., Shibata,K.,				


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Db      74 TTTGATATCTACACATGATGATGATCTATCTATGAAAAATAAGTAGCAGCTCCATAT 133
Oy      424 SerIleGlnAlaTyValAlaLysGluGlyValProSerGluGlyProGluThrIleValGlu 443
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Oy      564 HisLeuCySTrPProThrValAlProAsnProAlaGluSerSerIleAlaThrTy 581
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RESULT 6
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LOCUS      B0932D09-5 N1A Mouse Unfertilized Egg cDNA Library (long 1) Mus
DEFINITION      Musculus cDNA clone N1A:B0932D09 IMAGE:30475340 5', mRNA sequence.
ACCESSION      CF174021
VERSION      CF174021.1 GI:33283570
KEYWORDS      EST.
SOURCE      Mus musculus (house mouse)
ORGANISM      Mus musculus
REFERENCE      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS      Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
TITLE      1 (bases 1 to 637)
Piao, Y., Ko, N.T., Lim, M.K. and Ko, M.S.H.
Construction of long-transcript enriched cDNA libraries from
submitogram amounts of total RNAs by a universal PCR amplification
method
Genome Res. 11 (9), 1553-1558 (2001)
JOURNAL      MEDLINE
PUBMED      21429098
COMMENT      Contact: Dawood B. Dudekula
Laboratory of Genetics
National Institute on Aging/National Institutes of Health
333 Cassell Drive, Suite 4000, Baltimore, MD 21224-6820, USA
Email: cdna@gsun.grc.nia.nih.gov
Plate: B0932 row: D column: 09
Seq primer: M13 Reverse
High quality sequence stop: 637
POLYA-No.

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FEATURES
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1)"
/note="Vector: pCMV-SPORT6 (Invitrogen), Site 1: SalI;
Site 2: NotI; Mouse cDNA project by the Laboratory of
Genetics, National Institute on Aging (NIA), Intramural
Research Program, NIH (http://1gsun.grc.nia.nih.gov/cDNA).
This is a long-transcript enriched cDNA library (Ref.
Genome Res. 11: 1553-1558 (2001). [PMD: 11541991]. Total
RNAs were extracted from a pool of 148 unfertilized eggs.
Double-stranded cDNAs were synthesized with an Oligo(dT)
primer (Invitrogen):
5'-GGACTAGTTCAGATCGGACGCGCCCTTTTCTTTT-3',
treated with T4 DNA polymerase, and purified by
ethanol-precipitation. The cDNAs were ligated to
lone-linker LB-Sal4, purified by phenol/chloroform, and
separated from free linker by Centricon 100. Then, the
cDNAs were amplified by long-range high fidelity PCR using
Ex Taq polymerase (Takara) with a primer Sal4-S. The
products were purified by phenol/chloroform and Centricon
100. The cDNAs were digested with SalI and NotI enzymes
and cloned into SalI/NotI site of pCMV-SPORT6 plasmid
vector. The DH10B E. coli host was transformed with the
ligation mixture by the standard chemical method. The
average insert size is about 2.5 kb. The library was
constructed by Yulan Piao."

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ORIGIN

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Alignment Scores:
Pred. No.:      1.58e-39      Length:      637
Score:      468.50      Matches:      96
Percent Similarity:      63.59%      Conservative:      21
Best Local Similarity:      52.17%      Mismatches:      54
Query Match:      13.45%      Indels:      13
DB:      7      Gaps:      4

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US-10-006-265-2 (1-652) x CF174021 (1-637)

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Oy      67 ThrValLysArgThrTyAlaPheGlyGluLysHisAspAsnCyThrThrAsnSerSer 86
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Oy      87 ThrSerGluAsnAlaGlyLaserCySerPhePheLeuProArgIleThrIle-----Pro 104
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Oy      105 AspAsnTyThrIleGluValGluAlaGluAsnGlyAspGlyValIleLysSerHisMet 124
Db      395 GACATCTGACGTGTGAAGTACAAAGCTCAAAATGAGATGTAAGTAAATCTGACATC 454
Oy      125 ThrTyThrPArgLeuGluAsnIleAlaLysThrGluProProLysIlePheArgValLys 144
Db      455 ACATATTGGCATTTAATCTCATAGCAAAAACCAACCACTTAATTTTAAGTGAAT 514
Oy      145 ProValLeuGlyIleLysArgMetIleGlnIleGluThrPleLysPProGluLeuAlaPro 164
Db      515 CCAATT-----TGTATATAGAAATGTCACATACAAATG---AAACCGCGTGAAGAAAGACT 565

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QY 165 ValSerSerAspLeuYrThrLeuAcGpHeArgThrValAsnSerThrSerTrpMet 184
 Db 566 CCGGGGTTTCCTTCTAGTAGCAGCTTCCTCGGTTGAGAACTGTCAACAGTACCGACTGGAGC 625

QY 185 GluValAsnSph 188
 Db 626 GAAGTCATTTT 637

RESULT 7
 AK089305
 LOCUS 2804 bp mRNA linear HTC 03-APR-2004
 DEFINITION Mus musculus B6-derived CD11 +ve dendritic cells cDNA, RIKEN full-length enriched library, clone: F730003J03 Product: colony stimulating factor 3 receptor (granulocyte), full insert sequence.

ACCESSION AK089305.1 GI:26105194
 VERSION AK089305.1
 KEYWORDS HTC; CAP trapper.
 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE
 AUTHORS Carninci, P. and Hayashizaki, Y.
 TITLE High-efficiency full-length cDNA cloning
 JOURNAL Meth. Enzymol. 303, 19-44 (1999)
 MEDLINE 99279253
 PUBMED 10349636

REFERENCE
 AUTHORS Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Kono, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.
 TITLE Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes
 JOURNAL Genome Res. 10 (10), 1617-1630 (2000)
 MEDLINE 20499374
 PUBMED 11042159

REFERENCE
 AUTHORS Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P., Kono, H., Akiyama, J., Nishi, K., Kitsuai, T., Taahito, H., Itoh, M., Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A., Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K., Fujiwake, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watanabe, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsunaga, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y.
 TITLE RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer
 JOURNAL Genome Res. 10 (11), 1757-1771 (2000)
 MEDLINE 20530913
 PUBMED 11076861

REFERENCE
 AUTHORS The RIKEN Genome Exploration Research Group Phase II Team and the PANTOM Consortium.
 TITLE Functional annotation of a full-length mouse cDNA collection
 JOURNAL Nature 409, 685-690 (2001)
 MEDLINE 11076861

REFERENCE
 AUTHORS The PANTOM Consortium and the RIKEN Genome Exploration Research Group Phase I & II Team.
 TITLE Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs
 JOURNAL Nature 420, 563-573 (2002)
 MEDLINE 11076861

REFERENCE
 AUTHORS Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hashizume, W., Hayashida, K., Hayatsu, N., Hiramoto, K., Hiraoka, T., Hirozane, T., Horii, F., Imotani, K., Ishii, Y., Itoh, M., Kagawa, T., Kasukawa, T., Kato, H., Kawai, J., Kojima, Y., Kondo, S., Kono, H., Kouda, M., Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Murata, M., Nakamura, M., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Ohsato, N., Okazaki, Y., Saito, R., Saitoh, H., Sakai, C., Sakai, K., Sakazume, N., Sano, H., Sasaki, D., Shibata, K., Shinagawa, K., Shiraki, T., Sogabe, Y., Tagami, M., Tagawa, A., Takanashi, F., Takaku-Kahira, S., Takekura, Y., Tanaka, T., Tomaru, A., Toya, T., Yasunishi, A., Muramatsu, M. and Hayashizaki, Y.

TITLE
 JOURNAL
 Direct Submission
 Submitted (16-Apr-2002) Yoshinide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute, 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail: genome-res@sc.riken.jp, URL: http://genome.gsc.riken.jp/, Tel: 81-45-503-9222, Fax: 81-45-503-9216)

COMMENT
 cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.
 Tissues were provided by Dr. John Todd (Dept. of Medical Genetics Wellcome Trust Centre for Molecular Mechanisms in Disease Wellcome Trust/MRC building Addenbrookes Hospital Cambridge) whose assistance we gratefully acknowledge.
 Please visit our web site for further details.
 URL: http://genome.gsc.riken.jp/
 URL: http://phantom.gsc.riken.jp/
 Location/Qualifiers
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 putative"

misc_feature
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 putative"

ORIGIN
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 Pred. No.: 4,82e-38 Length: 2804
 Score: 464.50 Matches: 159
 Percent Similarity: 41.958 Conservative: 91
 Best Local Similarity: 26.688 Mismatches: 251
 Query Match: 13.338 Indels: 95
 DB: 3 Gaps: 26

US-10-006-265-2 (1-652) x AK089305 (1-2804)

QY 35 ProAlaLysProGluAsnLLeSerCysValTYrTYrArgLysAsn--LeuThrCys 53
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 Db 571 CCGCCAGCCCTCAAACTATCTGCTGCATGACCTCACCAACAGCCTGGCTGC 630
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QY 54 ThrTPSerProGlyLysGluThrSerTYr---ThnGlnTYrThValLysArgThTYr 72
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 Db 631 CAGTGGAGCCAGTCTGATGACCACTGCCACCACTGCTTCTTAAG----- 681
 |||||

QY 73 AlaPheGlyGluLysHisAspAsnCYrThrTrAsnSerSerThr----- 87
 |||||
 Db 682 AGCTTCAGAGAGCCGCCAC--TCTCATGACCAAGGAGACATCCCGATTTGTG 738
 |||||

QY 88 ---SerGluAsnArgLAsSerCysSerPheLeuProArgLLeThrLLeProAspAn 106
 |||||
 Db 739 GCMAAGAGAGGAGAGAACTGCTCCATCCCGGAAAAAACTGCTCTGACAGATAT 798
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QY 107 TYrThrLLeGluValGluLysGluLysGluLysGluLysGluLysSerHisSerThrTYr 126
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 Db 799 ATGGCCATCTGGATGTCAGAGATATATGATGATGATGATGATGATGATGATGATG 858
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QY 127 TrpArgLLeGluAsnLLeLysThrGluPropolyLLe-----PheArgValLys 144
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 Db 859 CTGACCCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 918
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QY 145 ProValLeu-----GlyLLeLysArgMetLLeGlnLLeGlnLLeGlnLLeGlnLLe 159
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Db 919 CCTGATGAGTCTCTCACACGCTGCTGCTGTGCTGATGAGTGAAGCATGAAAGCCC 978
Qy 160 ProGUleuAlaProValSerSerAspLeuGlySerThrLeuArgPheArgThrValAsn 179
Db 979 AGTGAATCATGAAACAGAGTGTGAACTTCCTGACAGCCACGACCATTAAGAGACCAAC 1038
Qy 180 SerThrSerTrpMetGluValAsnPheAlaValAsnArgAspLeuValAsnGlnThrTrp 199
Db 1039 -----TGACCTCTGCTGTGTCCACCTGCTTCCAGCAGAGACAG-----TTT 1080
Qy 200 AsnLeuThrGlyLeuGlnProPheThrGluTrpValIleAlaLeuArgCysAlaValAsn 219
Db 1081 GAGCTCTGGGGCTCATCAAGGCCACGACCTTACCATCCCTACAGATCGATGCG---ATTGCG 1137
Qy 220 GluSer-----LysPheTrpSerAspTrpSerGlnGluLysMetGlyMetThrGluGlu 237
Db 1138 TCATCTCTGCTGATCTGTGAGCCCTGAGACCCCGGCTGACAGCTGAGGCTTACCATG 1197
Qy 238 GluAlaPro---CysGlyLeuGluLeuTrpArgValLeuLysProAlaGluAlaAspGly 256
Db 1198 AAGGCCCCACCATCAAGACTGACACGCTGTCTCAAGAAAGAACATGAT---CCAGGG 1254
Qy 257 ArgArgProValArgLeuLeuTrpLysAlaArgAlaProValLeuGlu----- 274
Db 1255 ACAGTGAAGTGTGACAGCTGTCTGAAAGCCA-----AGCCCTGACAGAAAGACAGT 1305
Qy 275 ---LysThrLeuGlyTrpAsnIle---TrpTrpTrpProGluSerAsnThrAsnLeuThr 292
Db 1306 GGAAGATCCAGGGGTACTCTGTCTGAGATTCCCAAGATCATCAAGGACAGACATA 1365
Qy 293 GluThrMetAsnThrThrAsnGlnIleLeuGluIleLeuGlyGlySerPheTrp 312
Db 1366 CACCTTGCAACACACGACGCTGATCTTCTCTGCTGCTGACGAGGCCACAGAAC 1425
Qy 313 ValSerMetIleSerTrpAsnSerLeuGlyLysSerProValAlaThrLeuArgIlePro 332
Db 1426 GTGACCTTGTTGGCTTACAAAGACAGGAGCCTTCACTACCTACAGTG----- 1476
Qy 333 AlaIleGlnGluLysSerPheGlnCysIleGluValMetGlnAlaCysValAlaGluAsp 352
Db 1477 GTTTTCTCGAGAAC-----GAAAGT 1497
Qy 353 GlnLeuValValLysTrpGlnSerSerAlaLeuAspValAsnThrTrpMetIleGluTrp 372
Db 1498 CCAGCTGTGACCGGACTCATGCTGAGCCCAAGACCTTACACCATTCGTGGTACCTGG 1557
Qy 373 ---PheProAspValAspSerGluProThrThrLeuSerTrpGluSerValSerGlnAla 391
Db 1558 GAAGCCCCACGCTTCTGCTCAGGGCTATCTCATTTGAGTGGAAATGAGTTCTCCAGC 1617
Qy 392 ThrAsn-----TrpThrIleGln----- 397
Db 1618 TACATATACACGCTTAACTCTGATGATAGAACCTTAACGGGAACATCATGGAATTCTG 1677
Qy 398 ---GlnAspLysLeuLysProPheTrpCysTrpTrpAsnIleSerValTrpProMetLeuHis 416
Db 1678 TTAAGACACATTAATCTCTTCACTTCACTTCAAGATTAACATGAGCTCCCTGACCCA 1737
Qy 417 AspLysValGlyLysProTrpSerIleGlnAlaTrpAlaLysGluGlyValProSerGlu 436
Db 1738 GGCATCTGGGAGCCCTCTGTAATGTCTACACCTTCGCTGAGAGAGAGAGCTTCTTCAT 1797
Qy 437 GlyProGluThrLysValGluAsnIleGlyValLysThrValIleThrTrpLysGlu 456
Db 1798 GCTCCAGGCTGATCTTAACATGTTGGCAACCTGGGACAGCTGGAGTGG----- 1851
Qy 457 IleProLysSerGluLysGlyIleIle-----CysAsnTrpThrIlePheTrpGln 474
Db 1852 GTACTAGAGCCCTTACGCTGGAGTGAATACCTCCACCTACACCATTCCTTGGGCC 1911
Qy 475 AlaGluGlyGlyLysGlyPheSerLysThrValAsnSerSerIleLeuGlnTrpGlyLeu 494
Db 1912 GATCTGGGAGCACTCTCTTCCGTACCTCGAAGACATCTCCCTCCAGATCTTGTCTGT 1971

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Qy 495 GluSerLeuLysArgLysThrSerTrpIleValGlnValMetAlaAsnThrSerAlaGly 514
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Qy 515 GlyThrAsnGlyThrSerIleAsnPheLysThrLeuSerPheSerValPheGluIleIle 534
Db 2032 TCCACCAACAGTACAGGCTTACCTGAGACCCCTAGATTCATCTGACTTAAACATTTC 2091
Qy 535 LeuIleThrSerLeuIleGlyGlyLeuLeuLeuIleIleLeuThrValAlaTrp 554
Db 2092 CTG-----GGCATCTTGTCTTGTAGTACTTGTCCACTACCTGT 2130
Qy 555 GlyLeuLysProAsnLysLeuThrHisLeuLys----- 566
Db 2131 -----GTAGTACCTGGCTCTGTGCAACACGAGAAAGACTTCC 2172
Qy 567 ---TrpProThrValProAsnProAlaGluSerSerIleAlaThrTrp 581
Db 2173 TTCTGTGATGATGTGCCAGACCCACAGTACGATGCTGAGCTCTGTG 2220

RESULT 8
AY412152 2592 bp DNA linear GSS 16-DEC-2003
LOCUS Homo sapiens CSF3R gene, VIRUAL TRANSCRIPT, partial sequence,
DEFINITION genomic survey sequence.
ACCESSION AY412152
VERSION AY412152.1 GI:39768117
KEYWORDS GSS.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 2592)
AUTHORS Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejarival,A.,
Todd,M.A., Tanenbaum,D.M., Civeello,D.R., Lu,F., Murphy,B.,
Ferreira,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
Adams,M.D. and Cargill,M.
TITLE Direct Submission
JOURNAL Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,
Rockville, MD 20850, USA
COMMENT This sequence was made by sequencing genomic exons and ordering
them based on alignment.
FEATURES
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ORIGIN
Alignment Scores:
Pred. No.: 1,47e-37 Length: 2592
Score: 459.50 Matches: 165
Percent Similarity: 39.68% Conservative: 81
Best local Similarity: 26.61% Mismatches: 279
Query Match: 13.19% Indels: 95
DB: Gaps: 25

US-10-006-265-2 (1-652) x AY412152 (1-2592)
Qy 9 CysValAsnLeuGlyMetMetTrpThrTrpAlaLeuTrpMetLeuProSerLeuCysLys 28

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Db      1339 GGAAAGAAATGGAGAGCCAGCGGGTTTCTGTGAAGAGAAC---ATCAGGCCCTTTCA 1395
Qy      405 pcytyrAsnIleSerValtyrPromeIleuHISApblyValIGlupProtyrSerI 425
Db      1396 GCCTTATGAGATATGCTACTCTCTTGTACAGAGACACCATGGACCTCCCAAGCATGT 1455
Qy      425 eGlnAlaTyraAlaLysGluIGlValProSerGluGlyProGluThryLeuValuAnI 445
Db      1456 CTATGCTACTCTCAAGAAATGGCTCCCTCCAGCCGAGAGCTGCATCTTAAGACAT 1515
Qy      445 eGlyValLysThValThryLeuThryPlyPlyGluLeuProlYsSerGluArgLysGly 465
Db      1516 TGCAAGACCTGGGACAGCTGGAGTGGGCTGCTGAGTGGGAGAGAGGCC 1575
Qy      465 eIleCyAsnTyThrIlePheTyrglnAlaGluIGlyLysGlyPheSerTyThryVa 485
Db      1576 CCTTACCCTACATCATCTTCTTGAGCAACAGCTCAGAACCACTCTTCCCACTCCT 1635
Qy      485 lAnSerSerIleLeuGlnTyrglyLeuGluSerLeuLysArgLysThrySerTyrlLeVa 505
Db      1636 GAATGCTCTCCCGTGGCTTGTCTTCATGAGCTGGAGCCGCGCAGTGTATCAT 1695
Qy      505 lGlnValMetAlaAsnThrySerAlaGlyLysThryAsnGlyThrySerIleAsnPhelyTh 525
Db      1696 CCACTCATGCTGCGCACAGCCAGGCTGGGCGCACCAAGTACGCTCTCACCCCTGATGAC 1755
Qy      525 rIleuSerPheSerValPheGluIleLeuIleuIleThrySerIleGlyLysGlyLeu 545
Db      1756 CTTGACCCAGAGAGGCTGGAGCTACACATCATCTGGGCTTGGCTTCCCTCTGCTGTT 1815
Qy      545 uIleLeuIleIleLeuThryValAlaTyrglyLeuLysPlyProAsnLysLeuThryHis 565
Db      1816 GCTCACCTGCTCTGNGAGAACTGCTGCTGCTGCTGAGGCTCCCAAGAGAAATCCCT 1875
Qy      565 uCysTTPProThryValProAsnProAlaGluSerSerIleAlaThryTP----- 581
Db      1876 C---TGCCCAAGTGTCCCAAGCCAGCTCACAGACGCTGGCTCTGGTGGCCCAAT 1932
Qy      582 ----HisGlyAspAspPheLys-----AspLysLeuAs 591
Db      1933 CATGAGAGAGAGAGCTTCCAGCTGCCCGGCTTGGACGCCACCATCATCAAGCTCAC 1992
Qy      591 nLeuLysGluSerAspAsp 597
Db      1993 AGTGTGAGAGAGATGAA 2011

RESULT 10
CP915066
LOCUS      CP915066      651 bp      mRNA      linear      EST 05-NOV-2003
DEFINITION B0973F04-5 NIA Mouse Unfertilized Egg cDNA Library (Long 1) Mus
ACCESSION CP915066
VERSION    CP915066.1 GI:38186268
KEYWORDS   EST.
SOURCE     Mus musculus (house mouse)
ORGANISM   Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 651)
Plao,Y., Ko,N.T., Lim,M.K. and Ko,M.S.H.
Construction of long-transcript enriched cDNA libraries from
submicrogram amounts of total RNAs by a universal PCR amplification
method
Genome Res. 11 (9), 1553-1558 (2001)

JOURNAL    MEDLINE
PUBMED     11544199
COMMENT    Contact: Dawood B. Dudekula
Laboratory of Genetics
National Institute on Aging/National Institutes of Health
333 Cassell Drive, Suite 4000, Baltimore, MD 21224-6820, USA
Email: cdna@nigun.grc.nia.nih.gov
Plate: B0973 Row: F Column: 04
Seq primer: M13 Reverse

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FEATURES
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POLYA=No.
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Location/Qualifiers
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/clone_1ib="NIA Mouse Unfertilized Egg cDNA library (Long
1)"
/note="Vector: PCMV-SPORT6 (Invitrogen); Site 1: SalI;
Site 2: NotI; Mouse cDNA project by the Laboratory of
Genetics, National Institute on Aging (NIA), Intramural
Research Program, NIH (http://jgun.grc.nia.nih.gov/cDNA).
This is a long-transcript enriched cDNA library (Ref.
Genome Res. 11: 1553-1558 (2001). (PMID: 11544199)). Total
RNAs were extracted from a pool of 1488 unfertilized eggs.
Double-stranded cDNAs were synthesized with an oligo(dT)
primer (Invitrogen:
5'-pGACTAGTCTAGATCGCAGCGCGCCGCTTTTCTTTT-3'1,
treated with T4 DNA polymerase, and purified by
ethanol-precipitation. The cDNAs were ligated to
Lone-linker lR-SalI, purified by phenol/chloroform, and
separated from free linkers by Centricon 100. Then, the
cDNAs were amplified by long-range high fidelity PCR using
Ex Taq polymerase (Takara) with a primer SalI-S. The
products were purified by phenol/chloroform and Centricon
100. The cDNAs were digested with SalI and NotI enzymes
and cloned into SalI/NotI site of PCMV-SPORT6 plasmid
vector. The DH10B E. coli host was transformed with the
ligation mixture by the standard chemical method. The
average insert size is about 2.5 kb. The library was
constructed by Yulan Plao."

ORIGIN
Alignment Scores:
Pred. No.:      8,66e-32      Length:      651
Score:          397.00      Matches:      79
Percent Similarity: 64.90%      Conservative: 19
Best Local Similarity: 52.32%      Mismatches: 41
Query Match:     11.39%      Indels:      12
DB:              7          Gaps:      3

US-10-006-265-2 (1-652) x CP915066 (1-651)
Qy      6 GlnProSerCyValAsnLeuGlyMeMetTTPThryAlaLeuThryPmeLeuProSer 25
Db      229 CAGCCTCTGGGTGTGAACCGCTGGAATATGTGACCTTGGCACTGTGGCATCTCTTTC 288
Qy      26 LeuCyAlaPheSerLeuAlaLeuProAlaLysProGluAnIleSerCyValTy 45
Db      289 CTCTGCAAAATTCAGCTCGACAGTCCCGACTTAACCCAGAGAAACATTTCTGCGCTTT 348
Qy      46 TTTTThryArgLysAsnLeuThryThryThryPseProGlyLysGluThrySerTyThryGln 65
Db      349 TACTTGGACGAATTCGACTTGGACCTTGAAGCCAGAGAGAAACCAATGATGACAC 408
Qy      66 TTTThryValLysArgThryTyraLysPheGlyLysHisAspAsnCySerThryThryAsnSer 85
Db      409 TACATTGTGACTTGTGACTTATCTCTATGAAAA-----AAC 444
Qy      86 SerThrySerGluAsnArgLaseCySerPhePheLeuProArgIleThryle----- 103
Db      445 AATTATAGTACATCTACAGAGGCTTCATATTTCTTCCCGTCTGTGCATGAGCCC 504
Qy      104 ProAspAsnTyThryIleGluValaGluAsnGlyArgGlyValaIleLysSerHis 123
Db      505 CCAGACATCTGCAGTGTGAAGTACAAAGCTCAAAATGAGAGATGTAAGTTAATCTGAC 564

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Qy 124 MetThrTYTTPArgLeuGluAsnIleAlaLysThrGluProProLysIlePheArgVal 143
 Db 565 ATCATATTTGGCATTTATCTCCATAGCAAAACCAACCACTTAATTTTAAGTGTG 624
 Qy 144 LysProValLeuGlyIleLysArgMetIleGln 154
 Db 625 AATCCAATT-----TGTAATAGAAATGTTCAG 651

RESULT 11
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 LOCUS Mus musculus CSF3R gene, VIRUTAL TRANSCRIPT, partial sequence,
 DEFINITION AY412154
 ACCESSION AY412154 GI:39768119
 VERSION GSS.
 KEYWORDS
 ORGANISM Mus musculus (house mouse)
 SOURCE
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sclerognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 2535)
 Clark,A.G., Gnanowsk,i,S., Nielson,R., Thomas,P., Kejarival,A.,
 Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
 Ferreira,S., Wang,G., Zheng,X.H., White,T.J., Sminsky,J.J.,
 Adams,M.D. and Cargill,M.
 Inferring nonneutral evolution from human-chimp-mouse orthologous
 gene sites
 Science 302 (5652), 1960-1963 (2003)
 JOURNAL
 PUBMED 14671302
 2 (bases 1 to 2535)
 Clark,A.G., Gnanowsk,i,S., Nielson,R., Thomas,P., Kejarival,A.,
 Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
 Ferreira,S., Wang,G., Zheng,X.H., White,T.J., Sminsky,J.J.,
 Adams,M.D. and Cargill,M.
 Direct Submision
 Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,
 Rockville, MD 20850, USA
 This sequence was made by sequencing genomic exons and ordering
 them based on alignment.

FEATURES
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ORIGIN
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 Score: 395.50 Matches: 154
 Percent Similarity: 39.80% Conservative: 88
 Best Local Similarity: 25.33% Mismatches: 228
 Query Match: 11.35% Indels: 140
 DB: 9 Gaps: 24

US-10-006-265-2 (1-652) x AY412154 (1-2535)

Db 538 GCAAAAGAGGACAGAAACAATGCTCATCCCGCAAAAAAATTGCTCTGTACAGATAT 597
 Qy 107 TYTThrIleGluValAlaGluAsnGlyAspGlyValIleLysSerHisMetThrTyr 126
 Db 598 ATGGCATCTGGGTGCAAGAGAAATGTCTAGGGTCAGCAGATCCCAAGCTGTGC 657
 Qy 127 TrpArgLeuGluAsnIleAlaLysThrGluProProLysIle-----PheArgVal 144
 Db 658 CTCGACCCCATGATGTTGTGAATTGGAGCTCCCATGCTGCAGAGCCCTGCACATTGGC 717

145 ProValLeu-----GlyIleLysArgMetIleGlnIleGluTrpIleLys 159
 Db 718 CCTGATGAGTCTCTACACAGCCTGCTGCTGTGCTGAGCTGGAAACCATGGAAGCCC 777

160 ProGluLeuAlaProValSerSerAspLeuLysTyrThrLeuArgPheArgValAsn 179
 Db 778 AGTGAGTACATGAAACAGAGAGTGAACTTGCTACACGCCACAGCTCAAGAGCCAAC 837

180 SerThrSerTrpMetGluValAsnPheAlaLysAsnArgLysAspLysAsnGlnThrTyr 199
 Db 838 -----TGACTCTGTGTCTTCCACTCGCTTCCTCCAGCAAGACAG-----TTT 879

200 AsnLeuThrGlyLeuGlnProPheThrGluTyrValIleAlaLeuArgCysAlaValLys 219
 Db 880 GAGCTCTGGGGCTTCATCAGAGCCCAAGTCTACACCTTACAGATGCATGC---ATTGCG 936

220 GluSer-----LysPheTrpSerAspTrpSerGlnGluLysMetGlyMetThrGluGlu 237
 Db 937 TCATCTCTGCTGTGATCTGTGAGCCCTCGAGCC----- 972

238 GluLysProCysGlyLeuGluLeuTrpArgValLeuLys---ProAlaGluAlaAsp--- 255
 Db 973 -----GGCTTCAGCTTGAAGCTTCACTGAAGGGTCCCCACCTCAGACTGCG 1020

256 -----GlyArgArgProValArgLeuLeuTrp 264
 Db 1021 ACACGTGTGTGACAGAAAGCACTAGATCCAGGAGACAGTG-AGTGTCACTGTTCGG 1079

265 LysLysAlaArgGlyAlaProValLeuGluLysThrLeuGlyTyrAsnIleTrpTyrTyr 284
 Db 1080 AAGCAGAGAC----- 1088

285 ProGluSerAsnThrAsnLeuThrGluThrMetAsnThrTrpAsnGlnLeuGluLeu 304
 Db 1089 -----ATACACCTTGGCAACACAGCAGCTCATCTATCTTC 1127

305 HisLeuGlyGlyGluSerPheTrpValSerMetIleSerTyrAsnSerLeuGlyLysSer 324
 Db 1128 CTCCTGCCCTCAGAGGCCCAAGAGTGAACCTTGTGGCTTCAACAAGAGGAGCCTCT 1187

325 ProValAlaThrLeuArgIleProAlaIleGlnGluLysSerPheGlnCysIleGluVal 344
 Db 1188 TCACCTACTACAGTGTG-TTTTCTGGA----- 1213

345 MetGlnAlaCysValAlaIleGluAspGlnLeuValValLysTrpGlnSerSerAlaLeuAsp 364
 Db 1214 GAACGAAAGTGTCCAGCT-----GTGACCGAGCTCCATGCCATGGCCCAAGAC 1261

365 ValAsnThrTrpMetIleGluTrp---PheProAspValAspSerGluProThrThrLeu 383
 Db 1262 CTTAAACACATCTGGTGAAGCTGGAAAGCCCGACGCTTGCGCTAGGGCTATCTCAT 1321

384 SerTrpGluSerValSerGlnAlaThrAsn-----TrpThrIleGln--- 397
 Db 1322 GAGTGGGAATGAGCTTCTCCAGCTACAAATACAGCTATAGTCTGATGATGAACCT 1381

398 -----GlnAspLysLeuLysProPheTrpCysTyrAsn 408
 Db 1382 AACGGAAACATCACTGAATTTCTTTAAAGCAACAATAATCCCTTTCAGCTTACAGA 1441

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Db	Accession	Source	Organism	Reference Authors	Title	Journal Comment
Db	949	TTAAAGCATATCATGGGTCAAGGCTGGGCGGCTCTT---	TTAGATCTTAAAGTCTGAC	1005		
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Db	1006	ATCCAAATATAGACCAAAAGATGCTCTCAACTTGATATCCAGGTCCCTCTT---	GAAGATACA	1062		
Qy	193	LysAspLysAsnGlnThrTyraAsnLeuThrGluGlnProPheThrGluTyrValIle	212			
Db	1063	ATGTCCTCTCGAACCTCTTCCCTTCACTGTCAGAGACCTCAAGCCCTTTTAAAGAAATATGTGTTT	1122			
Qy	213	AlaLeuArgCysAlaValIleGluSer-----LysPheTrpSerAspTrpSerGlnGlu	230			
Db	1123	AGGATTCGG---TCCATTATAGGACACGTGGAGAGGCTACTGAGTGACTGGAGTGAAGAG	1179			
Qy	231	LysMetGlyMetThrGluGluGluValaProCys---GlyLeuGluLeuTrpArgValIleu	249			
Db	1180	GCTAGTGGGACCATATAGAGACAGACATCCAAACACCAAGTTTCTGGATATAGACA	1239			
Qy	250	LysProAlaGluAlaAspGlyArgArgProValArgLeuLeuTrpLysAlaArgGly	269			
Db	1240	AATCATCTCCATGGGACAGAAATATAGATCTGTACGGCTCATATGAGAGACCTGCCCTCTT	1299			
Qy	270	AlaProValLeuGluLysThrLeuGlyTyraSerIleTrpTyrTyrProGluSerAsnThr	289			
Db	1300	TCTGAAGCCATATGGGAAATCTTGATATATGAAGT-----ATTCTTACGACATCAAG	1355			
Qy	290	AsnLeuThrGluThrMetAsnThrThraSngInGlnLeuGluLeuGlyGlu	309			
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DEFINITION	K0283D09-5N NIA Mouse Unfertilized Egg cDNA library (long) Mus					
ACCESSION	CA561173					
VERSION	CA561173.1	GI:25105828				
KEYWORDS	EST.					
SOURCE	Mus musculus (house mouse)					
ORGANISM	Mus musculus					
REFERENCE	Euhayrta; Metazoa; Chordata; Craniata; Vertebrate; Euteleostomi;					
AUTHORS	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.					
TITLE	1 (bases 1 to 592)					
JOURNAL	Piao, Y., Karui, G.J., Dudekula, D.B., Qian, Y., Luo, A., Steagy, C.A.,					
COMMENT	Matlin, P., Abba, K., Tanaka, T. and Ko, M.S.H.					
	Systematic Analyses of NIA Mouse Unfertilized Egg cDNA library					
	(long)					
	Unpublished (2001)					
	Other ESTs: K0283D09-3					
	Contact: Dawood B. Dudekula					
	Laboratory of Genetics					
	National Institute on Aging/National Institutes of Health					
	333 Cassell Drive, Suite 4000, Baltimore, MD 21224-6820, USA					
	Email: cdha@igsun.grc.nia.nih.gov					
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	Seq primer: M13 Reverse					
	High quality sequence stop: 592					
	PolyA=no.					
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(Long)"
/notc=Vector; pSPORT1 (Invitrogen); Site_1: SalI; Site_2:
NotI; Mouse cDNA project by the Laboratory of Genetics,
National Institute on Aging (NIA), Intramural Research
Program, NIH (http://igsun.grc.nia.nih.gov/cDNA). This is
a long-transcript enriched cDNA library (Ref. Genome Res.
11: 1553-1558 (2001). [PMID: 11544193]). Total RNAs were
extracted from a pool of 148 unfertilized eggs.
Double-stranded cDNAs were synthesized with an Oligo(dT)
primer (Invitrogen:
5'-pGACtAGTTCTCATTCGACGGCGCCCTTTTTTTTTTTT-3'),
treated with T4 DNA polymerase, and purified by
ethanol-precipitation. The cDNAs were ligated to
Lone-linker L1-SalI, purified by phenol/chloroform, and
separated from free linkers by Centricon 100. Then, the
cDNAs were amplified by long-range high fidelity PCR using
Ex Taq polymerase (Takara) with a primer Sal14-8. The
products were purified by phenol/chloroform and Centricon
100. The cDNAs were digested with SalI and NotI enzymes
and cloned into SalI/NotI site of pSPORT1 plasmid vector.
The DH10B E. coli host was transformed with the ligation
mixture by the standard chemical method. The average
insert size is about 2.5 kb. The library was constructed
by Yulan Piao (NIA)."

ORIGIN

Alignment Scores:
Pred. No.: 1,86e-26 Length: 592
Score: 347.00 Matches: 67
Percent Similarity: 65.89% Conservative: 18
Best local Similarity: 51.94% Mismatches: 34
Query Match: 9.96% Indels: 10
DB: Gaps: 2

US-10-006-265-2 (1-652) x CAS61173 (1-592)

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QY 26 LeuCylslyspheSerleuaLaalaLeuProAlalyseProglubansilesCysValTyr 45
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QY 66 TyrThrAllysaRghTrTryAlaPhelGLVluShIsaspAncysThnRthAnsSer 85
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409 TACATTTGACTTGGACTTACTCTCTTAAGAAAA-----AGC 444
QY 86 SerThrsErglubsnaTgAlasErCysSePhepheLeuProAlIethrile----- 103
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QY 104 ProAspaNtyrThrllegluValglualaGlubansglyabgilyvalIlleySerHis 123
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505 CCAGACACATCGCAGTGTGGAAGTAGAACGTCMAAATGAGATGTGAAGTTAAATCTGAC 564
QY 124 MetThrTyrrPaArgLeugluAnlle 132
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565 ATCACAATTATGGCATTTAATCTCCATA 591

RESULT 15
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LOCUS K0279C07-5N NIA Mouse Unfertilized Egg cDNA Library (Long) Mus
DEFINITION
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musculus cDNA clone NIA:K0279C07 IMAGE:30052254 5', mRNA sequence.
 CA560924 GI:25105579
 EST.
 Mus musculus (house mouse)
 Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 479)
 Piao,Y., Kargul,G.J., Dudekula,D.B., Qian,Y., Luo,A., Steaggs,C.A.,
 Martin,P., Alba,K., Tanaka,T. and Ko,M.S.H.
 Systematic Analyses of NIA Mouse Unfertilized Egg cDNA Library
 (Long)

JOURNAL
 COMMENT
 Unpublished (2001)
 Other_ESTS: K0279C07-3
 Contact: Dawood B. Dudekula
 Laboratory of Genetics
 National Institute on Aging/National Institutes of Health
 333 Cassell Drive, Suite 4000, Baltimore, MD 21224-6820, USA
 Email: cdna@igsun.grc.nia.nih.gov
 Plate: K0279 row: C column: 07
 Seq primer: M13 Reverse
 High quality sequence stop: 479
 POLYA=NO.

FEATURES

SOURCE

Location/Qualifiers
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 (Long)"
 /note="Vector: pSPORT1 (Invitrogen); Site 1: SalI; Site 2:
 NotI; Mouse cDNA project by the Laboratory of Genetics,
 National Institute on Aging (NIA), Intramural Research
 Program, NIH (http://igsun.grc.nia.nih.gov/cDNA). This is
 a long-transcript enriched cDNA library (Ref. Genome Res.
 11: 1553-1558 (2001). [PMID: 11544191]. Total RNAs were
 extracted from a pool of 1488 unfertilized eggs.
 Double-stranded cDNAs were synthesized with an Oligo(dT)
 primer (Invitrogen:
 5'-pGACTAGTCTAGATCGCGAGCGCCCTTTT-3'),
 treated with T4 DNA polymerase, and purified by
 ethanol-precipitation. The cDNAs were ligated to
 lona-linker IL-SalI, purified by phenol/chloroform, and
 separated from free linkers by Centricon 100. Then, the
 cDNAs were amplified by long-range high fidelity PCR using
 Ex Tag polymerase (Takara) with a primer SalI-S. The
 products were purified by phenol/chloroform and Centricon
 100. The cDNAs were digested with SalI and NotI enzymes
 and cloned into SalI/NotI site of pSPORT1 plasmid vector.
 The DH10B E. coli host was transformed with the ligation
 mixture by the standard chemical method. The average
 insert size is about 2.5 kb. The library was constructed
 by Yulan Piao (NIA)."

ORIGIN

Alignment Scores:
 Pred. No.: 4.57e-26 Length: 479
 Score: 342.00 Matches: 66
 Percent Similarity: 65.62% Conservative: 18
 Best Local Similarity: 51.56% Mismatches: 34
 Query Match: 9.82% Indels: 10
 DB: 6 Gaps: 2

US-10-006-265-2 (1-652) x CA560924 (1-479)

QY 7 ProSerCyValaIenLeuGIyMeMetTrpThrPaIaLeuTrpMetLeuProSerLeu 26

DB 119 CCTCGGCTGTGAACGTGTGAATATGTGACCTTGGCACTGTGGCATCTCTTCTC 178
 QY 27 CysIySPheSerLeuAlaAlaLeuProAlaIySProGIuAnIleSerCyValITyTyr 46
 DB 179 TGCAAATTGACCTGGCAGTCTGCTCCGACTAGCCAGAAACATTTCTGGGCTTTTAC 238
 QY 47 TyraIySaenLeuThrCyethrTrpSerProGIySGIuThrSerTyThrGlnITyr 66
 DB 239 TTCACAGAAATCTGACTTGCATTTGAGACCAAGAAAGAACCAATGATACCACTAT 298
 QY 67 ThrValIySaenITyThraIaPheGIyGluIySaenCyethrThraenSerSer 86
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 QY 105 AspAenITyThrIleGIuAlaIaGIuAnGIyAspGIyValIleIySerHisMet 124
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 QY 125 ThrTyTTPaRyLeuGIuAnIle 132
 DB 455 ACATATTGGCATTTAATCTCATTA 478

Search completed: February 23, 2005, 19:23:40
 Job time : 6029.32 secs

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RESULT 1	ALIGNMENTS
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LOCUS	
DEFINITION	Novel hemopoietin receptor protein, NR10.
ACCESSION	BD091865
VERSION	BD091865.1 GI:22637476
KEYWORDS	WO 0075314-A/2.
SOURCE	Homo sapiens (human)
ORGANISM	Homo sapiens
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
AUTHORS	1 (bases 1 to 2440)
TITLE	Maeda,M. and Yaguchi,N.
JOURNAL	Novel hemopoietin receptor protein, NR10 Patent: WO 0075314-A 2 14-DEC-2000; CHUGAI RESEARCH INSTITUTE FOR MOLECULAR MEDICINE INC, MASATSUGU MAEDA, NORIKO YAGUCHI
COMMENT	OS Homo sapiens (human) PN WO 0075314-A/2 PD 14-DEC-2000 PF 01-JUN-2000 WO 2000JP003556 PR 02-JUN-1999 JP 99P 155797, 30-JUL-1999 JP 99P 217797 PI MASATSUGU MAEDA,NORIKO YAGUCHI PC C12N15/12, C12N5/10, C07K14/715, C07K16/28, C12P21/02, G01N33/53, G01N33/566 CC FH Key FT CDS Location/Qualifiers (523). (1278).

FEATURES
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Query Match: 100.00% Indels: 0
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US-10-006-265-4 (1-252) x BD091865 (1-2440)

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DB 523 ATGAAGCTCTCTCCAGCCTTCATGTGTTAACTGGGAGATGATGAGACCTGGCACTG 582
QY 21 TrpMetLeuProSerLeuCysLysPheSerLeuAlaAlaLeuProAlaLysProGluAsn 40
DB 583 TGGATGCTCCCTCAGCTGCAATTCAAGCTGCGAGCTCTGCGAGCTAAGCTGAGAAC 642
QY 41 LeSerCysValTyrTyrArgLysAsnLeuThrCysThrTrpSerProGlyLysGlu 60
DB 643 ATTTCCTGTCTACTACTAGTATAGAAAATTTAACCTGCACTTGAGACTCAGAGAAAGAA 702
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LOCUS
DEFINITION Sequence 21 from Patent WO0200721.

ACCESSION AX365169
VERSION AX365169.1 GI:18696927
KEYWORDS
SOURCE
ORGANISM

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Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

REFERENCE
AUTHORS Sprecher, C.A., Presnell, S.R., Gao, Z., Whitmore, T.E., Kuiper, J.L.
and Maurer, M.F.

TITLE Cytokine receptor zcytor17
JOURNAL Patent: WO 0200721-A 21 03-JAN-2002;
ZymoGenetics, Inc. (US)

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ORIGIN

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Pred. No.: 1,42e-125 Length: 1476
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Best Local Similarity: 99.60% Mismatches: 1
Query Match: 98.90% Indels: 0
DB: Gaps: 0

US-10-006-265-4 (1-252) x AX365169 (1-1476)

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DB 189 CTCCTCTCACTGCAAAATTCAGCTGCGAGCTCTGCCAGCTAAGCTGAAGCAATTTCC 248
QY 43 CysValTyrTyrArgLysAsnLeuThrCysThrTrpSerProGlyLysGluThrSer 62
DB 249 TGTGCTACTACTATAGAAAATTTAACTGCACTTGGAAGTCCAGAAAGGAAACCACT 308
QY 63 TyrThrGlnTyrThrValLysArgThrTyrAlaPheGlyGluLysHisAspAsnGlyThr 82
DB 309 TATACCCAGTACACAGTTTAAGAACTTAACGCTTTTGGAGAAAACATGATATATGTACA 368
QY 83 ThrAsnSerSerThrSerGluAsnArgAlaSerCysSerPhePheLeuProArgIleThr 102
DB 369 ACCAATAGTCTTACAAAGTAAATGCTGCTGTGCTCTTTTCTCTTCCCAAGATTAAG 428
QY 103 IleProAspAsnTyrThrIleGluValGluAlaGluAsnGlyAspGlyValIleLysSer 122
DB 429 ATCCCAAGATTAATTAACATTGAGGTGGAAGCTGAAAATGAGAGATGATTAATTAATCT 488
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Db 729 GGGCTGACGCTTTTACAGAAATATGTCATAGCTTCGCAATGTCCGTCAGAGATCAAAAG 788
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Db 789 TTCGGAATGACTGAGACCAAGAAAATGGGAATGACTGAGAGAAAGGACGACTACTC 848
Qy 243 ProAlaIleProValLeuSerThrLeuVal 252
Db 849 CCTGGATTCCTGCTGCTGCTGCTG 878
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AF106913
LOCUS AF106913 1761 bp mRNA linear PRI 01-DEC-2001
DEFINITION Homo sapiens CRJ3 protein (CRJ3) mRNA, complete cds.
ACCESSION AF106913
VERSION AF106913.1 GI:17221662
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE
AUTHORS Zhang, W., Man, T., He, L., Yuan, Z. and Cao, X.
TITLE A novel soluble type I cytokine receptor
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 1761)
AUTHORS Zhang, W., Man, T., He, L., Yuan, Z. and Cao, X.
TITLE Direct Submission
JOURNAL Submitted (13-NOV-1998) Department of Immunology, Shanghai
Brilliance Biotechnology Institute & Second Military Medical
University, 800 Xiangyin Road, Shanghai 200433, P.R.China
FEATURES
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KESKFWDSQEKMGTEEARPCGLELWVLPKPAADGRPVRLLMKKARAPYLEKT
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NMTIQDQKLKRFKCNISYVPMIDKNGEPYSIAYAKEGVPSPGPEPKYENIGKTY
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G"

US-10-006-265-4 (1-252) x AF106913 (1-1761)
Qy 1 MelYsLeuSerProGlnProSerCyValAsnLeuGlyMetMetTrpThrTrpAlaLeu 20
Db 114 ATGAAGCTCTCTCCCAAGCCCTTCAATGTGTAACTGGGGAAGATGTGACCTGGCAGCTG 173
Qy 21 TrpMetLeuProSerLeuCyValPheSerLeuAlaLeuProAlaLysProGluAsn 40
Db 174 TGGATGCTCCCTTACCTGCAATTCAAGCTTGCAAGCTTGCACGCTGAGAAC 233
Qy 41 IleSerCyValIleThrValArgLysAsnLeuThrCyThrTrpSerProGlyLysGlu 60
Db 234 ATTTCCTGTGTCTACTACTAAGAAAATTTAACTGCACTTGGAGTCCAGAAAGGAA 293
Qy 61 ThrSerTrpThrGlnIleThrValLysArgThrValAlaPheGlyGluLysHisAspAsn 80
Db 294 ACCAGTATACCCAGTACACAGTAAAGAGCACTTAAGCTTTTGGAGAAAACATGATAT 353
Qy 81 CyThrThrAsnSerSerThrSerGluAsnArgAlaSerCySerPhePheLeuProArg 100
Db 354 TGTACACCAATAGTCTACAGTGAATGTGCTTCTGCTCTTTTCTTCCCAAGA 413
Qy 101 IleThrIleProAspAsnIleThrIleGluValGluAlaGluAsnGlyAspGlyValIle 120
Db 414 ATTAAGATCCCAAGTAAATTAATACATGAGGTGAGAGTGAATAATGGAGATGTAT 473
Qy 121 LysSerHisMetThrIleTrpArgLeuGluAsnIleAlaLysThrGluProProLysIle 140
Db 474 AAATCTCATATGACATCTGAGATTAAGAACATAGGAACATGAACCACTTAAGATT 533
Qy 141 PheArgValLysProValIleGluIleLysArgMetIleGlnIleGluTrpIleLysPro 160
Db 534 TTCGTGTGAACCAAGTTTGAGCAACAAAGATGATTCAAATTAATGAATGAAGCT 593
Qy 161 GluLeuAlaProValIleSerSerAspLeuLysIleThrLeuArgPheArgThrValAsnSer 180
Db 594 GAGTTGGGCGCTGTTTATCATCGATTAAATACACACTGCTCAGACAGTCAACAGT 653
Qy 181 ThrSerTrpMetGluValAsnPhaAlaValAsnArglyAsnAllyAsnGlnThrThyAsn 200
Db 654 ACCAGCTGAGTGAAGTCACTGCTTAAGAACCGTAAAGATTAACCAAACTTACCAAC 713
Qy 201 LeuThrGlyLeuGlnProPheThrGluThrValIleAlaLeuA99CyBaAlaValLysGlu 220
Db 714 CTCACGGGCGCTGACCTTTTACAGAAATGTCATAGCTTCGCAATGTCCGCTCAAGAG 773
Qy 221 SerLysPheTrpSerAspTrpSerGlnGluLysMetGlyMetThrGluGluGly 238
Db 774 TCAGATTCCTGAGTGAAGTGAAGCAAGAAAATGGGAATGACTGAGAGAA 827
RESULT 4
BD091877 2119 bp DNA linear PAT 27-AUG-2002
LOCUS BD091877
DEFINITION Novel hemopoietin receptor protein, NR10.
ACCESSION BD091877
VERSION BD091877.1 GI:22637488
KEYWORDS WO 0075314-A/14.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE
AUTHORS Maeda, M. and Yaguchi, N.
TITLE Novel hemopoietin receptor protein, NR10
JOURNAL Patent: WO 0075314-A 14 14-DEC-2000;
CHUGAI RESEARCH INSTITUTE FOR MOLECULAR MEDICINE INC, MASATSUGU
MEDA, NORIO YAGUCHI
COMMENT
OS Homo sapiens (human)
PN WO 0075314-A/14
PD 14-DEC-2000
PF 01-JUN-2000 WO 2000JP003556
PR 02-JUN-1999 JP 99P 155797,30-JUL-1999 JP 99P 217797 P1

MASATSUGU MAEDA, NORIKO YAGUCHI
PC C12N15/12, C12N5/10, C07K14/715, C07K16/28, C12P21/02, G01N33/53,
CC G01N33/566

FEATURES
source Location/Qualifiers
FT key (11) . (1996) .
CDS Location/Qualifiers
1. .2119
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"

ORIGIN

Alignment Scores:
Pred. No.: 3,11e-120 Length: 2119
Score: 1292.00 Matches: 238
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 95.14% Indels: 0
DB: 6 Gaps: 0

US-10-006-265-4 (1-252) x BD091877 (1-2119)

QY 1 MetLysLeuSerProGlnProSerCysValAsnLeuGlyMetMetTrpThrTrrPalaleu 20
DB 11 ATGAAGCTCTCTCCAGCCTTCATGTGTAACTGGGGATGATGGACCTGGCAGCTG 70
QY 21 TrpMetLeuProSerLeuCysLysPheSerLeuAlaAlaLeuProAlaLysProGluAn 40
DB 71 TGGATGCTCCCTCCACTGCAATTGAGCTTGAGCTTGACCTGAAAGCTGAGAAC 130
QY 41 ILeSerCysValTyrTyrTrrArgLysAsnLeuThrCysThrTrpSerProGlyLysGlu 60
DB 131 ATTTCCTGTGTACTACTATAGAAAAATTAACTGCACCTGGAGTCCAGAAAGAA 190
QY 61 ThrSerTyrThrGlnTyrThrValLysArgThrTrrAlaPheGlyGlyLysHisAspAsn 80
DB 191 ACCAGTTAATACCAGATACAGATTAAGAGAACTTAAGCTTTTGAGAAAAACATGATAT 250
QY 81 CysThrThrAsnSerSerThrSerGluAsnArgAlaSerCysSerPhePheLeuProArg 100
DB 251 TGTACACCAATAGTTCTCAAGTGAATAATCGTGTCTGCTCTTTTCCCTTCAGAA 310
QY 101 ILeThrIleProAspAsnTyrThrIleGluValGluAlaGluAsnGlyAspGlyValIle 120
DB 311 ATTAAGATCCCAATATTAATTAACATTGAGCTGGAAGCTGAAAATGGAGATGCTGTAAT 370
QY 121 LysSerHisMetThrTyrTrrArgLeuGluAsnIleAlaLysThrGluProProLysIle 140
DB 371 AATATCATATGACATATGAGATTAAGAACATATGCGAAACCTGAACACCACTAAGATT 430
QY 141 PheArgValLysProValLeuGlyIleLysArgMetIleGlnIleGluTrpIleLysPro 160
DB 431 TTCGGGTGAACCAATTTTGGGCATCAACGAATATTCAAATTAATGATTAAGCCCT 490
QY 161 GluLeuAlaProValSerSerAspLeuLysTyrThrLeuArgPheArgThrValAsnSer 180
DB 491 GAGTTGGCGCGCTTTCATCTGATTTAAATACACCTTCGATTCAGAGACAGCAACAGT 550
QY 181 ThrSerTrpMetGluValAsnPheAlaLysAsnArgLysAspLysAsnGlnThrTrrAsn 200
DB 551 ACCAGCTGATGAGATCAACTTCGCTTAAGAACCTTAAGATTAACCAACGATCAAC 610
QY 201 LeuThrGlyLeuGlnProPheThrGluTrrValIleAlaLeuArgCysAlaValLysGlu 220
DB 611 CTCACGGGGGTGAGCCTTTTACAGAAATAGTATAGCTCTTGCGATGTGGCGTCAAGAG 670
QY 221 SerLysPheTrpSerAspTrpSerGlnGluLysMetGlyMetThrGluGluGlu 238
DB 671 TCAAAGTTCTGGAGTGACTGAGACCAAGAAAAATGGGAATGACTGAGAGAA 724

RESULT 5
AX467335

LOCUS AX467335 2238 bp DNA linear PAT 16-JUL-2002
DEFINITION Sequence 5 from Patent WO0229080.
ACCESSION AX467335
VERSION AX467335.1 GI:21900585
KEYWORDS
SOURCE
ORGANISM
Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homindae; Homo.
REFERENCE
AUTHORS Cosman, D.J., Mosley, B.A., Bird, T.A., Dubose, R.F. and Wiley, S.R.
TITLES Hematopoietin receptors hpr1 and hpr2
JOURNAL Patent: WO 0229060-A 5 11-Apr-2002;
Immunex Corporation (US)
FEATURES
source Location/Qualifiers
1. .2238
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

ORIGIN

Alignment Scores:
Pred. No.: 3,33e-120 Length: 2238
Score: 1292.00 Matches: 238
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 95.14% Indels: 0
DB: 6 Gaps: 0

US-10-006-265-4 (1-252) x AX467335 (1-2238)

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DB 1 ATGAAGCTCTCTCCAGCCTTCATGTGTAACTGGGGATGATGGACCTGGCAGCTG 60
QY 21 TrpMetLeuProSerLeuCysLysPheSerLeuAlaAlaLeuProAlaLysProGluAn 40
DB 61 TGGATGCTCCCTCCACTGCAATTGAGCTTGAGCTTGACCTGAAAGCTGAGAAC 120
QY 41 ILeSerCysValTyrTyrTrrArgLysAsnLeuThrCysThrTrpSerProGlyLysGlu 60
DB 121 ATTTCCTGTGTACTACTATAGAAAAATTAACTGCACCTGGAGTCCAGTAAAGCTGAGAA 180
QY 61 ThrSerTyrThrGlnTyrThrValLysArgThrTrrAlaPheGlyGlyLysHisAspAsn 80
DB 181 ACCAGTTAATACCAGATACAGATTAAGAGAACTTAAGCTTTTGAGAAAAACATGATAT 240
QY 81 CysThrThrAsnSerSerThrSerGluAsnArgAlaSerCysSerPhePheLeuProArg 100
DB 241 TGTACACCAATAGTTCTCAAGTGAATAATCGTGTCTGCTCTTTTCCCTTCAGAA 300
QY 101 ILeThrIleProAspAsnTyrThrIleGluValGluAlaGluAsnGlyAspGlyValIle 120
DB 301 ATTAAGATCCCAATATTAATTAACATTGAGCTGGAAGCTGAAAATGGAGATGCTGTAAT 360
QY 121 LysSerHisMetThrTyrTrrArgLeuGluAsnIleAlaLysThrGluProProLysIle 140
DB 361 AATATCATATGACATATGAGATTAAGAACATATGCGAAACCTGAACACCACTAAGATT 420
QY 141 PheArgValLysProValLeuGlyIleLysArgMetIleGlnIleGluTrpIleLysPro 160
DB 421 TTCGGGTGAACCAATTTTGGGCATCAACGAATGATCAATTAAGATTAAGCCCT 480
QY 161 GluLeuAlaProValSerSerAspLeuLysTyrThrLeuArgPheArgThrValAsnSer 180
DB 481 GAGTTGGCGCGCTTTCATCTGATTTAAATACACCTTCGATTCAGAGACAGCAACAGT 540
QY 181 ThrSerTrpMetGluValAsnPheAlaLysAsnArgLysAspLysAsnGlnThrTrrAsn 200
DB 541 ACCAGCTGATGAGATCAACTTCGCTTAAGAACCTTAAGATTAACCAACGATCAAC 600
QY 201 LeuThrGlyLeuGlnProPheThrGluTrrValIleAlaLeuArgCysAlaValLysGlu 220

Db 601 CTCACGGGCTGCACCTTTTACAGATATGTCATAGCTCTGCAGATGTCGGTCAAGAG 660

Qy 221 SerlyspHetTPSerAptTPSerGlnGluYmMetGlyMetThnGluGlu 238

Db 661 TCNAAGTTCGAGAGCTGAGCCAGCAAGAAAAATGGAAATGATGAGGAGAA 714

RESULT 6

AX365216

LOCUS AX365216 2295 bp DNA linear PAT 15-FEB-2002

DEFINITION Sequence 68 from Patent WO0200721.

ACCESSION AX365216

VERSION AX365216.1 GI:18696970

KEYWORDS

SOURCE

ORGANISM

synthetic construct

other sequences; artificial sequences.

REFERENCE

1 Sprecher, C.A., Presnell, S.R., Gao, Z., Whitmore, T.E., Kujiper, J.L., and Maurer, M.F.

TITLE Cytokine receptor zcytor17

JOURNAL Patent: WO 0200721-A 68 03-JAN-2002;

FEATURES

source

1. .2295

Location/Qualifiers

/organism="synthetic construct"

/mol_type="unassigned DNA"

/db_xref="taxon:32630"

/note="Polynucleotide encoding human zcytor17-Fc4 fusion"

1. .2295

/note="unnamed protein product"

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/transl_table=11

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/db_xref="GI:18696971"

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ORIGIN

Alignment Scores:

Pred. No.: 3,43e-120 Length: 2295

Score: 1292.00 Matches: 238

Percent Similarity: 100.00% Conservative: 0

Best Local Similarity: 100.00% Mismatches: 0

Query Match: 95.14% Indels: 0

Gaps: 0

DB: 6

US-10-006-265-4 (1-252) x AX365216 (1-2295)

Qy 1 MetlyaleuSerProGlnProSerCyValAblenleuGlyMetMetThnThnAlaleu 20

Db 1 ATGAAGCTCTCTCCCGACCTTCATGTTTAACTGGGGAGATGATGAGACCTGGGCACTG 60

Qy 21 TrpMetleuProSerleuCyValyPheSerleuAlaleuProAlaleuProGluAan 40

Db 61 TGGATGCTCCCTTCACTGTGAAATTCAGCGCTGGAGCTGCGACGTAAGCTGAGAAC 120

Qy 41 TleserCyValTyTyTyTArGlyAblenleuThnTySthnTPSerProGlyLylyGlu 60

Db 121 ATTTCCTGTGCTCTACTATAGGAAAAATTTAACTGACCTTGAGAGTCCGAGAAAGGAA 180

Qy 61 ThreerTyThnGlnTyThnValyAblenThnTyTAlarPheGlyGlyLylyHlaAblan 80

Db 181 ACCAGTTATACCCAGTACAGAGTTAAGGAACCTTAACGCTTTTGGAGAAAAATCATATAT 240

Qy 81 CysThnThraAnSerSerThSerGluAblenAglaserCySerPhePheleuProArg 100

Db 241 TGTACACCAATAGTTCACAAAGTGAAGAAATGTCCTTCGTCTCTTTTTCCTTCCAAAGA 300

Qy 101 TleThrIleProAblenTyThnIleGluValGluAgluAanGlyAAspGlyValIle 120

Db 301 ATACAGATCCCAAGTAAATTAATACATGAGGTGGAAGCTGAAATGGAGATGGTATATT 360

Qy 121 LysSerHisMetThnTyTTPArgleuGluAanIleAlalySthnGluProProLyseIle 140

Db 361 AAATCTCATATGACATACCTGAGATTGAGAAACATAGGAAACATGAAACCATTAAGATT 420

Qy 141 PheArgValLyPProValleuGlyIleleAArgMetIleGlnIleGluTPIleLyPPro 160

Db 421 TTCGGTGGAAACCAAGTTTGGCATCAACGAATGATTCAAATTGATGATGAAGCCT 480

Qy 161 GluIleuAlaProValSerSerAblenTyTyThnThnleuAArgPheArgThnValAnSer 180

Db 481 GAGTTGGCGCTGTTTCATCTGATTTAAATAACACACTTCGATTCAGACAGTCAACAGT 540

Qy 181 ThreerTPMetGluValAblenPheAlalyAblenArgLyAAspLyAAsnGlnThnTyAn 200

Db 541 ACCAGCTGAGAGAGAGTCACTTGCCTAGAACCGTAAAGATTAACCAACCAACGTAACAC 600

Qy 201 LeuThrglyleuGlnProPheThnGluTyValIleAlaleuAArgCyValIleValyGlu 220

Db 601 CTCACGGGCTGCACCTTTTACAGATATGTCATAGCTCTGCAGATGTCGGTCAAGAG 660

Qy 221 SerlyspHetTPSerAptTPSerGlnGluYmMetGlyMetThnGluGlu 238

Db 661 TCNAAGTTCGAGAGCTGAGCCAGCAAGAAAAATGGAAATGATGAGGAGAA 714

RESULT 7

AX467333

LOCUS AX467333 2480 bp DNA linear PAT 16-JUL-2002

DEFINITION Sequence 3 from Patent WO0229060.

ACCESSION AX467333

VERSION AX467333.1 GI:21900584

KEYWORDS

SOURCE

Homo sapiens (human)

ORGANISM

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE

1 Cosman, D.J., Mosley, B.A., Bird, T.A., Dubose, R.F. and Wiley, S.R.

TITLE Hematopoietin receptors hprt1 and hprt2

JOURNAL Patent: WO 0229060-A 3 11-Apr-2002;

FEATURES

source

1. .2480

Location/Qualifiers

/organism="Homo sapiens"

/mol_type="unassigned DNA"

/db_xref="taxon:9606"

ORIGIN

Alignment Scores:

Pred. No.: 3.79e-120 Length: 2480

Score: 1292.00 Matches: 238

Percent Similarity: 100.00% Conservative: 0

Best Local Similarity: 100.00% Mismatches: 0

Query Match: 95.14% Indels: 0

Gaps: 0

DB: 6

US-10-006-265-4 (1-252) x AX467333 (1-2480)

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Qy 21 TrpMetleuProSerleuCyValyPheSerleuAlaleuProAlaleuProGluAan 40

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Qy 61 ThrSerTyThrsGlnTyThrVallylsargThrTyAlaPheGlyGlylyshIsaapasn 80
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Db 312 ACCAGATTATACCAATATATATACCATTTGAGGTGAAAGCTGAAATGAGATGATAT 371
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Qy 81 CySerThrThrsanSerThrSerGluasnArgAlaSerCysSerPhePheLeuProArg 100
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Db 372 TGTACAAACCAATAGTTCTCAAGTGAATAATCGCTTCGCTCTTTTCTTCCCAAGA 431
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Qy 101 lIeThrIleProaspentTyThrIleGluValGluasnGlylysaPglyValIle 120
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|||
Qy 121 lYsSerHisMetThrTyrrTrpArgLeuGluasnIleAlaIleThrGluProPolysile 140
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Db 492 AATCTCATATGACATCTGAGATTTAGAACATACGAAACTGAACTCAAGATT 551
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Qy 141 PheArgVallylsProValleuglyIlelysaArgMetIleGlnIleGluTrpIlelyPro 160
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Db 552 TTCGGTGGAAACAGTTTGGGCATCAACGAATGATTCAAAATTGAATGATAAGCCT 611
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Qy 161 GluLeuAlaProValSerSerAspIleuTyThrIleuArgPheArgThrValIleSer 180
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Db 612 GAGTTGGCGCTTTTCATCTGATTTAAATACACCTTGATTCAGGACGCAACAGT 671
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Qy 181 ThrSerTyThrsGlnTyThrVallylsargAlaIlePheAlaIleThrGluProPolysile 200
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Qy 221 SerTyPheThrPserAspTrpSerGlnGluIleuMetGlyMetThrGluGlu 238
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Db 792 TCAAGTTCTGAGTAGTACGAGCCAAAGAAAATGGGAATGACTGAGGAAGA 845
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RESULT 8
AX365201 2903 bp DNA linear PAT 15-FEB-2002
LOCUS Sequence 53 from Patent WO0200721.
ACCESSION AX365201
VERSION AX365201.1 GI:18696955
KEYWORDS
SOURCE
ORGANISM Homo sapiens (human)
Mammalia; Eutheria; Chordata; Craniata; Vertebrata; Euteleostomi;
Bukaryaota; Metazoa; Primates; Catarrhini; Homnidae; Homo.
Sprecher,C.A., Presnell,S.R., Gao,Z., Whitmore,T.E., Krijger,J.L.
and Maurer,M.F.
1
Cytokine receptor zcyfor17
Patent: WO 0200721-A 53 03-JAN-2002;
ZymoGenetics, Inc. (US)
FEATURES
source
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/organism="Homo sapiens"
/mol_type="unassigned DNA"
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ORIGIN

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Alignment Scores:
Pred. No.: 4,6e-120 Length: 2903
Score: 1292.00 Matches: 238
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 95.14% Indels: 0
DB: 6 Gaps: 0

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US-10-006-265-4 (1-252) x AX365201 (1-2903)

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Qy 21 TrpMetLeuProSerLeuCySerlyspheSerleuAlaIleProAlaIlyspProGluasn 40
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Db 557 TGGATGCTCCCTTCACTCTGCAAAATTCAGCCTGGCAGCTCTGCCAGCTAAGCTGAGAAC 616
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Qy 41 lIeSerCyVallyrTyrrArglysaenLeuThrCySerThrPserProGlylysglu 60
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Db 617 ATTTCCTGTCCTACACTATAGAAAATTTAACTGCACCTGAGTTCAGGAAAGAA 676
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Qy 61 ThrSerTyThrsGlnTyThrVallylsargThrTyAlaPheGlyGluIlyshIsaapasn 80
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Db 677 ACCAGTTAACCCAGATACAGATTAGAGAACCTTGCGCTTTGGAGAAAACATGATATAT 736
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Qy 81 CySerThrThrsanSerThrSerGluasnArgAlaSerCysSerPhePheLeuProArg 100
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Db 737 TGTACAAACCAATAGTTCTTCAAGTGAATAATCGCTCTGCTCTTTTCTTCCCAAGA 796
|||
Qy 101 lIeThrIleProaspentTyThrIleGluValGluasnGlylysaPglyValIle 120
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Db 797 ATACAGATCCCAATATATATACCATTTGAGGTGAAAGCTGAAATGAGATGATGATAT 856
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Qy 121 lYsSerHisMetThrTyrrTrpArgLeuGluasnIleAlaIleThrGluProPolysile 140
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Db 857 AATCTCATATGACATCTGAGATTTAGAACATACGAAACTGAACTCAAGATT 916
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Qy 141 PheArgVallylsProValleuglyIlelysaArgMetIleGlnIleGluTrpIlelyPro 160
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Db 917 TTCGGTGGAAACAGTTTGGGCATCAACGAATGATTCAAAATTGAATGATAAGCCT 976
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Qy 161 GluLeuAlaProValSerSerAspIleuTyThrIleuArgPheArgThrValIleSer 180
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Db 977 GAGTTGGCGCTTTTCATCTGATTTAAATACACCTTGATTCAGGACGACGATCAACAGT 1036
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Qy 181 ThrSerTyThrsGlnTyThrVallylsargAlaIlePheAlaIleThrGluProPolysile 200
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Qy 201 LeuThrGlyleuGlnProPheThrGluTyrrValIleAlaIleuArgCysAlaVallysglu 220
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RESULT 9
AY499342 2903 bp mRNA linear PRI 10-JUL-2004
LOCUS AY499342
DEFINITION Homo sapiens interleukin 31RA splice variant x4 (IL31RA) mRNA,

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complete cds, alternatively spliced.

ACCESSION
AY499342 GI:46276462

KEYWORDS

SOURCE
Homo sapiens (human)

ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.

REFERENCE

1 (bases 1 to 2903)
Dillon,S.R., Sprecher,C., Hammond,A., Bilsborough,J.,
Rosenfeld-Franklin,M., Presnell,S.R., Haugen,H.S., Maurer,M.,
Harder,B., Johnston,J., Bort,S., Modri,S., Kuijper,J.,
Bukowski,T., Shea,P., Dong,D.L., Dasovich,M., Grant,F.J.,
Lockwood,L., Levin,S.D., Leciel,C., Maggie,K., Day,H., Topouzis,S.,
Kramer,J., Kuestner,R., Chen,Z., Foster,D., Parrish-Novak,J. and
Gross,J.A.
Interleukin 31, a cytokine produced by activated T cells, induces
dermatitis in mice
Nat. Immunol. 5 (7), 752-760 (2004)

TITLE

JOURNAL
Nat. Immunol. 5 (7), 752-760 (2004)

REFERENCE

AUTHORS

2 (bases 1 to 2903)
Dillon,S.R., Sprecher,C., Hammond,A., Rosenfeld-Franklin,M.,
Presnell,S.R., Haugen,H., Bilsborough,J., Maurer,M., Harder,B.,
Johnston,J., Bort,S., Modri,S., Kuijper,J., Bukowski,T., Shea,P.,
Dong,D., Dasovich,M., Lockwood,L., Levin,S., Leciel,C., Maggie,K.,
Kramer,J., Kuestner,R., Chen,Z., Foster,D., Parrish-Novak,J. and
Gross,J.A.
Direct Submission
Submitted (10-DEC-2003) Bioinformatics, ZymoGenetics, Inc., 1201
Eastlake Avenue East, Seattle, WA 98102, USA

FEATURES

SOURCE

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ORIGIN

Alignment Scores:

Pred. No.: 4.6e-120 Length: 2903

Score: 1292.00 Matches: 238

Percent Similarity: 100.00% Conservative: 0

Best Local Similarity: 100.00% Mismatches: 0

Query Match: 95.14% Indels: 0

DB: 9 Gaps: 0

US-10-006-265-4 (1-252) x AY499342 (1-2903)

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Db 1157 TCAAAGTTCTGAGTGAAGTGAAGCAAGAAATGGAATGACTGAGAAAGAA 1210

RESULT 10

LOCUS BD091864 2969 bp DNA linear PAT 27-AUG-2002

DEFINITION Novel hemopoietin receptor protein, NR10.

ACCESSION BD091864 GI:22637475

VERSION BD091864.1

KEYWORDS Homo sapiens (human)

ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 2969)

AUTHORS Maeda,M. and Yaguchi,N.

TITLE Novel hemopoietin receptor protein, NR10

JOURNAL Patent: WO 0075314-A 1 14-DEC-2000;

CHUGAI RESEARCH INSTITUTE FOR MOLECULAR MEDICINE INC, MASATSUGU

MAEDA, NORIKO YAGUCHI

OS Homo sapiens (human)

PN WO 0075314-A/1

PR 01-JUN-2000 WO 2000JP003556

PR 02-JUN-1999 JP 99P 155797,30-JUL-1999 JP 99P 217797 P1

PC MASATSUGU MAEDA,NORIKO YAGUCHI

PC G12N15/12,C12N5/10,C07K14/715,C07K16/28,C12P21/02,G01N33/53,

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CC FH Key Location/Qualifiers

FEATURES FT CDS (523)..(2478).
location/Qualifiers
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ORIGIN

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Score:	1292.00	Matches:	238
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Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	95.14%	Indels:	0
DB:	6	Gaps:	0

US-10-006-265-4 (1-252) x BD091864 (1-2969)

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QY 21 TrpMetLeuProSerLeuCysLysPheSerLeuAlaAlaLeuProAlaLysProGluAsn 40
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QY 41 IleSerCysValTyrTyrTyrArgLysAsnLeuThrCysThrTrpSerProGlyLysGlu 60
DB 643 ATTTCTGTCCTACTCTACTAGAGAAATTTAACTTGCACCTTGGAGTCCAGAGAAAGAA 702
QY 61 ThrSerTyrThrGlnTyrThrValLysArgThrTyrAlaPheGlyGlyLysHisAspAsn 80
DB 703 ACCAGTTATACCCAGTACAGAGTTAAGAGAACTTAAGCTTCCGAGAGAAACATGATTAAT 762
QY 81 CysThrThrAsnSerSerThrSerGluAsnArgAlaSerCysSerPhePheLeuProArg 100
DB 763 TGTACAAACCAATGTTCTTACAGTGAATAATCGTCTCGCTCTTTTCTTCCCAAGA 822
QY 101 IleThrIleProAspAsnTyrThrIleGluValGluAlaGluAsnGlyAspGlyValIle 120
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RESULT 11
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LOCUS AX365165 1299 bp DNA linear PAT 15-FEB-2002
DEFINITION Sequence 17 from Patent WO0200721.
ACCESSION AX365165
VERSION AX365165.1 GI:18696923
KEYWORDS

SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

REFERENCE 1
AUTHORS Sprecher,C.A., Presnell,S.R., Gao,Z., Whitmore,T.E., Kujiper,J.L.
and Maurer,M.F.

TITLE Cytokine receptor zcytor17
JOURNAL Patent: WO 0200721-A 17 03-JAN-2002;
ZymoGenetics, Inc. (US)

FEATURES

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Location/Qualifiers

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ORIGIN

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US-10-006-265-4 (1-252) x AX365165 (1-1299)

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DB 189 CTCCCTCACTCTGCAAAATTCAGCTGGCAGCTGCGACGCTAAGCTGAGAACATTTCC 248
QY 43 CysValTyrTyrTyrArgLysAsnLeuThrCysThrTrpSerProGlyLysGluTrpSer 62
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DEFINITION Homo sapiens interleukin 31RA splice variant x2 (IL31RA) mRNA,
complete cds, alternatively spliced.
ACCESSION AY499340
VERSION AY499340.1 GI:46276458
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 1299)
AUTHORS Dillon,S.R., Sprecher,C., Hammond,A., Bilborough,J.,
Rosenfeld-Franklin,M., Presnell,S.R., Haugen,H.S., Maurer,M.,
Harder,B., Johnston,J., Bort,S., Mudri,S., Kuijper,J.L.,
Bukowski,T., Shea,P., Dong,D.L., Dasovich,M., Grant,F.J.,
Lockwood,L., Levin,S.D., LeCiel,C., Maggie,K., Day,H., Topouzis,S.,
Kramer,J., Kuestner,R., Chen,Z., Foester,D., Parrish-Novak,J. and
Gross,J.A.
Interleukin 31, a cytokine produced by activated T cells, induces
dermatitis in mice
Nat. Immunol. 5 (7), 752-760 (2004)
15184896
2 (bases 1 to 1299)
AUTHORS Dillon,S.R., Sprecher,C., Hammond,A., Rosenfeld-Franklin,M.,
Presnell,S.R., Haugen,H., Bilborough,J., Maurer,M., Harder,B.,
Johnston,J., Bort,S., Mudri,S., Kuijper,J., Bukowski,T., Shea,P.,
Dong,D., Dasovich,M., Lockwood,L., Levin,S., LeCiel,C., Maggie,K.,
Kramer,J., Kuestner,R., Chen,Z., Foester,D., Parrish-Novak,J. and
Gross,J.A.
Direct Submission
Submitted (10-DEC-2003) Bioinformatics, ZymoGenetics, Inc., 1201
Eastlake Avenue East, Seattle, WA 98102, USA
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162. 1136
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Pred. No.: 1,73e-119 Length: 1299
Score: 1282.00 Matches: 236
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 94.40% Indels: 0
Gaps: 0
US-10-006-265-4 (1-252) x AY499340 (1-1299)
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Db 129 CTCTCTCCCGACCTTCACTGTGTAACTCGGAGATGATGTGACCTGGGCACTGTGAGT 188
QY 23 LeuProSerLeuCysIysPheSerLeuAlaIleuProAlaIysProGluAsnIleSer 42
Db 189 CTCCCTCACTCTGAAATTAATTCAGCTGACCTCTGCGAGCTTAAGCTGAGAACTTTCC 248
QY 43 CysValTyrTyrTyrArgIysAsnLeuThrCysThrTPSerProGlyIysGluThrSer 62
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QY 223 PheTTPSerAspTPSerGlnGluIlyMetGlyMetThrGluGlu 238
Db 789 TTCTGAGTGACTGAGCCAGCAAGAAAATGGAATGACTGAGAGAA 836
RESULT 13
LOCUS AY499341 2393 bp mRNA linear PRI 10-JUL-2004
DEFINITION Homo sapiens interleukin 31RA splice variant x3 (IL31RA) mRNA,
complete cds, alternatively spliced.
ACCESSION AY499341
VERSION AY499341.1 GI:46276460
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 2393)
AUTHORS Dillon,S.R., Sprecher,C., Hammond,A., Bilborough,J.,
Rosenfeld-Franklin,M., Presnell,S.R., Haugen,H.S., Maurer,M.,
Harder,B., Johnston,J., Bort,S., Mudri,S., Kuijper,J.L.,

Bukowski, T., Shea, P., Dong, D.L., Dasovich, M., Grant, F.J.,
 Lockwood, L., Levin, S.D., Leciel, C., Maggile, K., Day, H., Topouzis, S.,
 Kramer, J., Kuestner, R., Chen, Z., Foster, D., Parish-Novak, J. and
 Gross, J.A.
 Interleukin 31, a cytokine produced by activated T cells, induces
 dermatitis in mice
 Nat. Immunol. 5 (7), 752-760 (2004)
 15184896
 2 (bases 1 to 2393)
 Dillon, S.R., Sprecher, C., Hammond, A., Rosenfeld-Franklin, M.,
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 Johnston, J., Bort, S., Mudri, S., Kuijper, J., Bukowski, T., Shea, P.,
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 Kramer, J., Kuestner, R., Chen, Z., Foster, D., Parish-Novak, J. and
 Gross, J.A.
 Direct Submission
 Submitted (10-DEC-2003) Bioinformatics, ZymoGenetics, Inc., 1201
 Eastlake Avenue East, Seattle, WA 98102, USA
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ORIGIN

Alignment Scores:
Pred. No.: 3,71e-119 Length: 2402
Score: 1282.00 Matches: 236
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 94.40% Indels: 0
DB: 6 Gaps: 0

US-10-006-265-4 (1-252) x AX365149 (1-2402)

QY 3 LeuSerProGlnProSerCysValAsnLeuGlyMetMetTyrThrAlaLeuTyrMet 22
DB 138 CTCTCTCCCAAGCCCTTCACTGTGTAACTGGGGAATGATGTGACCTGGGCACCTGTGGATG 197
QY 23 LeuProSerLeuCysLysPheSerLeuAlaAlaLeuProAlaLysProGluAsnIleSer 42
DB 198 CTCCTCTACCTCTGCAAAATTCAGCTGGCAGCTCTGCGAGCTTAAGCTTGAGAACATTTCC 257
QY 43 CysValTyrTyrTyrArgLysAsnLeuThrCysThrTyrPseProGlyLysGluThrSer 62
DB 258 TGTGTCTACTACTATAGAAAAATTTAACTGCACTTGAGAGTCCAGAAAGAAACACAGT 317
QY 63 TyrThrGlnTyrThrValLysArgThrTyrAlaPheGlyGluLysHisAspAsnCysThr 82
DB 318 TATACCCGATCACAGTTAGAGAACTTAACGCTTTTGGAGAAAAACATGATTAATGTACA 377
QY 83 ThrAsnSerSerThrSerGluAsnArgLaseCysSerPhePheLeuProArgIleThr 102
DB 378 ACCAATAGTCTACAGAGAAATCGCTGCTGCTCTTTTCTTCCCAAGAAATACG 437
QY 103 IleProAspAsnTyrThrIleGluValGluAlaGluAsnGlyAspGlyValIleLysSer 122
DB 438 ATCCAGATTAATTAACCATTTAGAGTGAAGCTGAAATGAGATGGTAAATTAATCT 497
QY 123 HisMetThrTyrTyrPArgLeuGluAsnIleAlaLysThrGluProLysIlePheArg 142
DB 498 CATATGACATCTGAGAGATTAGAGAACATAGCGAAACCTGAACCTTAAGATTTTCCGT 557
QY 143 ValLysProValIleGluLysArgMetIleGlnIleGluTyrIleLysProGluLeu 162
DB 558 GTGAACCAAGTTTGGGCAATCAACGAATGATTAATTAAGTGAAGCTGAGTTG 617
QY 163 AlaProValSerSerAspLeuLysTyrThrLeuArgPheArgThrValAsnSerThrSer 182
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QY 183 TyrMetGluValAsnPheAlaLysAsnArgLysAspLysAsnGlnThrTyrAsnLeuThr 202
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QY 203 GlyLeuGlnProPheThrGluTyrValIleAlaLeuArgCysAlaValLysGluSerLys 222
DB 738 GGGCTGCGCCTTTTACGAATATGTCAATGCTGCGCATGTGCGGTAAAGAGTCAAG 797
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LOCUS AX358838 2445 bp DNA linear PAT 13-FEB-2002
DEFINITION Sequence 91 from Patent WO0193983.
ACCESSION AX358838
VERSION AX358838.1 GI:18675320
KEYWORDS
ORGANISM Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

REFERENCE

1 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
Baker, K.P., Desnoyers, L., Gerritsen, M.E., Goddard, A.,
Godowski, P.J., Grimaldi, J.C., Gunney, A.U., Smith, V., Stephan, J.P.,
Watanabe, C.K. and Wood, W.I.
Secreted and transmembrane polypeptides and nucleic acids encoding
the same

TITLE

JOURNAL Patent: WO 0193983-A 91 13-DEC-2001;

FEATURES

Location/Qualifiers
1..2445
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/mol_type="unassigned DNA"
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ORIGIN

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Score: 1282.00 Matches: 236
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Query Match: 94.40% Indels: 0
DB: 6 Gaps: 0

US-10-006-265-4 (1-252) x AX358838 (1-2445)

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QY 23 LeuProSerLeuCysLysPheSerLeuAlaAlaLeuProAlaLysProGluAsnIleSer 42
DB 316 CTCCTCTACCTCTGCAAAATTCAGCTGGCAGCTCTGCGAGCTTAAGCTTGAGAACATTTCC 375
QY 43 CysValTyrTyrTyrArgLysAsnLeuThrCysThrTyrPseProGlyLysGluThrSer 62
DB 376 TGTGTCTACTACTATAGAAAAATTTAACTGCACTTGAGAGTCCAGAAAGAAACACAGT 435
QY 63 TyrThrGlnTyrThrValLysArgThrTyrAlaPheGlyGluLysHisAspAsnCysThr 82
DB 436 TATACCCGATCACAGTTAGAGAACTTAACGCTTTTGGAGAAAAACATGATTAATGTACA 495
QY 83 ThrAsnSerSerThrSerGluAsnArgLaseCysSerPhePheLeuProArgIleThr 102
DB 496 ACCAATAGTCTACAGAGAAATCGCTGCTGCTCTTTTCTTCCCAAGAAATACG 555
QY 103 IleProAspAsnTyrThrIleGluValGluAlaGluAsnGlyAspGlyValIleLysSer 122
DB 556 ATCCAGATTAATTAACCATTTAGAGTGAAGCTGAAATGAGATGGTAAATTAATCT 615
QY 123 HisMetThrTyrTyrPArgLeuGluAsnIleAlaLysThrGluProLysIlePheArg 142
DB 616 CATATGACATCTGAGAGATTAGAGAACATAGCGAAACCTGAACCTTAAGATTTTCCGT 675
QY 143 ValLysProValIleGluLysArgMetIleGlnIleGluTyrIleLysProGluLeu 162
DB 676 GTGAACCAAGTTTGGGCAATCAACGAATGATTAATTAAGTGAAGCTGAGTTG 735
QY 163 AlaProValSerSerAspLeuLysTyrThrLeuArgPheArgThrValAsnSerThrSer 182
DB 736 GCGCTGTTCATCTGATTTAAATTAACACACTTCGATTCAGGACAGTCAACGATCCAGC 795
QY 183 TyrMetGluValAsnPheAlaLysAsnArgLysAspLysAsnGlnThrTyrAsnLeuThr 202
DB 796 TGGATGGAAAGTCACTTCGTAAAGAACGTAAAGATTAACCAACCTAACCTCAGC 855
QY 203 GlyLeuGlnProPheThrGluTyrValIleAlaLeuArgCysAlaValLysGluSerLys 222
DB 856 GGGCTGCGCCTTTTACGAATATGTCAATGCTGCGCATGTGCGGTAAAGAGTCAAG 915
QY 223 PheTyrSerAspTyrPseGlnGlyLysMetGlyMetThrGluGluGlu 238
DB 916 TTTCTGAGTGACTGAGAGCCAAAGAAAAATGGGAATGACTGAGAGAA 963

Search completed: February 23, 2005, 15:24:16
Job time : 3193.89 secs

GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Run on: February 23, 2005, 05:20:17 ; Search time 372.207 Seconds

(without alignments)
4007.918 Million cell updates/sec

Title: US-10-006-265-4

Perfect score: 1358

Sequence: 1 MKLSPPQSCVNLGMMWTAL.....GMTBECKLTPALPVLSTLV 252

Scoring table:

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Ygapop 10.0, Ygapext 0.5
Fgapop 6.0, Fgapext 7.0
Delop 6.0, Delext 7.0

Searched: 4390206 seqs, 2959870667 residues

Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:
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-LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=blomsu62 -TRANS=human40.cdi
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-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : N.Geneseq_16Dec04:*

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1358	100.0	2440	4	AAC92338 Human hae
2	1343	98.9	1476	6	ABA93784 Human zcy
3	1343	98.9	1476	11	ADL26677 Human zcy
4	1292	95.1	2119	4	AAC92350 Human hae
5	1292	95.1	2295	6	ABA93821 Human zcy

6	1292	95.1	2295	10	ADD68179 Human zcy
7	1292	95.1	2295	11	ADL26602 Human zcy
8	1292	95.1	2480	6	ADD38772 Human hae
9	1292	95.1	2903	6	ABA93808 Human zcy
10	1292	95.1	2903	10	ADD68146 Human zcy
11	1292	95.1	2903	11	ADL26569 Human zcy
12	1292	95.1	2969	4	AAC92337 Human hae
13	1282	94.4	1299	6	ABA93781 zcyox17
14	1282	94.4	1299	11	ADL26675 Human zcy
15	1282	94.4	2386	6	ABA93767 Human zcy
16	1282	94.4	2402	11	ADL26673 Human zcy
17	1282	94.4	2445	6	ABK33581 CDNA enco
18	1282	94.4	2445	6	ABL88257 Human PRO
19	1282	94.4	2445	6	ABL95746 Human ang
20	1282	94.4	2445	8	ACA68542 Human hum
21	1282	94.4	2445	8	ABT44271 Human PRO
22	1282	94.4	2445	9	ABT44554 Human PRO
23	1282	94.4	2445	9	ACD82221 Human sec
24	1282	94.4	2445	9	ABT43927 Human mem
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34	1282	94.4	2445	10	ADB72982 Novel hum
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36	1282	94.4	2445	10	ADC21810 Human PRO
37	1282	94.4	2445	10	ADC49841 Novel hum
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ALIGNMENTS

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ID AAC92338 standard; CDNA; 2440 BP.
AC AAC92338;
26-MAR-2001 (first entry)
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KW Human; haemopoietin receptor; NR10.1; NR10.2; NR10.3; NR10;
KW immunoregulation; haematopoietic cell regulation; transmembrane;
KW immune disorder; haematopoietic disorder; autoimmune disease; allergy;
KW metal allergy; pollen allergy; se.
XX OS Homo sapiens.
XX PN WO200075314-A1.
XX PD 14-DEC-2000.
XX PF 01-JUN-2000; 2000WO-JP003556.
XX PR 02-JUN-1999; 99JP-00155797.
XX PR 30-JUL-1999; 99JP-00217797.
PA (CHUG-) CHUGAI RES INST MOLECULAR MEDICINE INC.
XX Maeda M, Yaguchi N.
PI

```

XX WPI; 2001-061720/07.
DR P-PSDB; AAB51243.
XX Hematopoietin receptor protein NR10 for screening potential ligands for
PT treatment of immune and hematopoietic disorders such as autoimmune
PT diseases and allergies.
XX
XX Claim 1; Fig 6-7; 127pp; Japanese.
XX
CC The present sequence encodes a human haemopoietin receptor protein
CC (NR10), specifically designated NR10.2. NR10 occurs as a transmembrane
CC protein and a soluble protein. NR10 is a haemopoietin receptor molecule
CC which participates in immunoregulation and haematopoietic cell regulation
CC in vivo, and is useful in searching for haematopoietic factors capable of
CC binding to the receptor. NR10 can be used for the identification of
CC substances for the treatment and prevention of immune and haematopoietic
CC disorders including autoimmune diseases and allergies such as metal and
CC pollen allergy
XX
SQ Sequence 2440 BP; 738 A; 508 C; 524 G; 670 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 2,48e-141 Length: 2440
Score: 1358.00 Matches: 252
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 4 Gaps: 0

US-10-006-265-4 (1-252) x AAC92338 (1-2440)
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QY 21 TrpMetLeuProSerLeuCysLysPheSerLeuAlaLeuProAlaLysProGluAsn 40
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QY 41 LLeSerCysValLysTrpTrpArgLysAsnLeuTrpCysThrTrpSerProGlyLysGlu 60
Db 643 ATTTCTGCTGTCTACTACTATAGAAAAAATTAACTGCACTTGAGTCCAGAAAGAA 702
QY 61 ThrSerTrpThrGlnTrpThrValLysArgThrTrpAlaPheGlyGlyLysAsn 80
Db 703 ACCAGTTATACCAAGTACAGATTAGAGAACTTACGCTTCCGAGAAAAACATGATTAAT 762
QY 81 CysThrThzAsnSerSerThrSerGluAsnArgAlaSerCysSerPhePheLeuProArg 100
Db 763 TGTACAAACCAATGTTCTTACAGTGAATAATCGTGCTTCGTCCTTTTCTTCCAAAG 822
QY 101 LLeThrLLeProAspPheTrpThrLLeGluValGluAlaGluAsnGlyLysGlyVal 120
Db 823 ATATACATCCCAATATATATACCATTTGAGTGAAGCTGAAAAATGAGATGATGTAATT 882
QY 121 LysSerHisMetThrTrpTrpArgLysGluAsnLLeAlaLysThrGluProProLys 140
Db 883 AAATTCATATGACATCTGAGATTAAGAAACATACGAAACCTGAAACCACTTAAGATT 942
QY 141 PheArgValLysProValLeuGlyLLeLysArgMetLLeGlnLLeGluTrpLLeLysPro 160
Db 943 TTCGGTGTGAACCAAGTTTGGGATCAAAACGAAATGATTAATTAATTAATTAAGCTT 1002
QY 161 GluLeuAlaProValSerSerAspLysLysTrpThrLeuArgPheArgThrValAsnSer 180
Db 1003 GAGTTGGCGCTTTTCATCTGATTTAAATACACACTTGATTTCCAGACGCAACAGT 1062
QY 181 ThrSerTrpMetGluValAsnPheAlaLysAsnArgLysAspLysAsnGlnTrpTrpAsn 200
Db 1063 ACCAGCTGGATGAGCAACTTCGCTAAGAACCCGTAAAGATTAACCAACAGTCTAAC 1122
QY 201 LeuThrGlyLeuGlnProPheThrGluTrpValLLeAlaLeuArgCysAlaValLysGlu 220

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Db 1123 CTCACGGGCGCTCAGCCTTTTACAGAAATGATGATAGCTCTCGCATGTCGGTCAAGGAG 1182
QY 221 SerLysPheTrpSerAspTrpSerGlnGlyLysMetGlyWetThrGluLugLysLys 240
Db 1183 TCAAAATTCTGAGATGATCTGAGAGCCAGAAAAATGGGATATGATGAGAAAGAGCAAG 1242
QY 241 LeuLeuProAlaLLeProValLeuSerThrLeuVal 252
Db 1243 CTACTCCCTGCGATTCCCTCTCTCTACTCTGCTG 1278

RESULT 2
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XX ABA93784;
AC
XX
XX 01-MAY-2002 (first entry)
DT
XX
XX Human zcytor17 soluble form encoding cDNA SEQ ID NO:21.
DE
XX
XX Zcytor17; chromosome 5; 5q11; cytokine receptor; immunomodulatory;
XX antiinflammatory; antiviral; antineumatic; antiarthritic; cytostatic;
XX muscular; lymphoid; immune; inflammatory; splenic; blood; bone;
XX infection; immunosuppression; cytotoxicity; leucopenia; Crohn's disease;
XX autoimmune disease; rheumatoid arthritis; multiple sclerosis; cancer;
XX inflammatory disease; pancreatitis; inflammatory bowel disease; ss.
XX
XX Homo sapiens.
OS
XX
XX WO200200721-A2.
PN
XX
XX 03-JAN-2002.
PD
XX
XX 26-JUN-2001; 2001WO-US020484.
PR
XX
XX 26-JUN-2000; 2000US-0214282P.
PR 29-JUN-2000; 2000US-0214955P.
PR 08-FEB-2001; 2001US-0267963P.
XX
XX (ZYMO ) ZYMOGENETICS INC.
PA
XX
XX Sprecher CA, Preenell SR, Gao Z, Whitmore TE, Kuijper JL;
PI Maurer MF;
PI
XX
XX WPI; 2002-090519/12.
DR P-PSDB; ABB05733.
XX
XX Isolated polynucleotide encoding a cytokine receptor zcytor17 which is
PT useful for treating and diagnosing lymphoid, immune, inflammatory,
PT splenic, blood or bone disorders.
XX
XX Example 2; Page 178-180; 235pp; English.
PS
XX
XX The present invention describes a cytokine receptor designated zcytor17.
CC Zcytor17 has immunomodulatory, antiinflammatory, antiviral, cytostatic,
CC antihematic, antiarthritic and muscular activities. The zcytor17
CC proteins are useful for treating and diagnosing lymphoid, immune,
CC inflammatory, splenic, blood or bone disorders. Agonists or anti-
CC zcytor17 antibodies are useful in stimulating cell-mediated immunity and
CC for stimulating lymphocyte proliferation, such as in the treatment of
CC infections involving immunosuppression, including certain viral
CC infections. They are also useful for inducing cytotoxicity and for
CC treating leukopenias. Antagonist of zcytor17 polypeptides are useful for
CC treating autoimmune diseases (e.g. rheumatoid arthritis and multiple
CC sclerosis), inflammatory diseases (e.g. Crohn's disease), cancer,
CC pancreatitis, and inflammatory bowel disease. Zcytor17 was mapped to
CC chromosome 5, specifically to the 5q11 chromosomal region. ABA93767 to
CC ABA93843 and ABB05730 to ABB05745 represent sequences used in the
CC exemplification of the present invention
XX
XX Sequence 1476 BP; 414 A; 326 C; 338 G; 398 T; 0 U; 0 Other;
SQ

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XX      SQ      Sequence 1476 BP; 414 A; 326 C; 338 G; 398 T; 0 U; 0 Other;
Alignment Scores:
Pred. No.:      5,68e-140      Length:      1476
Score:          1343.00      Matches:      249
Percent Similarity: 99.60%      Conservative: 0
Best Local Similarity: 99.60%      Mismatches: 1
Query Match:    98.90%      Indels:      0
DB:            11      Gaps:      0
US-10-006-265-4 (1-252) x ADL26677 (1-1476)
QY      3      LeuSerProGlnProSerCysValAsnLeuGlyMetMetTrpThrTrpAlaLeuTrpMet 22
DB      129  CTCCTCCCCAGGCTTCATGCTGTTAACTCGGGATATGCGACCTGGGCACTGTGGATG 188
QY      23      LeuProSerLeuCysAlysPheSerLeuAlaLeuProAlaLysProGluAsnIleSer 42
DB      189  CTCCTCTCACTCGAAATTCAGCTCGGACGCTCTGCCAGCTAAAGCTGAGAACATTTCC 248
QY      43      CysValTyrTyrTyrArgLysAsnLeuThrCysThrTrpSerProGlyLysGluTrpSer 62
DB      249  TGTGCTACTACTATAGGAAAAAATTTAACTGCACTTGAGTCAGAGAAAGAAACCAAGT 308
QY      63      TyrThrGlnTyrThrValLysArgThrTyrAlaPheGlyGluLysHisAspAsnCysThr 82
DB      309  TATACCCAGTACACAGTTAAAGAACTTACGCTTTTGAGAAAAAATGATTAATTTGATCA 368
QY      83      ThrAsnSerSerThrSerGluAsnArgAlaSerCysSerPhePheLeuProArgIleThr 102
DB      369  ACCAATAGTTCTTACAGTAGTGAATCGTGCTCGTCTTTTTCCTCCAAAGATTAACG 428
QY      103     IleProAspAsnTyrThrIleGluValGluAlaGluAsnGlyAspGlyValIleLysSer 122
DB      429  ATCCCGATTAATATACCATTTGAGGAGGAGAGCTGAAAAATGAGATGCTTAATTAATCT 488
QY      123     HisMetThrTyrTrpArgLeuGluAsnIleAlaLysThrGluProProlLysIlePheArg 142
DB      489  CAAATGACATCTCGAGATTAGAAACATAGCGAAAAATGAAACCACTTAAGATTTCCGT 548
QY      143     ValLysProValLeuGlyLysArgMetIleGlnIleGluTrpIleLysProGluLeu 162
DB      549  GTGAAACCAAGTTTGGGCAATCAACGAATGATTCAAATTGAATGATTAAGCTGAGTTG 608
QY      163     AlaProValSerSerLeuLysTyrThrLeuArgPheArgThrValAsnSerThrSer 182
DB      609  GCGCTGTTTCATCTGATTTAAATACACACTTCGATTCAGGACAGTCAACAGTACACAGC 668
QY      183     TrpMetGluValAsnPheAlaLysAsnArgLysAspLysAsnGlnThrTyrAsnLeuThr 202
DB      669  TGGATGGAATCAACTTCGCTAGAAACCGTAAGATTAAGAACCAACGTAACCTCAGC 728
QY      203     GlyLeuGlnProPheThrGluTyrValIleAlaLeuArgCysAlaValLysGluSerLys 222
DB      729  GGGCTCAGGCTTTTACAGAAATATGATCATGCTCGGATGTGCGGTCAAGAGAGTCAAG 788
QY      223     PheTrpSerAspTrpSerGlnGluLysMetGlyMetThrGluGluGluLysLysLeu 242
DB      789  TTCTGAGTACTGAGGCAAGAAAAAATGGGAATGATGAGGAAGCAAGCAAGTACTC 848
QY      243     ProAlaIleProValLeuSerThrLeuVal 252
DB      849  CTGCGATTCCGCTCTGCTGCTGCTG 878

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DE      Human haemopoietin receptor protein NR10.3 encoding cDNA SEQ ID NO:16.
XX      Human: haemopoietin receptor; NR10.1; NR10.2; NR10.3; NR10;
XX      immunoregulation; haematopoietic cell regulation; transmembrane;
XX      immune disorder; haematopoietic disorder; autoimmune disease; allergy;
XX      metal allergy; pollen allergy; ss.
XX      Homo sapiens.
XX      MO200075314-A1.
XX      14-DEC-2000.
XX      01-JUN-2000; 2000MO-JP003556.
XX      02-JUN-1999; 99JP-00155797.
XX      30-JUL-1999; 99JP-00217797.
XX      (CHUG-) CHUGAI RES INST MOLECULAR MEDICINE INC.
XX      Maeda M, Yaguchi N;
XX      WPI, 2001-061720/07.
XX      P-PSDB; AAB51244.
XX      Hematopoietin receptor protein NR10 for screening potential ligands for
XX      treatment of immune and hematopoietic disorders such as autoimmune
XX      diseases and allergies.
XX      Claim 1; Fig 13-14; 127pp; Japanese.
XX      The present sequence encodes a human haemopoietin receptor protein
XX      (NR10), specifically designated NR10.3. NR10 occurs as a transmembrane
XX      protein and a soluble protein. NR10 is a haemopoietin receptor molecule
XX      which participates in immunoregulation and haematopoietic cell regulation
XX      in vivo, and is useful in searching for haematopoietic factors capable of
XX      binding to the receptor. NR10 can be used for the identification of
XX      CC substances for the treatment and prevention of immune and haematopoietic
XX      disorders including autoimmune diseases and allergies such as metal and
XX      pollen allergy
XX      SQ      Sequence 2119 BP; 643 A; 459 C; 504 G; 513 T; 0 U; 0 Other;
Alignment Scores:
Pred. No.:      4.98e-134      Length:      2119
Score:          1292.00      Matches:      238
Percent Similarity: 100.00%      Conservative: 0
Best Local Similarity: 100.00%      Mismatches: 0
Query Match:    95.14%      Indels:      0
DB:            4      Gaps:      0
US-10-006-265-4 (1-252) x AAC92350 (1-2119)
QY      1      MetLysLeuSerProGlnProSerCysValAsnLeuGlyMetMetTrpThrTrpAlaLeu 20
DB      11  ATGAAGCTCTCTCCCCAGGCTTCATGCTGTTAACTGGGATGATGAGACCTGGGCACTG 70
QY      21      TrpMetLeuProSerLeuCysAlysPheSerLeuAlaLeuProAlaLysProGluAsn 40
DB      71  TGGATGCTCCCTCATCTGCAATTCAGCTCGGACGCTCTGCCAGCTTAAGCTTGGAAC 130
QY      41      IleSerCysValTyrTyrTyrArgLysAsnLeuThrCysThrTrpSerProGlyLysGlu 60
DB      131  ATTTCCTGCTCTACTACTACTAGAAAAATTTAACTGCACTTGAGATCCAGAAAAAGAA 190
QY      61      ThrSerTyrThrGlnTyrThrValLysArgThrTyrAlaPheGlyGluLysHisAspAsn 80
DB      191  ACCAGTTATACCCAGTACAGATTAAGAACTTACGCTTTTGAGAAAAAATGATTAAT 250
QY      81      CysThrThrAsnSerSerThrSerGluAsnArgAlaSerCysSerPhePheLeuProArg 100
DB      251  TGTAAACCAATATGTTCAAGTAGTGAATCGTGCTGCTCTTTTCTTCCAAAG 310

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CC	Zcytor17 has immunomodulatory, antiinflammatory, antiviral, cyostatic,
CC	anti rheumatic, antidiabetic and muscular activities. The zcytor17
CC	proteins are useful for treating and diagnosing lymphoid, immune,
CC	inflammatory, splenic, blood or bone disorders. Agonists or anti-
CC	zcytor17 antibodies are useful in stimulating cell-mediated immunity and
CC	for stimulating lymphocyte proliferation, such as in the treatment of
CC	infections involving immunosuppression, including certain viral
CC	infections. They are also useful for inducing cytotoxicity and for
CC	treating leukopenias. Antagonist of zcytor17 polypeptides are useful for
CC	treating autoimmune diseases (e.g. rheumatoid arthritis and multiple
CC	sclerosis), inflammatory diseases (e.g. Crohn's disease), cancer,
CC	pancreatitis, and inflammatory bowel disease. Zcytor17 was mapped to
CC	chromosome 5, specifically to the 5q11 chromosomal region. ABA93767 to
CC	ABA93843 and ABB05730 to ABB05745 represent sequences used in the
CC	exemplification of the present invention
XX	
SQ	Sequence 2295 BP; 659 A; 578 C; 565 G; 493 T; 0 U; 0 Other;
	Alignment Scores:
Pred. No.:	5.6e-134 Length: 2295
Score:	1292.00 Matches: 238
Percent Similarity:	100.00% Conservatave: 0
Best Local Similarity:	100.00% Mismatches: 0
Query Match:	95.14% Indels: 0
DB:	Gaps: 0
US-10-006-265-4 (1-252) x ABA93821 (1-2295)	
QY	1 MetLysLeuSerProGlnProSerCysValAsnLeuGlyMetMetTrpThrTPPALeu 20
Db	1 ATGAAGCTCTCTCCCCAGCGTTTCATGTGTAAACCTGGGAGTGTGGACCTGGCACTG 60
QY	21 TrpMetLeuProSerLeuCysAlpSphSerLeuAlaIleLeuProAlaLysProGluAsn 40
Db	61 TGGAGTGCTCCCTCACTCTGCNAAATTACGCTGGACGCTCTGCACCTAAGCCTGGAGAAC 120
QY	41 IleserCysValTyfTyfTyfZrArgLysAsnLeuthnCysThfTrpSerProGilyLysGlu 60
Db	121 ATTCTCTGTGTACTACTCATATGAAAAATTTAACCTGCACCTTGAGTCCAGAAAAGGA 180
QY	61 ThrSerTyfTrhgIntTyfThrVallysbArghTrYraIaphegilyGluLyshiSaapasn 80
Db	181 ACCAGATTATACCACAATAACAGATTAAAGAACCTTACGCTTTGGAGAAAAACATGATTAAT 240
QY	81 CysThrTrhAnserSerThrsertGluAsnAgJasercYsserPhepheLeuProArg 100
Db	241 TGTAACAACCAATAGTTCTTACAAGTAAATCGTGCTCGCTCTTTTCTTCCAAGA 300
QY	101 IleThrIleProASPAsmTyfThrllegilVslgluAlagLuAsnglYAspglyValile 120
Db	301 ATTAGCATGCCAGATTAATTATTCATTGAGTGGANAGCTGAAAATGSAAGATGCTGAATT 360
QY	121 LysSerHisMetThyTyfTrpArgLeugluAsnIllealalySthrgIuProProlysiile 140
Db	361 AAATCTCATATGACATACATCGAGATTAGGAACATATAGCAAACATCACACTTAAGATT 420
QY	141 PheaArgValLysProvalleuGllylleYsbargMetIlegInlegIutrpIlelyPro 160
Db	421 TTCCCTGTGAAAACCAAGTTTGGGCACTCAAAACCAATGATTCCAATTGAAAGGATTAAGCCT 480
QY	161 GlueuAlaProvalSerSerAspLeuLysTyfTrhrlleuArgPheArghThrValJaanser 180
Db	481 GAGTTGGGGCGCTGTTTCAITCTGATTTTAATAATACACCTTCGATTCCAGGACAGTCAACGT 540
QY	181 ThsSerTrpMetGluValAsnPhenAlalySaenArgLysAspLysAbanglInthTyraen 200
Db	541 ACCAGCTGGATGGAAAGTCAACTGCTTAAGAACCGTAAGGATTAATAAACCAACAGTCAAC 600
QY	201 LeuthrgilyLeuGlnProPheThrgIutyrrValillealeuArgCysAlavalleyglu 220
Db	601 CTCACGGGGCGCTGACGCTTTTACAGAAATATGTCAATAGCTCTCGATGTGCGGTCAAGAG 660
QY	221 SerLysPheTrpSerAspTrhSerGlnglLylsMetsgIymetThsgIungluGlu 238

Db 661 TCAGAGTCTGAGTGAAGTGAAGCAAGAAAGAAATGGAATGACTGAGGAAGAA 714
RESULT 6
ADD68179
ID ADD68179 standard; cDNA; 2295 BP.
XX
XX ADD68179;
XX
XX
XX 15-JAN-2004 (first entry)
XX
XX Human zcytor17-Fc4 fusion cDNA SEQ ID NO:38.
XX
XX se; gene; human; zcytor17; antiinflammatory; dermatological;
XX immunosuppressive; antimicrobial; vaccine; inflammatory disease;
XX inflammatory bowel disease; ulcerative colitis; Crohn's disease;
XX atopic dermatitis; eczema; psoriasis; endotoxaemia; septicemia;
XX toxic shock syndrome; infectious disease.
XX
XX Chimeric.
XX Homo sapiens.
XX
XX
XX Key Location/Qualifiers
XX CDS 1..2295
XX /tag= a
XX /product= "zcytor17-Fc4 fusion"
XX
XX MO2003060090-A2.
XX
XX 24-JUL-2003.
XX
XX 21-JAN-2003; 2003WO-US001984.
XX
XX 18-JAN-2002; 2002US-0350325P.
XX 25-APR-2002; 2002US-0375323P.
XX 19-DEC-2002; 2002US-0435315P.
XX
XX (ZYMO) ZYMOGENETICS INC.
XX
XX
XX Sprecher CA, Kuiper JL, Dasovich MM, Grant FU, Hammond AK,
XX Novak UE, Gross JA, Dillon SR;
XX
XX WPI; 2003-618179/58.
XX
XX P-PsDB; ADD68180.
XX
XX
XX New zcytor17 ligand polypeptides, useful for treating inflammatory
XX diseases, such as inflammatory bowel disease, ulcerative colitis, Crohn's
XX disease, atopic dermatitis, eczema, psoriasis, endotoxaemia, septicemia.
XX
XX Example 8; SEQ ID NO 38; 372pp; English.
XX
XX
XX The invention relates to a novel isolated zcytor17 ligand polypeptide. A
XX polypeptide of the invention has antiinflammatory, dermatological,
XX immunosuppressive, and antimicrobial activity, and may have a use in a
XX vaccine. The polypeptide is useful for treating inflammatory diseases,
XX such as inflammatory bowel disease, ulcerative colitis, Crohn's disease,
XX atopic dermatitis, eczema, psoriasis, endotoxaemia, septicemia, toxic
XX shock syndrome or infectious diseases. The present sequence is used in
XX the exemplification of the invention.
XX
XX
XX Sequence 2295 BP; 659 A; 578 C; 565 G; 493 T; 0 U; 0 Other;
XX
XX
XX Alignment Scores:
XX Pred. No.: 5.6e-134 Length: 2295
XX Score: 1292.00 Matches: 238
XX Percent Similarity: 100.00% Conservative: 0
XX Best Local Similarity: 100.00% Mismatches: 0
XX Query Match: 95.14% Indels: 0
XX DB: 10 Gaps: 0
XX
XX US-10-006-265-4 (1-252) x ADD68179 (1-2295)
XX
XX
XX 1 MetLysLeuSerProGlnProSerCysValAsnLeuGlyMetMetTrpThrTrpAlaLeu 20

Db 1 ATGAAGCTCTCTCCCGAGCTTCATGTGTTAACTCGGGGATGATGGACCTGGGCACACTG 60
QY 21 TrpMetLeuProSerLeuCysLysPheSerLeuAlaAlaLeuProAlaLysProGluAsn 40
Db 61 TGAATGCTCTTCACTGCAAAATTCAGCTGGGAGCTCTCCAGCTTAAGCTGTGAAC 120
QY 41 IleSerCysValTyrTyrTyrTyrArgLysAsnLeuThrCysThrTrpSerProGlyLysGlu 60
Db 121 ATTTCTGTGTCTACTACTATAGAAAAATTTAACTGTCACTTGGAGTCCAGAAAAAGAA 180
QY 61 ThrSerTyrThrGlnTyrThrValLysArgThrTyrAlaPheGlyGlyLysHisAspAsn 80
Db 181 ACCAGTTAAACCCAGATACACAGTTAAGAACTTACGCTTTGGAGAAAAACATGTAAT 240
QY 81 CysThrThrAsnSerSerThrSerGluAsnAsgAlaSerCysSerPhePheLeuProArg 100
Db 241 TGTACAAACCAATAGTTCTACAAAGTAAATCGTCTCGTCTTTTTCCTCCACAGA 300
QY 101 ILeThrIleProAspAsnTyrThrIleGluValGluAlaGluAsnGlyAspGlyValIle 120
Db 301 ATTAAGATCCAGATATATTATACATTGAGCTGGAAGCTGAAAATGGAGATGGTGAAT 360
QY 121 LysSerHisMetThrTyrTrpArgLeuGluAsnIleAlaLysThrGluProLysIle 140
Db 361 AATCTCATATGACATACTGAGATTAGAAACATAGCAAAACTGAACCATTAAGATT 420
QY 141 PheArgValLysProValLeuGlyIleLysArgMetIleGlnIleGluTrpIleLysPro 160
Db 421 TTCCGGTGAACCAAGTTTGGGCATCAAAACAAATGATTCAATATGAAATGAAGTAAAGCCT 480
QY 161 GluLeuAlaProValSerSerAspLeuLysTyrThrLeuArgPheAspThrValAsnSer 180
Db 481 GAGTTGGCGCCGTTCATCTGATTTAAATACACACTTCGATTCAAGACAGTCAACACT 540
QY 181 ThrSerTrpMetGluValAsnPheAlaLysAsnArgLysAspLysAsnGlnThrTyrAsn 200
Db 541 ACCAGCTGATGAAGTCAACTTCCTTAAGAACCCGTAAAGATAAAACCAACGTAACAAC 600
QY 201 LeuThrGlyLeuGlnProPheThrGluTyrValIleAlaLeuAspCysAlaValLysGlu 220
Db 601 CTCACGGGGCTCAGCTTTTACAGAAATGTGCATAGCTCTCGCATGTGGGTCAAGAG 660
QY 221 SerLysPheTrpSerAspTrpSerGlnGlyLysMetGlyMetThrGluGluGlu 238
Db 661 TCAGAGTCTGAGTGAAGTGAAGCAAGAAAGAAATGGAATGACTGAGGAAGAA 714
RESULT 7
ADL26602
ID ADL26602 standard; DNA; 2295 BP.
XX
XX
XX ADL26602;
XX
XX 20-MAY-2004 (first entry)
XX
XX Human zcytor17-Fc4 fusion protein DNA.
XX
XX
XX antiinflammatory; antiulcer; dermatological; antiallergic; antipsoriatic;
XX antibacterial; immunosuppressive; cell proliferation inhibitor;
XX immune response inhibitor; inflammatory response inhibitor;
XX multimeric cytokine receptor; heterodimeric cytokine receptor; cancer;
XX cytokine-binding domain; class I cytokine receptor; hematopoietic cell;
XX zcytor17lig-induced proliferation; zcytor17lig-induced differentiation;
XX hematopoietic progenitor cell; zcytor17lig-induced inflammation;
XX inflammatory disease; inflammatory bowel disease; ulcerative colitis;
XX Crohn's disease; atopic dermatitis; eczema; psoriasis; endotoxaemia;
XX septicemia; toxic shock syndrome; zcytor17lig; zcytor17; Fc4;
XX fusion protein; gene; ds.
XX
XX Homo sapiens.
XX Synthetic.
XX
XX US2003215838-A1.

XX 20-NOV-2003.
 PD 21-JAN-2003; 2003US-00351157.
 XX 18-JAN-2002; 2002US-0350325P.
 XX 14-JUN-2002; 2002US-0389108P.
 PR 19-DEC-2002; 2002US-0435361P.
 XX (SPRE/) SPRECHER C A.
 PA (GROZ/) GRO Z.
 PA (KUIJ/) KUIJPER J L.
 PA (DASO/) DASOVICH M M.
 PA (GRAN/) GRANT F J.
 PA (PRES/) PRESNEL S R.
 PA (WHIT/) WHITMORE T E.
 PA (HAMM/) HAMMOND A K.
 PA (NOVA/) NOVAK J E.
 PA (GROS/) GROSS J A.
 PA (DILL/) DILLON S R.
 XX Sprecher CA, Gao Z, Kuijper JL, Dasovich MM, Grant FJ,
 PI Presnell SR, Whitmore TE, Hammond AK, Novak JE, Gross JA, Dillon SR;
 DR WPI; 2003-876545/81.
 XX P-PSDB; ADL26603.
 DR Novel multimeric or heterodimeric cytokine receptors useful for treating
 PT chronic inflammatory disease such as inflammatory bowel disease,
 PT ulcerative colitis, acute inflammatory disease such as endotoxaemia,
 PT septicemia.
 PT
 PS Example 8; SEQ ID NO 38; 205pp; English.
 XX
 CC The invention describes an isolated multimeric or heterodimeric cytokine
 CC receptor (I) having at least one polypeptide having 90 percent sequence
 CC identity with a 732 (S1) or 649 (S2) amino acid sequence given in
 CC specification, and where (I) binds a ligand comprising a 164 (S3) amino
 CC acid sequence, given in specification, or at least one polypeptide
 CC comprising residue 20-227 of (S1). (I) is useful for killing cancer cells
 CC and producing an antibody to (I) and a cytokine-binding domain of a class
 CC I cytokine receptor. A composition (C1) comprising (I) and a cytokine-
 CC binding domain of a class I cytokine receptor and a vehicle is useful
 CC for: reducing hematopoietic cells and hematopoietic progenitor cells in
 CC a mammal; inhibiting zcytor17lig-induced proliferation or differentiation
 CC of hematopoietic cells and hematopoietic progenitor cells; reducing
 CC zcytor17lig-induced inflammation; treating a mammal afflicted with an
 CC inflammatory disease in which zcytor17lig plays a role. The disease is a
 CC chronic inflammatory disease such as inflammatory bowel disease,
 CC ulcerative colitis, Crohn's disease, atopic dermatitis, eczema and
 CC psoriasis. The disease is acute inflammatory disease such as
 CC endotoxaemia, septicemia, toxic shock syndrome and infectious disease.
 CC An immune response inhibiting composition is useful for inhibiting an
 CC immune response in a mammal exposed to an antigen or pathogen. An
 CC inflammatory response inhibiting composition is useful for suppressing an
 CC inflammatory response in a mammal with inflammation. An antibody that
 CC specifically binds to (I) is useful for detecting the presence of a
 CC multimeric or heterodimeric cytokine receptor in a biological sample.
 CC This sequence encodes a soluble human zcytor17-human Fc4 (not defined)
 CC fusion protein.
 CC
 XX
 SO Sequence 2295 BP; 659 A; 578 C; 565 G; 493 T; 0 U; 0 Other;
 Alignment Scores:
 Pred. No.: 5.6e-134 Length: 2295
 Score: 1293.00 Matches: 238
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 95.14% Indels: 0
 DB: 11 Gaps: 0

QY 1 MetLysLeuSerProGlnProSerCyValAsnLeuGlyMetMetTrpThrTrpAlaLeu 20
 DB 1 ATGAAGCTCTCTCCCAACCTTCACTGCTGGGGATGATGATGACCTGGGACACTG 60
 QY 21 TrpMetLeuProSerLeuCyValPheSerLeuAlaAlaLeuProAlaLysProGluAsn 40
 DB 61 TGGATGCTCCCTTCACTCTGCAAAATTCAGCTGGAGACTGCGCAAGCTTGAAGAC 120
 QY 41 IleSerCyValTrpTrpTrpArgLysAsnLeuThrTrpTrpSerProGlyValGlu 60
 DB 121 ATTCTGTGTCTACTACTATAGAAAATTTAACTGCACTTGGAGTGGAGAAAGAA 180
 QY 61 ThSerTrpTrpGlnTrpValLysArgTrpThrTrpAlaPheGlyGluLysPheAspAsn 80
 DB 181 ACCAGTTTACCAGTACACAGTTAGAGAACTTACGTTTGGAGAAAACATGATAT 240
 QY 81 CysTrpThrAsnSerSerThrSerGluAsnArgLysSerCySerPhePheLeuProArg 100
 DB 241 TGTACAAACAAATAGTTCACAAAGTGAATAATCGTCTGCTCTTTTTCCTTCAAGA 300
 QY 101 IleThrIleProAspAsnTrpThrIleGluValGluAlaGluAsnGlyValIle 120
 DB 301 ATAACGATCCAGATTAATTAATACATTCAGGTGAGAGCTGAATAATGAGATGTAAT 360
 QY 121 LysSerHisMetTrpTrpArgLeuGluAsnIleAlaLysTrpGluProProLysIle 140
 DB 361 AATCTCATATGACATCTGAGATTTAGAAACATAGCAAACTGAACCATTAAGATT 420
 QY 141 PheArgValLysProValLeuGlyIleLysArgMetIleGlnIleGluTrpIleLysPro 160
 DB 421 TTCGCTGGAACCAAGTTTGGCATCAACGAATGATTAATGAATGATTAAGCT 480
 QY 161 GluLeuAlaProValSerSerAspLeuLysTrpThrLeuArgPheArgThrValAsnSer 180
 DB 481 GAGTTGGGCGCTGTTTATCATCTGATTAATAACACACTTCATTCAGACAGTCAACGCT 540
 QY 181 ThSerTrpMetGluValAsnPheAlaLysAsnArgLysAspLysAsnGlnThrTrpAsn 200
 DB 541 ACCAGCTGATGAGATGACATCTGCTAGAACCTGTAAGATTAACCAACCACTACAC 600
 QY 201 LeuThrGlyLeuGlnProPheThrGluTrpValIleAlaLeuArgCyValaValIleGlu 220
 DB 601 CTCACGGGGGCGCAGCCCTTTTACAGAAATATGTCATACCTGCGCATGCGGCTCAAGAG 660
 QY 221 SerLysPheTrpSerAspTrpSerGlnGluLysMetGlyMetThrGluGlu 238
 DB 661 TCAAAGTTCTGAGTGACTGAGCCAGCAAAATAATGGAAATGACTGAGAAAGAA 714
 RESULT 8
 AAD38772
 ID AAD38772 standard; cDNA; 2480 BP.
 XX
 AC AAD38772;
 XX
 DT 23-SEP-2002 (first entry)
 XX
 DE Human haematopoietin receptor 1 (HPR1) cDNA.
 XX
 KW Human; haematopoietin receptor; receptor; HPR1; HPR2; cell proliferation;
 KW pancytopenia; leukopenia; anaemia; thrombocytopaenia; osteoporosis;
 KW neurodegenerative disorder; leukaemia; carcinoma; haematologic disorder;
 KW cancer; myelodysplastic syndrome; idiopathic thrombocytopenic purpura;
 KW ITP; sickle cell vasocclusive crisis; myelofibrosis; myeloid metaplasia;
 KW osteoclast disorder; periodontitis; acute polyneuropathy; Bell's palsy;
 KW anorexia nervosa; chronic fatigue syndrome; Creutzfeldt-Jacob disease;
 KW demyelinating neuropathy; Guillain-Barre syndrome; Gulf war syndrome;
 KW vertebral disc disease; myasthenia gravis; chronic neuronal degeneration;
 KW stroke; fatigue; tumour; sarcoma; osteoporosis; obesity; infertility;
 KW ischaemic disease; gene; ss.
 KW
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers

ID ABA93808 standard; cDNA: 2903 BP.
 XX ABA93808;
 AC
 XX
 DT 01-MAY-2002 (first entry)
 XX
 DE Human zcytor17 cDNA sequence SEQ ID NO:53.
 XX
 KM Zcytor17; chromosome 5; 5q11; cytokine receptor; immunomodulatory;
 KM antiinflammatory; antiviral; antirheumatic; antiarthritic; cytostatic;
 KM muscular; lymphoid; immune; inflammatory; splenic; blood; bone;
 KM infection; immunosuppression; cytotoxicity; leukopenia; Crohn's disease;
 KM autoimmune disease; rheumatoid arthritis; multiple sclerosis; cancer;
 KM inflammatory disease; pancreatitis; inflammatory bowel disease; ss.
 XX
 OS Homo sapiens.
 XX
 PN MO20020721-A2.
 XX
 PD 03-JAN-2002.
 XX
 PF 26-JUN-2001; 2001WO-US020484.
 XX
 PR 26-JUN-2000; 2000US-0214282P.
 PR 29-JUN-2000; 2000US-0214955P.
 PR 08-FEB-2001; 2001US-0257963P.
 XX
 PA (ZYMO) ZYMOGENETICS INC.
 XX
 PI Sprecher CA, Presnell SR, Gao Z, Whitmore TE, Kuijper JL,
 PI Meurer MF,
 PI
 XX WPI; 2002-090519/12.
 DR P-PSDB; ABB05741.
 XX
 PT Isolated polynucleotide encoding a cytokine receptor zcytor17 which is
 PT useful for treating and diagnosing lymphoid, immune, inflammatory,
 PT splenic, blood or bone disorders.
 PT
 PS Example 1; Page 199-203; 235pp; English.
 XX
 CC The present invention describes a cytokine receptor designated zcytor17.
 CC zcytor17 has immunomodulatory, antiinflammatory, antiviral, cyrostatic,
 CC antineumatic, antiarthritic and muscular activities. The zcytor17
 CC proteins are useful for treating and diagnosing lymphoid, immune,
 CC inflammatory, splenic, blood or bone disorders. Agonists or anti-
 CC zcytor17 antibodies are useful in stimulating cell-mediated immunity and
 CC for stimulating lymphocyte proliferation, such as in the treatment of
 CC infections involving immunosuppression, including certain viral
 CC infections. They are also useful for inducing cytotoxicity and for
 CC treating leukopenias. Antagonist of zcytor17 polypeptides are useful for
 CC treating autoimmune diseases (e.g. rheumatoid arthritis and multiple
 CC sclerosis), inflammatory diseases (e.g. Crohn's disease), cancer,
 CC pancreatitis, and inflammatory bowel disease. Zcytor17 was mapped to
 CC chromosome 5, specifically to the 5q11 chromosomal region. ABA93767 to
 CC ABA93843 and ABB05730 to ABB05745 represent sequences used in the
 CC exemplification of the present invention
 XX
 SQ Sequence 2903 BP; 862 A; 620 C; 664 G; 757 T; 0 U; 0 Other;
 XX
 Alignment Scores:
 Pred. No.: 7.91e-134 Length: 2903
 Score: 1292.00 Matches: 238
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 95.14% Indels: 0
 DB: 6 Gaps: 0
 US-10-006-265-4 (1-252) x ABA93808 (1-2903)
 QY 1 MetlyeuserProginProSerCyvaValaenleuglyMeMcetTTPThrTPAlaIeu 20
 DB 497 ATGAAGCTCTCTCCCGACCTTCACTGTGTTAACTGGGGAATGATGTGGAAGCTGCGCACTG 556

QY 21 TrpMetIeuProSerIeuCyelVePheSerIeuAlaIaIeuProAlaIeProGluasn 40
 DB 557 TGGATGCTCCCTTACTCTGAAATTCAGCCCTGGACCTGCGACCTGAACCTGAGAAC 616
 QY 41 IleSerCyvaValTYrTYrTYrArgIyaAsnIeuThrCySThrTPSerProGlyLysGlu 60
 DB 617 ATTTCTGTGTCTACTACTATAGAAAAATTTAACTGCACTTGAGCTGCAAGCAAGAA 676
 QY 61 ThrseryThrgInlyrThrValIyayrGthrTYrAlaPheGlyGluVshIaAspAsn 80
 DB 677 ACCAGTATATCCCGACGATACAGATTAAAGAACTTACCTTTGGAGAAAAACATGATAT 736
 QY 81 CyethrThrAsnSerSerThrseryGluAsnArgIaSerCysserPhePheIeuProArg 100
 DB 737 TGTACCAACCAATATCTTACAAAGTGAATCGCTCTGTCTCTTTTCTTCCCAAGA 796
 QY 101 IleThrIleProAspAntTYrThrIleGluValGluIaIuAengIyaSPGlyValIle 120
 DB 797 ATACGATCCCAATATTAATTAATTCATTGAGGTGGAAGCTGAAAAATGAGATGTAT 856
 QY 121 LysSerHisMetThrTYrTPArgIeuGluAsnIleAlaIySThrGluProProLysIle 140
 DB 857 AAATCTCATATGACATACGAGATTAGAGAACATACGAAACTGAACCACTTAAGATT 916
 QY 141 PheArgValIySProValIleuglyIleIyayrGmetIleGnIleGluTPPleIyPro 160
 DB 917 TTCGGTGTGAACCAAGTTTTGGGCATCAACGAATGATTCAAATGATGATTAAGCT 976
 QY 161 GluIeuAlaProValISerSerAspLeuIySTyrThrIeuArgPheArgThrValAsnSer 180
 DB 977 GAGTTGGCGCTGTATTATCTGATTTAAATACACACTTCGATTCAAGACGTAAACGT 1036
 QY 181 ThrseryThrMetGluValaenPheAlaIyAsnArgIyaSPlyAsnGlnThrTyAsn 200
 DB 1037 ACCAGCTGATGAAAGTCACTTCGTAAAGAACCGTAAGATTAACCAACCACTAAC 1096
 QY 201 LeuThrgIyLeuGlnProPheThrgIuTYrValIleAlaIeuArgCyvaIaValIyGlu 220
 DB 1097 CTCACGGGGCTGCGCTTTTACGAATATGTCTATACCTCTGCGATGTGCGTAAAGAG 1156
 QY 221 SerlySPheTPSerAspTPSerGlnIyIyMetGlyMetThrgIuGlu 238
 DB 1157 TCMAAGTTCTGAGTGTGACTGAGCCAGCAAAAAATGGGAATGACTGAGAA 1210
 RESULT 10
 ID ADD68146 standard; cDNA: 2903 BP.
 AC ADD68146;
 XX
 DT 15-JAN-2004 (first entry)
 XX
 DE Human zcytor17 cDNA SEQ ID NO:4.
 XX
 KM ss; gene; human; zcytor17; antiinflammatory; dermatological;
 KM immunosuppressive; antimicrobial; vaccine; inflammatory disease;
 KM inflammatory bowel disease; ulcerative colitis; Crohn's disease;
 KM atopic dermatitis; eczema; psoriasis; endotoxaemia; septicemia;
 KM toxic shock syndrome; infectious disease.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT CDS 497..2485
 FT /*tag= a
 FT /product= "zcytor17"
 XX
 FN WO2003060090-A2.
 XX
 PD 24-JUL-2003.
 XX
 PF 21-JAN-2003; 2003WO-US001984.

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XX 18-JAN-2002; 2002US-0350325P.
PR 25-APR-2002; 2002US-0375323P.
PR 19-DEC-2002; 2002US-0435315P.
XX (ZYMO) ZYMOGENETICS INC.
XX
XX Sprecher CA, Kuiper JL, Dasovich MM, Grant FJ, Hammond AK;
PI Novak JE, Gross JA, Dillon SR;
XX
XX MPI: 2003-618179/58.
DR P-PSDB; ADL68147.
XX
XX New zcytor17 ligand polypeptides, useful for treating inflammatory
PT diseases, such as inflammatory bowel disease, ulcerative colitis, Crohn's
PT disease, atopic dermatitis, eczema, psoriasis, endotoxaemia, septicemia.
XX
XX Example 3; SEQ ID NO 4; 372pp; English.
XX
XX The invention relates to a novel isolated zcytor17 ligand polypeptide. A
CC polypeptide of the invention has antiinflammatory, dermatological,
CC immunosuppressive, and antimicrobial activity, and may have a use in a
CC vaccine. The polypeptide is useful for treating inflammatory diseases,
CC such as inflammatory bowel disease, ulcerative colitis, Crohn's disease,
CC atopic dermatitis, eczema, psoriasis, endotoxaemia, septicemia, toxic
CC shock syndrome or infectious diseases. The present sequence is used in
CC the exemplification of the invention.
XX
XX Sequence 2903 BP; 862 A; 620 C; 664 G; 757 T; 0 U; 0 Other;
SQ
XX
XX Alignment Scores:
Pred. No.: 7.91e-134 Length: 2903
Score: 1292.00 Matches: 238
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 95.14% Indels: 0
DB: Gaps: 0
XX
US-10-006-265-4 (1-252) x ADL68146 (1-2903)
XX
QY 1 MetLysLeuSerProGlnProSerCysValAsnLeuGlyMetThrPthTAlaLeu 20
DB 497 ATGAACTCTCTCCAGCCTTCATGTGTTAACCTGGGATGATGAGACCTTGACCTG 556
QY 21 TrpMetLeuProSerLeuGlyPheSerLeuAlaLeuProAlaLysProGlyAsn 40
DB 557 TGGATCTCCTTCACTTGCAGAAATTCAGCCTGGAGCTTGCAGCTTAAGCTTGAAAC 616
QY 41 LeuSerCysValTyrTyrTyrArgLysAsnLeuThrCysThrTrpSerProGlyLysGlu 60
DB 617 ATTCTCTGTGTACTACTATAGAAAATTAACTGCACTTGAGATCCAGAAAAGAA 676
QY 61 ThrSerTyrThrGlnTyrThrValLysArgThrTyrAlaPheGlyGlyLysHisAspAsn 80
DB 677 ACCAGTTAAACCCAGACACAGTTAAGAGAACTTACGCTTTGAGAAAACATGATTAAT 736
QY 81 CysThrThrAsnSerSerThrSerGluAsnArgAlaSerCysSerPhePheLeuProArg 100
DB 737 TGTACAACCAATAGTCTACAAAGTGAATCGTCTCTCTCTTTTCTTCCACAAGA 796
QY 101 IleThrIleProAspAsnTyrThrIleGluValGluAlaGluAsnGlyAspGlyValIle 120
DB 797 ATAAACATCCCAATATTAATTAACATTTGAGGTGGAAGCTGAATAAGAGATGATTAAT 856
QY 121 LysSerHisMetThrTyrTrpArgLeuGluAsnIleAlaLysThrGluProPheLysIle 140
DB 857 AAATCTCATATGACATACGAGATTAAGAACATACGCGAAACCTGAACCTTAAGATT 916
QY 141 PheArgValLysProValLeuGlyIleLysArgMetIleGlnIleGluTrpIleLysPro 160
DB 917 TTCGGTGTGAACCAAGTTTGGGATCAACAGATGATTAATTAATGATGATTAAGCCCT 976
QY 161 GluLeuAlaProValSerSerAspLeuLysTyrThrLeuArgPheArgThrValAsnSer 180

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DB 977 GAGTTGGCGCGCTGTTCAATCTGATTTAAATACACACTTCGATTCAGGACACTCAACACT 1036
QY 181 ThrSerTrpMetGluValAsnPheAlaLysAsnArgLysAspLysAsnGlnThrTyrAsn 200
DB 1037 ACCAGCTGATGAAAGTCACTTCGCTAAGAACCTGAAGATTAACCAACGTCACAC 1096
QY 201 LeuThrGlyLeuGlnProPheThrGluTyrValIleAlaLeuArgCysAlaValLysGlu 220
DB 1097 CTCACGGGGCTGACGCTTTTACAGAAATATGTCATAGCTCTGCGATGTGCGGTCAAGAG 1156
QY 221 SerLysPheThrPheSerTrpSerGlnGlyLysMetGlyMetThrGluGluGlu 238
DB 1157 TCAAAAGTTCTGAGTCACTGAGCCAGAAAATAAGGAAATGACTGAGAGAGAA 1210
XX
XX RESULT 11
ADL26569
ID ADL26569 standard; cDNA; 2903 BP.
XX
XX AC ADL26569;
XX
XX 20-MAY-2004 (first entry)
XX
XX Human cytokine receptor zcytor17 DNA seqid 4.
DE
XX
XX antiinflammatory; antiulcer; dermatological; antiallergic; antipsoriatic;
XX antibacterial; immunosuppressive; cell proliferation inhibitor;
XX immune response inhibitor; inflammatory response inhibitor;
XX multimeric cytokine receptor; heterodimeric cytokine receptor; cancer;
XX cytokine-binding domain; class I cytokine receptor; hematopoietic cell;
XX zcytor171g-induced proliferation; zcytor171g-induced differentiation;
XX hematopoietic progenitor cell; zcytor171g-induced inflammation;
XX inflammatory disease; inflammatory bowel disease; ulcerative colitis;
XX Crohn's disease; atopic dermatitis; eczema; psoriasis; endotoxaemia;
XX septicemia; toxic shock syndrome; zcytor17; human; gene; ss.
XX
XX Homo sapiens.
XX
XX US2003215838-A1.
XX
XX 20-NOV-2003.
XX
XX 21-JAN-2003; 2003US-00351157.
XX
XX 18-JAN-2002; 2002US-0350325P.
PR 14-JUN-2002; 2002US-0389108P.
PR 19-DEC-2002; 2002US-0435361P.
XX
XX (SPRE/) SPEECHER C A.
PA (GAOZ/) GAO Z.
PA (KUJ/) KUIJPER J L.
PA (DASO/) DASOVICH M M.
PA (GRAN/) GRANT F J.
PA (PRES/) PRESNELL S R.
PA (WHIT/) WHITMORE T E.
PA (HAMM/) HAMMOND A K.
PA (NOVA/) NOVAK J E.
PA (GROS/) GROSS J A.
PA (DILL/) DILLON S R.
XX
XX Sprecher CA, Gao Z, Kuiper JL, Dasovich MM, Grant FJ;
PI Presnell SR, Whitmore TE, Hammond AK, Novak JE, Gross JA, Dillon SR;
XX
XX MPI: 2003-876545/81.
DR P-PSDB; ADL26570.
XX
XX Novel multimeric or heterodimeric cytokine receptors useful for treating
PT chronic inflammatory disease such as inflammatory bowel disease,
PT ulcerative colitis, acute inflammatory disease such as endotoxaemia,
PT septicemia.
XX
XX Example 3; SEQ ID NO 4; 205pp; English.
XX

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Alignment Scores:	
Pred. No.:	7, 91e-134
Score:	1292.00
Percent Similarity:	100.00%
Best Local Similarity:	100.00%
Query Match:	95.14%
OB:	11
Length:	2903
Matches:	238
Conservative:	0
Mismatches:	0
Indels:	0
Gaps:	0

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DB: 11 Gaps: 0
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Db 497 ATGAGCTCTCTCCCAAGCCTTCATGTGTTAACCTGGGATGATGTGGACCTGGCACTG 55

Db 557 TGGATGCTCCCTTCACTCTGCAATTCAAGCCTGAGAC 61

DB 61 / ATTCCGTCGTCACCTAAGGAAAATTACCTGCACCTTGGAGTCCAGGAAGGA 6 /

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2018-2019

121 LVSSerHisMetThrTyrTPArqlLeuGluAsnIleAlaIysThrgIupProProIyVile 14

Qy 141 pheargvallysprovalleuglyllyllybargmettleglntprlyllyspro 16

161 G L E U A I a P r o V a l S e r S e r A s p l e u l y s t y r T h r l e u a r g p h e a r g T h r V a l a s n S e r 188

Db 977 GAGTTGGCCCTGTTTCATCTGATTTAAATACACACTTCGATTCAGGACAGTCAACAGT 1000

AC	AAC92337;
XX	
DT	26-MAR-2001 (first entry)
XX	
DE	Human haemopoietin receptor protein NR10.1 encoding cDNA SEQ ID NO:1.
XX	
KM	Human; haemopoietin receptor; NR10.1; NR10.2; NR10.3; NR10;
KM	immunoregulation; haematopoietic cell regulation; transmembrane;
KM	immune disorder; haematopoietic disorder; autoimmune disease; allergy;
KW	metal allergy; pollen allergy; ss.

OS Homo sapiens.

PN WO200075314-A1.

PD 14-DEC-2000.

PF 01-JUN-2000; 2000WO-JP003556.

PR 02-JUN-1999; 99JP-00155797.

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(GIVE) TWO FOUR AND SEVENTEEN TWO

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DR P-PSDB; AAB51242.
.....

PT Hematopoietin receptor protein NR10 for screening potential ligands for

PT diseases and allergies.

PS Claim 1; Fig 3-5; 127pp; Japanese.

CC The present sequence encodes a human haemopoietin receptor protein

CC protein and a soluble protein. NR10 is a haemopoietin receptor molecule

CC in vivo, and is useful in searching for haematopoietic factors capable of binding to the receptor m10 for the identification of

CC substances for the treatment and prevention of immune and haematopoietic disorders including autoimmune diseases and allergies such as eczema and

CC pollen allergy

Sequence 2969 BP; 939 A; 618 C; 662 G; 750 T; 0 U; 0 Other;

Alignment Scores:

Prod No.	Length	Score
9 170-134	10000	3069

Score:	1292.00	Matches:	238
Percent of max:	100.00%	Combinations:	0

Best Local Similarity:	100.00%	Mismatches:	0
Overall Match:	95.14%	Indels:	0

DB: 4
Gaps: 0

US-10-006-265-4 (1-252) x AAC92337 (1-2969)

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QY      1 MetLysLeuSerProGlnProSerCysValAsnLeuGlyMetMetTrpThrTrpAlaLeu 20
Db      523 ATGAAGCTCTCTCCAGGCTTCATGTTAACTGGGATGATGGACCTGGGACACTG 582
QY      21 TrpMetLeuProSerLeuCysLysPheSerLeuAlaAlaLeuProAlaLysProGluAsn 40
Db      583 TGGATGCTCCCTCACTCGCAAAATTCAGCCTGGAGCTCTGGCACCTGAAGCCTGGAAC 642
QY      41 HisSerCysValTyrTyrTyrArgLysAsnLeuThrCysThrTrpSerProGlyLysGlu 60
Db      643 ATTTCTGTGTCTACTACTATAGAAAAATTTAACTGCACTTGGAGTCCAGAAAGGAA 702
QY      61 ThrSerTyrThrGlnTyrThrValLysArgThrTyrAlaPheGlyGluLysHisAspAsn 80
Db      703 ACCAGTTAAACCCAGTACACAGTTAAGAACTTAACCTTTGGAGAAAAACATGATTAAT 762
QY      81 CysThrThrAsnSerSerThrSerGluAsnArgAlaSerCysSerPhePheLeuProArg 100
Db      763 TGTACAAACCAATAGTTCTCAAGTGAATAATCGTCTCTTTTCCCTCCAGAA 822
QY      101 IleThrIleProAspAsnTyrThrIleGluValGluAlaGluAsnGlyAspGlyValIle 120
Db      823 ATTAACGATCCCGATATATATACATTGAGGTGAAGCTGAATAATGAAATGGTGTAAAT 882
QY      121 LysSerHisMetThrTyrTrpArgLeuGluAsnIleAlaLysThrGluProProlLysIle 140
Db      883 AATATCATATGACATCACTGGAGATTAGAAACATAGCCAAAACTGAACCACTAAGATT 942
QY      141 PheArgValLysProValLeuGlyIleLysArgMetIleGlnIleGluTrpIleLysPro 160
Db      943 TTCCCGTGAAACCAAGTTTGGGCATCAACGATGATTTCAATTAATGATGAATGAAGCCT 1002
QY      161 GluLeuAlaProValSerSerAspLeuLysTyrThrLeuArgPheArgThrValAsnSer 180
Db      1003 GAGTTGGCCCTGTTTCATCTGATTTAAATACACTTCGATTCAGGACAGCAACAGT 1062
QY      181 ThrSerTrpMetGluValAsnPheAlaLysAsnArgLysAspLysAsnGlnThrTyrAsn 200
Db      1063 ACCAGCTGATGGAAGTCAACTTCGCTAAGAACCGTAAGATTAACCAACAGTCAAC 1122
QY      201 LeuThrGlyLeuGlnProPheThrGluTyrValIleAlaLeuArgCysAlaValLysGlu 220
Db      1123 CTCACGGGGCTCGACGCTTTTACAGAAATATGTCATGCTCGAGATGTCGGGTCAAGAG 1182
QY      221 SerLysPheThrSerAspTrpSerGlnLysLysMetGlyMetThrGlnGluGlu 238
Db      1183 TCAAAAGTTCTGAGAGTGAAGCCAAAGAAAAATGGGAATGACTGAGAGAAAGA 1236

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RESULT 13
ABA93781
ID      ABA93781 standard; cDNA; 1299 BP.
XX      ABA93781;
AC      ABA93781;
XX      01-MAY-2002 (first entry)
DT      Zcytor17 soluble form truncated in the fibronectin domain cDNA SEQ.17.
XX      DE
XX      Zcytor17, chromosome 5; 5q11; cytokine receptor; immunomodulatory;
XX      antiinflammatory; antiviral; antirheumatic; antiarthritic; cystostatic;
XX      muscular; lymphoid; immune; inflammatory; splenic; blood; bone;
XX      infection; immunosuppression; cytotoxicity; leukopenia; Crohn's disease;
XX      autoimmune disease; rheumatoid arthritis; multiple sclerosis; cancer;
XX      inflammatory disease; pancreatitis; inflammatory bowel disease; ss.
XX      Homo sapiens.
XX      OS
XX      MO200200721-A2.
XX      PN
XX      03-JAN-2002.
XX      PD
XX      26-JUN-2001; 2001WO-US020484.
XX      PF

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XX      26-JUN-2000; 2000US-0214282P.
PR      29-JUN-2000; 2000US-0214955P.
PR      08-FEB-2001; 2001US-0267963P.
XX      (ZYMO ) ZYMOGENETICS INC.
PA      Sprecher CA, Presnell SR, Gao Z, Whitmore TE, Kujper JL;
PI      Maurer MF;
XX      MPI; 2002-090519/12.
XX      P-PSDB; ABB05732.
XX      DR
XX      Isolated polynucleotide encoding a cytokine receptor zcytor17 which is
XX      useful for treating and diagnosing lymphoid, immune, inflammatory,
XX      splenic, blood or bone disorders.
XX      Example 2, Page 174-176; 235pp; English.
XX      The present invention describes a cytokine receptor designated zcytor17.
XX      Zcytor17 has immunomodulatory, antiinflammatory, antiviral, cystostatic,
XX      antirheumatic, antarthritic and muscular activities. The zcytor17
XX      proteins are useful for treating and diagnosing lymphoid, immune,
XX      inflammatory, splenic, blood or bone disorders. Agonists or anti-
XX      zcytor17 antibodies are useful in stimulating cell-mediated immunity and
XX      for stimulating lymphocyte proliferation, such as in the treatment of
XX      infections involving immunosuppression, including certain viral
XX      infections. They are also useful for inducing cytotoxicity and for
XX      treating leukopenias. Antagonist of zcytor17 polypeptides are useful for
XX      treating autoimmune diseases (e.g. rheumatoid arthritis and multiple
XX      sclerosis), inflammatory diseases (e.g. Crohn's disease), cancer,
XX      pancreatitis, and inflammatory bowel disease. Zcytor17 was mapped to
XX      chromosome 5, specifically to the 5q11 chromosomal region. ABA93767 to
XX      ABA93843 and ABB05730 to ABB05745 represent sequences used in the
XX      exemplification of the present invention.
XX      Sequence 1299 BP; 402 A; 276 C; 306 G; 315 T; 0 U; 0 Other;
SQ
XX
XX      Alignment Scores:
XX      Pred. No.: 3,2e-133 Length: 1299
XX      Score: 1282.00 Matches: 226
XX      Percent Similarity: 100.00% Conservative: 0
XX      Best Local Similarity: 100.00% Mismatches: 0
XX      Query Match: 94.40% Indels: 0
XX      DB: 6 Gaps: 0
XX      US-10-006-265-4 (1-252) x ABA93781 (1-1299)
QY      3 LeuSerProGlnProSerCysValAsnLeuGlyMetMetTrpThrTrpAlaLeuTrpMet 22
Db      129 CTCTCTCCAGGCTTCATGTTAACTGGGATGATGGACCTGGGCACTGGGATG 188
QY      23 LeuProSerLeuCysLysPheSerLeuAlaAlaLeuProAlaLysProGluAsnIleSer 42
Db      189 CTCCTCTCACTCGCAAAATTCAGCCTGGACGCTGCCAGCTAAACCTGAAGAACTTCC 248
QY      43 CysValTyrTyrTyrArgLysAsnLeuThrCysThrTrpSerProGlyLysGluThrSer 62
Db      249 TGTGTCTACTACTATAGAAAAATTTAACTGACCTGAGTCCAGAAAGAAACCACT 308
QY      63 TyrThrGlnTyrThrValLysArgThrTyrAlaPheGlyGluLysHisAspAsnCysThr 82
Db      309 TATACCAAGTACACAGTTAAGAACTTAACGCTTTTGGAGAAAAACATGATTAATGTACA 368
QY      83 ThrAsnSerSerThrSerGluAsnArgAlaSerCysSerPhePheLeuProArgIleThr 102
Db      369 ACCAAATAGTTCTTACCAAGTGAATAATCGTGTCTCTCTTTTCCCTCCAGAAATACG 428
QY      103 IleProAspAsnTyrThrIleGluValGluAlaGluAsnGlyAspGlyValIleLysSer 122
Db      429 ATCCCAATATTAATCACTTGAAGGTGAAGCTGAATAATGAGATGGTGTAAATTAATCT 488
QY      123 HisMetThrTyrTrpArgLeuGluAsnIleAlaLysThrGluProProlLysIlePheArg 142

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Db 489 CATATGATATCTGAGATTAGAGAACATAGAGAAACGACCTTAAGATTTCCCT 548
 Qy 143 VallysPVoallleuglylleyayrgetlleglntpilleysProgluleu 162
 Db 549 GTGAACACGATTGGGCATCAACGAATGATTCAAATGGAATGAAGCTGAGTTG 608
 Qy 163 AAlaProValSerSerAspLeuLeyrThrLeuAagPheArgThrValAsnSerThrSer 182
 Db 609 GCGGCTGTTTCACTGATTAAATACACACTTCATTACAGACGTCAACAGTACCAAGC 668
 Qy 183 TrpMetGluValAsnPheAlaLysAsnArgLysAspLysAsnGlnThrTyrAsnLeuThr 202
 Db 669 TGGATGGAAGTCAACTTGCCTAAGAACCTTAAGATTAACCAACCTCAACCTCAAGC 728
 Qy 203 GlyLeuGlnProPheThrGluTyrValIleAlaLeuArgCysAlaValIleGluSerLys 222
 Db 729 GGGCTGCGACCTTTTACAGAAATATGTCAATGCTGCGATGTGCGGTCAAGAGTCAAG 788
 Qy 223 PheTrpSerAspTrpSerGlnGluLysMetGlyMetThrGluGlu 238
 Db 789 TTCTGAGTGACTGAGCCAAAGAAAAATGGGAATGACTGAGGAAGAA 836
 RESULT 14
 ID ADL26675 standard; cDNA; 1299 BP.
 AC ADL26675;
 XX 20-MAY-2004 (first entry)
 DT
 XX Human cytokine receptor zcytor17 DNA seqid 112.
 DE
 XX antiinflammatory; antitumor; dermatological; antiallergic; antipsoriatic;
 KM antibacterial; immunosuppressive; cell proliferation response inhibitor;
 KM immune response inhibitor; inflammatory response inhibitor;
 KM multimeric cytokine receptor; heterodimeric cytokine receptor; cancer;
 KM cytokine-binding domain; class I cytokine receptor; hematopoietic cell;
 KM zcytor17lig-induced proliferation; zcytor17lig-induced differentiation;
 KM hematopoietic progenitor cell; zcytor17lig-induced inflammation;
 KM inflammatory disease; inflammatory bowel disease; ulcerative colitis;
 KM Crohn's disease; atopic dermatitis; eczema; psoriasis; endotoxaemia;
 KM septicemia; toxic shock syndrome; zcytor17; human; gene; ss.
 KM
 XX Homo sapiens.
 OS
 XX
 PN US2003215838-A1.
 XX
 PD 20-NOV-2003.
 XX
 PF 21-JAN-2003; 2003US-00351157.
 XX
 PR 18-JAN-2002; 2002US-0350325P.
 PR 14-JUN-2002; 2002US-0389108P.
 PR 19-DEC-2002; 2002US-0435361P.
 XX
 PA (SPRE/) SPRECHER C A.
 PA (GAOZ/) GAO Z.
 PA (KUIJ/) KUIJPER J L.
 PA (DASO/) DASOVICH M M.
 PA (GRAN/) GRANT F J.
 PA (PRES/) PRESNELL S R.
 PA (WHIT/) WHITMORE T E.
 PA (HAMM/) HAMMOND A K.
 PA (NOVA/) NOVAK J E.
 PA (GROS/) GROSS J A.
 PA (DILL/) DILLON S R.
 XX
 PI Sprecher CA, Gao Z, Kuijper JL, Dasovich MM, Grant FJ,
 PI Presnell SR, Whitmore TE, Hammond AK, Novak JE, Gross JA, Dillon SR,
 XX WPI; 2003-876545/81.
 DR P-PSDB; ADL26676.

XX Novel multimeric or heterodimeric cytokine receptors useful for treating
 PT chronic inflammatory disease such as inflammatory bowel disease,
 PT ulcerative colitis, acute inflammatory disease such as endotoxaemia,
 PT septicemia.
 PS Disclosure; SEQ ID NO 112; 205bp; English.
 CC
 CC The invention describes an isolated multimeric or heterodimeric cytokine
 CC receptor (I) having at least one polypeptide having 90 percent sequence
 CC identity with a 732 (S1) or 649 (S2) amino acid sequence given in
 CC specification, and where (I) binds a ligand comprising a 164 (S3) amino
 CC acid sequence, given in specification, or at least one polypeptide
 CC comprising residue 20-227 of (S1). (I) is useful for killing cancer cells
 CC and producing an antibody to (I) and a cytokine-binding domain of a class
 CC I cytokine receptor. A composition (C1) comprising (I) and a cytokine-
 CC binding domain of a class I cytokine receptor and a vehicle is useful
 CC for: reducing haematopoietic cells and hematopoietic progenitor cells in
 CC a mammal; inhibiting zcytor17lig-induced proliferation or differentiation
 CC of hematopoietic cells and hematopoietic progenitor cells; reducing
 CC zcytor17lig-induced inflammation; treating a mammal afflicted with an
 CC inflammatory disease in which zcytor17lig plays a role. The disease is a
 CC chronic inflammatory disease such as inflammatory bowel disease,
 CC ulcerative colitis, Crohn's disease, atopic dermatitis, eczema and
 CC psoriasis. The disease is acute inflammatory disease such as
 CC endotoxaemia, septicemia, toxic shock syndrome and infectious disease.
 CC An immune response inhibiting composition is useful for inhibiting an
 CC immune response in a mammal exposed to an antigen or pathogen. An
 CC inflammatory response inhibiting composition is useful for suppressing an
 CC inflammatory response in a mammal with inflammation. An antibody that
 CC specifically binds to (I) is useful for detecting the presence of a
 CC multimeric or heterodimeric cytokine receptor in a biological sample.
 CC This sequence encodes a human zcytor17 cytokine receptor that can be used
 CC in a comparison with other zcytor17 receptors.
 CC
 SQ Sequence 1299 BP; 402 A; 276 C; 306 G; 315 T; 0 U; 0 Other;
 Alignment Scores:
 Pred. No.: 3.2e-133 Length: 1299
 Score: 1282.00 Matches: 236
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 Query Match: 94.40% Indels: 0
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 Db 129 CTCTCTCCCGACCTTCAATGATGTTAACCTGGGATGATGTGGACCTGGCACTGTGATG 188
 Qy 23 LeuProSerLeuCyLysPheSerLeuAlaLeuProAlaLysProGluAsnIleSer 42
 Db 189 CTCCTCCACCTCGCAATTCAGCTCGAGCTCTGCACGTAAAGCTGAGAAACATTTCC 248
 Qy 43 CysValIlyrTyrTyrAglYasnLeuThrCysThrTrpSerProGlyLysGluThrSer 62
 Db 249 TGTGTCTACTACTATAGAAAAATTAACTGCCTTGAGGTCCAGAAAAAGAAACAGT 308
 Qy 63 TyrThrGlnTyrThrValLysArgThrTyrAlaPheGlyGluLysHISAspAsnCysThr 82
 Db 309 TATACCAAGTACACAGTAAAGAACTTACGCTTTTGGAGAAAACATGATATTGTACA 368
 Qy 83 ThrAsnSerSerThrSerGluAsnArgAlaSerCysSerPhePheLeuProArgIleThr 102
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 Qy 103 IleProAspAsnTyrThrIleGluValGluAlaGluAsnGlyAspGlyValIleLysSer 122
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 Qy 123 HisWetThrTyrTrpArgLeuGluAsnIleAlaLysThrGluProProLysIlePheArg 142

Db 489 CATATGACATACCTGAGATTAGAGAACATAGCGAAAACTGAACCACTTAAGATTTTCCTG 548
 QY 143 ValIysProValIleuGlyIleIysArgMetIleGlnIleGluTrpIleIysProGluLeu 162
 Db 549 GTGAACCAAGTTTGGGCAATCAACGAATGATTCAATGATTAAGCTTGAGTTG 608
 QY 163 AlaProValSerSerAspIleuIysTrpTrpIleuArgPheArgThrValIAsnSerThrSer 182
 Db 609 GGGCTGTTTCATCTGATTTAAATAACACCTTCGATTGAGCAGTCAACAGTACACAG 668
 QY 183 TrpMetGluValAsnPheAlaIysAsnArgIysAspIysAsnGlnThrTrpAsnLeuThr 202
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 QY 203 GlyLeuGlnProPheThrGluTrpValIleAlaIleuArgCysAlaValIysGluSerIys 222
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 QY 223 PheTrpSerAspTrpSerGlnGluIysMetGlyMetThrGluGlu 238
 Db 789 TTCTGAGTGACTGAGCCAGAAAAAATGGAAATGATGAGAGAGAA 836
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 ID ABA93767 standard; cDNA; 2386 BP.
 AC ABA93767;
 XX
 DT 01-MAY-2002 (first entry)
 XX
 DE Human zcytor17 cDNA sequence SEQ ID NO:1.
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 KM zcytor17; chromosome 5; 5q11; cytokine receptor; immunomodulatory;
 KM antiinflammatory; antiviral; antirheumatic; antiarthritic; cycostatic;
 KM muscular; lymphoid; immune; inflammatory; splenic; blood; bone;
 KM infection; immunosuppression; cytotoxicity; leukopenia; Crohn's disease;
 KM autoimmune disease; rheumatoid arthritis; multiple sclerosis; cancer;
 KM inflammatory disease; pancreatitis; inflammatory bowel disease; ss.
 XX
 OS Homo sapiens.
 XX
 PN WO200200721-A2.
 PD 03-JAN-2002.
 XX
 PF 26-JUN-2001; 2001MO-US020484.
 XX
 PR 26-JUN-2000; 2000US-0214282P.
 PR 29-JUN-2000; 2000US-0214955P.
 PR 08-FEB-2001; 2001US-0267963P.
 XX
 PA (ZYMO) ZYMOGENETICS INC.
 XX
 PI Sprecher CA, Prensell SR, Gao Z, Whitmore TE, Kuijper JL;
 PI Maurer MF;
 PI
 DR MPI; 2002-090519/12.
 DR P-PSDB; ABB05730.
 XX
 PT Isolated polynucleotide encoding a cytokine receptor zcytor17 which is
 PT useful for treating and diagnosing lymphoid, immune, inflammatory,
 PT splenic, blood or bone disorders.
 XX
 PS Claim 2; Page 161-166; 235pp; English.
 XX
 CC The present invention describes a cytokine receptor designated zcytor17.
 CC zcytor17 has immunomodulatory, antiinflammatory, antiviral, cycostatic,
 CC antineumatic, antiarthritic and muscular activities. The zcytor17
 CC proteins are useful for treating and diagnosing lymphoid, immune,
 CC inflammatory, splenic, blood or bone disorders. Agonists or anti-
 CC zcytor17 antibodies are useful in stimulating cell-mediated immunity and
 CC for stimulating lymphocyte proliferation, such as in the treatment of
 CC infections involving immunosuppression, including certain viral

CC infections. They are also useful for inducing cytotoxicity and for
 CC treating leukopemias. Antagonist of zcytor17 polypeptides are useful for
 CC treating autoimmune diseases (e.g. rheumatoid arthritis and multiple
 CC sclerosis), inflammatory diseases (e.g. Crohn's disease), cancer,
 CC pancreatitis, and inflammatory bowel disease. Zcytor17 was mapped to
 CC chromosome 5, specifically to the 5q11 chromosomal region. ABA93767 to
 CC ABA93843 and ABB05730 to ABB05745 represent sequences used in the
 CC exemplification of the present invention

SQ Sequence 2386 BP; 711 A; 525 C; 575 G; 575 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.:	Length:	Matches:	Conservative:	Mismatches:	Indels:
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Best Local Similarity:	100.00%				
Query Match:	94.40%				
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US-10-006-265-4 (1-252) x ABA93767 (1-2386)

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QY	23	LeuProSerLeuCysIlePheSerIleuAlaIleuProAlaIysProGluAsnIleSer	42
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QY	43	CysValIysTrpTrpArgIysAsnLeuThrCysThrTrpSerProGluIysGluThrSer	62
Db	258	TGTGTCTACTACTATATGAAAAATTTAACTCTCAGTTCAGTTCAGAAAGAAACAGT	317
QY	63	TrpThrGlnTrpThrValIysArgThrTrpAlaPheGluGluIysHisAspAsnCysThr	82
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QY	83	ThrAsnSerSerThrSerGluAsnArgIAserCysSerPhePheLeuProArgIleThr	102
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QY	103	IleProAspAsnTrpThrIleGluValGluIleAsnGlyAspGlyValIleIysSer	122
Db	438	ATCCCAAGATAATTAATCACTTACGAGTGAAGCTGAATAATGAGATGTATAATCA	497
QY	123	HisMetThrTrpTrpArgIleuGlnIleAlaIysThrGluProProIysIlePheArg	142
Db	498	CATATGACATACCTGAGATTAGAGAACATAGCAAACTGAACCACTTAAGATTTCCG	557
QY	143	ValIysProValIleuGlyIleIysArgMetIleGlnIleGluTrpIleIysProGluLeu	162
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QY	163	AlaProValSerSerAspIleuIysTrpTrpIleuArgPheArgThrValIAsnSerThrSer	182
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Db	678	TGGATGGAAGTCAACTCGCTTAAGAACCGTAAAGATTAACCAACGTAACCTCAG	737
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 Job time : 382.207 secs

GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Run on: February 23, 2005, 08:59:57 ; Search time 116.023 Seconds
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Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	262.5	19.3	1977	2	US-08-825-558-3
3	262.5	19.3	1977	2	US-09-312-611-3
4	262.5	19.3	2369	1	US-07-797-556-1
5	262.5	19.3	2369	1	US-08-308-881-1
6	262.5	19.3	2369	2	US-09-058-263-1
7	262.5	19.3	2369	2	US-09-059-099-1
8	262.5	19.3	2369	2	US-09-058-264-1
9	262.5	19.3	2369	4	US-09-455-962-1
10	262.5	19.3	2369	5	PCR-US95-06530-1
11	262.5	19.3	2754	2	US-08-825-558-5
12	262.5	19.3	2754	3	US-09-312-611-5

13	262.5	19.3	3085	3	US-08-795-473B-4	Sequence 4, Appl1
14	262.5	19.3	3085	4	US-09-439-856-4	Sequence 4, Appl1
15	262.5	19.3	3085	4	US-09-023-655-1131	Sequence 1131, Ap
16	262.5	19.3	3477	4	US-09-313-942-25	Sequence 25, Appl
17	262.5	19.3	3507	4	US-09-313-942-23	Sequence 23, Appl
18	262.5	19.3	3218	3	US-09-012-072-1	Sequence 1, Appl1
19	233	17.2	1218	3	US-09-120-601-1	Sequence 1, Appl1
20	233	17.0	1690	3	US-09-071-224-1	Sequence 1, Appl1
21	231	17.0	1724	3	US-09-071-224-5	Sequence 5, Appl1
22	231	17.0	1790	4	US-09-866-028-31	Sequence 31, Appl
23	231	17.0	1790	4	US-09-944-457-31	Sequence 31, Appl
24	231	17.0	1813	3	US-09-071-224-3	Sequence 3, Appl1
25	211	15.5	1305	3	US-09-012-072-3	Sequence 3, Appl1
26	211	15.5	1305	3	US-09-120-601-3	Sequence 3, Appl1
27	211	15.5	1347	3	US-09-120-601-5	Sequence 5, Appl1
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37	171	12.6	1525	4	US-09-828-995B-95	Sequence 95, Appl
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42	159	11.7	2800	3	US-08-702-665A-4	Sequence 4, Appl1
43	156.5	11.5	2855	1	US-07-923-976-5	Sequence 3, Appl1
44	156.5	11.5	2943	1	US-07-923-976-3	Sequence 3, Appl1
45	156.5	11.5	2943	4	US-09-023-655-1086	Sequence 1086, Ap

ALIGNMENTS

RESULT 1
US-09-700-820C-17
; Sequence 17, Application US/09700820C
; Patent No. 6610485
; GENERAL INFORMATION:
; APPLICANT: Tsuchiya, Masayuki
; APPLICANT: Saito, Makiyoshi
; APPLICANT: Ohtomo, Toshihiko
; TITLE OF INVENTION: NOVEL METHOD FOR GENE CLONING
; FILE REFERENCE: 06501-070001
; CURRENT APPLICATION NUMBER: US/09/700,820C
; PRIOR FILING DATE: 1998-05-20
; PRIOR APPLICATION NUMBER: JP 10/138652
; PRIOR FILING DATE: 1999-04-30
; PRIOR APPLICATION NUMBER: PCT/JP99/02341
; PRIOR FILING DATE: 1998-05-20
; PRIOR APPLICATION NUMBER: JP 10/279876
; PRIOR FILING DATE: 1998-10-01
; NUMBER OF SEQ ID NOS: 39
; SEQ ID NO 17
; LENGTH: 2995
; TYPE: DNA
; ORGANISM: Mus musculus
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (29) .. (2839)
US-09-700-820C-17

Alignment Scores:
Pred. No.: 7.63e-22
Score: 265.50
Percent Similarity: 52.88%
Best Local Similarity: 31.25%
Query Match: 19.55%
DB: 4
Length: 2995
Matches: 65
Conservative: 45
Mismatch: 83
Indels: 15
Gaps: 9

US-10-006-265-4 (1-252) X US-09-700-820C-17 (1-2995)

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Db 464 CCGATTAACCTACCAATTTGACTTGCTGATGTGAATGAGGGGAAGATATCTGTGCGAC 523
Qy 55 TrpSerProgluLysGluThrSerTyr--ThrGlnTyrValLysArgThrTyrAla 73
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Qy 74 PheGlyGluTyrHisAspAsnCysThrThrAsnSerSerThrSerGluAsnArgAlaSer 93
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Qy 94 CysSerPhe---PheLeuProArgIleThrIleProAspAsnTyrThrIleGluValGlu 112
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Db 800 TTAAAGCTATCATGGGTGACGTTCAGAGGCTGGGGCGGTCT--TTAGATCTAAAGCTGAC 856
Qy 173 LeuArgPheArgThrValAsnSerThrSerThrMetGluValAsnPheAlaLysAsnArg 192
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Db 914 ATGTCCTCTCGAACTCTCTTCACGTGCGAGAGACCTCAAGCCTTTTACGAAATATGTGTT 973
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RESULT 2
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; Sequence 3, Application US/08825558
; Patent No. 5965724
; GENERAL INFORMATION:
; APPLICANT: SHARKEY, ANDREW
; APPLICANT: SMITH, STEPHEN K.
; APPLICANT: DELLOW, KIMBERLEY A.
; TITLE OF INVENTION: Gp 130 Lacking the Transmembrane Domain
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: STERN, KESSLER, GOLDSTEIN & FOX
; STREET: 1100 NEW YORK AVENUE
; CITY: WASHINGTON
; STATE: DC
; COUNTRY: USA
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/825,558
; FILING DATE: 19-MAR-1997
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:

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1 NAME: ESMOND, ROBERT W.
2 REGISTRATION NUMBER: 32, 893
3 REFERENCE/DOCKET NUMBER: 0623.0530001
4 TELECOMMUNICATION INFORMATION:
5 TELEPHONE: (202)371-2600
6 TELEFAX: (202)371-2540
7 INFORMATION FOR SEQ ID NO: 3:
8 SEQUENCE CHARACTERISTICS:
9 LENGTH: 1977 base pairs
10 TYPE: nucleic acid
11 STRANDEDNESS: both
12 TOPOLOGY: linear
13 MOLECULE TYPE: cDNA
14 FEATURE:
15 NAME/KEY: CDS
16 LOCATION: 1..1974
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18 US-08-825-558-3

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US-09-312-611-3
Sequence 3, Application US/09312611
Patent No. 6380160
GENERAL INFORMATION:
APPLICANT: SHARKEY, ANDREW
APPLICANT: SMITH, STEPHEN K.
APPLICANT: DELLOW, KIMBERLEY A.
TITLE OF INVENTION: Gp130 Lacking the Transmembrane Domain
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESSES:
ADDRESSEE: STERN, KESSLER, GOLDSTEIN & FOX
STREET: 1100 NEW YORK AVENUE
CITY: WASHINGTON
STATE: DC
COUNTRY: USA
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/312,611
FILING DATE: 17-MAY-1999
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: ESMOND, ROBERT W.
REGISTRATION NUMBER: 32,893
REFERENCE/DOCKET NUMBER: 0623, 0530002
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)371-2540
FAX: (202)371-2540
INFORMATION FOR SEQ ID NO: 3:
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TYPE: nucleic acid
STRANDEDNESS: both
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 1..1974
US-09-312-611-3
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Pred. No.: 9.2e-22 Length: 1977
Score: 262.50 Matches: 65
Percent Similarity: 51.85% Conservative: 47
Best Local Similarity: 30.09% Mismatches: 75
Query Match: 19.33% Indels: 29
DB: 3 Gaps: 11
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Db 436 TGGGATGGTGAAGGAAACACACTGTGAGCAAACTTCATTTAAATCTGAATGGCA 495
Qy 71 ThrTyrAlaPheGlyGlu-----LysHisAsp-----AsnCyThrThrAsn 84
Db 496 ACACACAAGTTTGGCTGATTCGAAGCAAAACGTGACACCCACCTCATGCACTGTGAT 555
Qy 85 SerSerThrSerGluAsnArgAlaSerCySerPhePheLeuProArgIleThrIlePro 104
Db 556 TATTTCTACT-----GTGTAFTTGTCT----- 576
Qy 105 AspAsnTyrThrIleGluValGluIleAsnGlyValAspGlyValIleLysSer---His 123
Db 577 ---AACATTGAAGTGTGGTGAAGCAGAAATGCCCTTGGGAAGCTTACATCATCATCAT 633

Qy 124 MetThrTyrTrpArgLeuGluAsnIleAlaLysThrGluProProLysIlePheArgVal 143
Db 634 ATCAATTTGATCCTGTAATTAAGT---AAGCCCAATCCGCCCATTAATTTACATG 690
Qy 144 LysProValLeuGlyIleLysArgMetIleGlnIleGluTrpIleLysProGluLeuAla 163
Db 691 ATCAACTCAGAGGAAGTCTCAGATCTTAATATGATGACCAACCCAAAGTATTAAAG 750
Qy 164 ProValSerSerAspLeuTyrTyrThrLeuArgPheArgThrValAsnSerThrTyr 183
Db 751 AGTGTATAATA---CTAAATATATACATTCAAATATGAGCAAAAGATGCCCTCAACTGG 807
Qy 184 MetGluValAsnPheAlaLysAsnArgLysAspLysAsnGlnThrTyrAsnLeuThrGly 203
Db 808 AGCCAGATTCCT---CCTGAAGACACAGCATCCACCCGATCTTCACTCATGTCACAGAC 864
Qy 204 LeuGlnProPheThrGluTyrValIleAlaLeuArgCysAlaValLysGluSerLys--- 222
Db 865 CTTAACCTTTTACAGAAATATGTTTAGAGATTGCTGTATGAAGGAAGATGTAAAGGA 924
Qy 223 PheTTPSerAspTTPSerGlnGluLysMetGlyMetThrGluGlu 238
Db 925 TACTGAGTGAAGTGAAGGAAGCAAGTGGATCACTATGAAGAT 972
RESULT 4
US-07-797-556-1
Sequence 1, Application US/07797556
Patent No. 5262522
GENERAL INFORMATION:
APPLICANT: Geating, David P.
TITLE OF INVENTION: Receptor for Oncostatin M and Leukemia
TITLE OF INVENTION: Inhibitory Factor
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Immunex Corporation
STREET: 51 University Street
CITY: Seattle
STATE: WA
COUNTRY: USA
ZIP: 98101
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/797,556
FILING DATE: 19911122
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Seese, Kathryn A.
REGISTRATION NUMBER: 32,172
REFERENCE/DOCKET NUMBER: 2607
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-587-0430
FAX: 206-587-0606
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 2369 base pairs
TYPE: NUCLEIC ACID
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA to mRNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: N-terminal
ORIGINAL SOURCE:
TISSUE TYPE: human placenta
IMMEDIATE SOURCE:
CLONE: B10G/DDC303
FEATURE:
NAME/KEY: CDS

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/ LOCATION: 244..2369
/ FEATURE:
/ NAME/KEY: mat_peptide
/ LOCATION: 310..2369
/
/ FEATURE: sig_peptide
/ LOCATION: 244..309
/
US-07-797-556-1

Alignment Scores:
Pred. No.: 1,23e-21 Length: 2369
Score: 262.50 Matches: 65
Percent Similarity: 51.85% Conservative: 47
Best Local Similarity: 30.09% Mismatches: 75
Query Match: 19.33% Indels: 29
DB: 1 Gaps: 11

US-10-006-265-4 (1-252) x US-07-797-556-1 (1-2369)
QY 35 ProAlaLysProGluAsnIleSerCysValTyrTyrArgLysAsnLeuThrCysThr 54
Db 619 CCAGAAAACCTAAATTTGAGTTGCACTTGCAAGAGGGAAGAAAATGAGGTGTAG 678
QY 55 TTPSerProGlyLysGluThrSerTyr---ThrGlnTyrThrValLys-----Arg 70
Db 679 TGGGATGCTGGAAGGAAACACACTTGAGCAAACTTCACTTAAATCTGAATGGGCA 738
QY 71 ThTyrAlaPheGlyGlu-----LysHisAsp-----AsnCysThrThrAsn 84
Db 739 ACACACAAGTTCCTATTGCAAAAGCAAAAGTGAACCCCACTTCATGACCTGTGAT 798
QY 85 SerSerThrSerGluAsnArgAlaSerCysSerPhePheLeuProArgIleThrIlePro 104
Db 799 TATTCTACT-----GTCGATTTTCTC----- 819
QY 105 AspAsnTyrThrIleGluValGluAlaGluAsnGlyAspGlyValIleLysSer---His 123
Db 820 ---AACATTGAAGCTCGGTGAAGAGAGAAATGCCCTTGGGAAGGTTACATCAGATCAT 876
QY 124 MetThrTyrTrpArgLeuGluAsnIleAlaLysThrGluProProLysIlePheArgVal 143
Db 877 ATCAATTTTGATCCTGATATTAAGTG---AGCCCAATCCGCCACATTAATTTATGATG 933
QY 144 LysProValLeuGlyIleLysArgMetIleGlnIleGluTrpIleLysProGluLeuAla 163
Db 934 ATCAACTCAGAGAGACTGCTACTATCTTAATTTGACATGACCAACCAAGTATTTAG 993
QY 164 ProValSerSerAspLeuLysTyrThrLeuArgPheArgThrValAsnSerThrSerTrp 183
Db 994 AGTGTTATATA---CTAAATATTAACATTCATATATAGGACCAAGATGCTCAACTTG 1050
QY 184 MetGluValAsnPheAlaLysAsnArgLysAspLysAsnGlnIleThrValAsnLeuThrGly 203
Db 1051 AGCCAGATTCCT---CCTGAAGACACAGCATCCACCCGATCTTCATTCAGTCCAAAGAC 1107
QY 204 LeuGlnProPheThrGluTyrValIleAlaLeuArgCysAlaValLysGluSerLys--- 222
Db 1108 CTTAAACCTTTTCAGAAATATGTGTTAGGATTCGCTGATATGAAGAAGATGTTAAGGCA 1167
QY 223 PheTTPSerAspTTPSerGlnGluLysMetGlyMetThrGluGluGlu 238
Db 1168 TACTGAGAGTACTGAGTGAAGAAAGCAAGTGGATCACCTATGAAAGAT 1215

RESULT 5
US-08-308-881-1
/ Sequence 1, Application US/08308881
/ Patent No. 5783672
/ GENERAL INFORMATION:
/ APPLICANT: Mosley, Bruce
/ APPLICANT: Mosley, David J.
/ TITLE OF INVENTION: Receptor for Oncostatin M
/ NUMBER OF SEQUENCES: 11
/ CORRESPONDENCE ADDRESS:
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/ ADDRESSER: Immunex Corporation
/ STREET: 51 University Street
/ CITY: Seattle
/ STATE: WA
/ COUNTRY: USA
/ ZIP: 98101
/
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: Apple Macintosh
/ OPERATING SYSTEM: Apple 7.1
/ SOFTWARE: Microsoft Word, Version 5.1a
/
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/308,881
/ FILING DATE: 12-SEP-1994
/ CLASSIFICATION: 435
/
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 08/249,553
/ FILING DATE: 26-MAY-1994
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Seese, Kathryn A.
/ REGISTRATION NUMBER: 32,172
/ REFERENCE/DOCKET NUMBER: 2614-A
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (206) 587-0430
/ TELEFAX: (206) 233-0644
/ TELEX: 756822
/
/ INFORMATION FOR SEQ ID NO: 1:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 2369 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ MOLECULE TYPE: cDNA to mRNA
/ HYPOTHEICAL: NO
/
/ ANTI-SENSE: NO
/
/ FRAGMENT TYPE: N-terminal
/ ORIGINAL SOURCE:
/ TISSUE TYPE: human placenta
/ IMMEDIATE SOURCE:
/ CLONE: B10G/pDC303
/
/ FEATURE:
/ NAME/KEY: CDS
/ LOCATION: 244..2369
/
/ FEATURE:
/ NAME/KEY: mat_peptide
/ LOCATION: 310..2369
/
/ FEATURE:
/ NAME/KEY: sig_peptide
/ LOCATION: 244..309
/
US-08-308-881-1

Alignment Scores:
Pred. No.: 1,23e-21 Length: 2369
Score: 262.50 Matches: 65
Percent Similarity: 51.85% Conservative: 47
Best Local Similarity: 30.09% Mismatches: 75
Query Match: 19.33% Indels: 29
DB: 1 Gaps: 11

US-10-006-265-4 (1-252) x US-08-308-881-1 (1-2369)
QY 35 ProAlaLysProGluAsnIleSerCysValTyrTyrArgLysAsnLeuThrCysThr 54
Db 619 CCAGAAAACCTAAATTTGAGTTGCACTTGCAAGAGGGAAGAAAATGAGGTGTAG 678
QY 55 TTPSerProGlyLysGluThrSerTyr---ThrGlnTyrThrValLys-----Arg 70
Db 679 TGGGATGCTGGAAGGAAACACACTTGAGACAAACTTCACTTAAATCTGAATGGGCA 738
QY 71 ThTyrAlaPheGlyGlu-----LysHisAsp-----AsnCysThrThrAsn 84
Db 739 ACACACAAGTTCCTATTGCAAAAGCAAAAGTGAACCCCACTTCATGACCTGTGAT 798
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Qy 85 SerSerThrSerGluuAenrAlaSerCySerPhePheLeuProArgIleThrIlePro 104
    |||||
Db 799 TATTTCTACT-----GTGATTTTGTCT----- 819
Qy 105 AspaenrYrThrIleGluValGluAlaGluAenrGlyAspGlyValIleLeuSer---His 123
    |||||
Db 820 ---AACATTGAAGTCTGGGTAGAGAGAGAAATGCCCTTGGGAAGGTATCATCAGATCAT 876
Qy 124 MetThrYrTrpArgLeuGluAenrIleAlaLeuThrGluProProGlyIlePheArgVal 143
    |||||
Db 877 ATCAATTTTGATCCGTATATTAAGG---AAGCCCAATCCGCCATATTTATTCAGAG 933
Qy 144 LysProValIleGluIleLeuArgMetIleGluIleGluTrpIleLysProGluLeuAla 163
    |||||
Db 934 ATCAACTCAGAGAAATGCTGTAGTATCTTAAATTCACATGACCAACCAAGTATTAAAG 993
Qy 164 ProValSerSerAspLeuValYrThrIleuArgPheArgThrValAsnSerThrSerTrp 183
    |||||
Db 994 AGTGTATTAATA---CTAAATATATTAACATTCATATAGACCAAGATGCTCAACTTGG 1050
Qy 184 MetGluValAenrPheAlaLysAenrGlyAspGlyAsnGlnThrYrAsnLeuThrGly 203
    |||||
Db 1051 AGCCGAGATTCTCT---CTGAAGACACAGCATCCACCCGATCTTCATCTCCAGAC 1107
Qy 204 LeuGlnProPheThrGluTrpValIleAlaLeuArgCyAlaValIleGluSerLys--- 222
    |||||
Db 1108 CTTAAACCTTTTACAGAAATATGTGTTTAGGATTCGCTGATATAGAGAAAGATGTAAGGGA 1167
Qy 223 PheTrpSerAspTrpSerGlnGluLysMetGlyMetThrGluGlu 238
    |||||
Db 1168 TACTGAGTGAAGTGAAGTGAAGACAGCAAGTGGATCAGCTATGAAGAT 1215

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RESULT 6
US-09-058-263-1
Sequence 1, Application US/09058263
Patent No. 5891997

GENERAL INFORMATION:
APPLICANT: Mosley, Bruce
TITLE OF INVENTION: Receptor for Oncostatin M
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: Immunex Corporation
STREET: 51 University Street
CITY: Seattle
STATE: WA
COUNTRY: USA
ZIP: 98101
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Macintosh
OPERATING SYSTEM: Apple 7.1
SOFTWARE: Microsoft Word, Version 5.1a
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/058,263
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/308,881
FILING DATE: 12-SEP-1994
APPLICATION NUMBER: US 08/249,553
FILING DATE: 26-MAY-1994
ATTORNEY/AGENT INFORMATION:
NAME: Seese, Kathryn A.
REGISTRATION NUMBER: 32,172
REFERENCE/DOCKET NUMBER: 2614-A
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 587-0430
TELEFAX: (206) 233-0644
TELEX: 756822
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 2369 base pairs

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; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: CDNA to mRNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE: N-terminal
; ORIGINAL SOURCE:
; TISSUE TYPE: human placenta
; IMMEDIATE SOURCE:
; CLONE: B10G/PDC303
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 244..2369
; FEATURE:
; NAME/KEY: mat_peptide
; LOCATION: 310..2369
; FEATURE:
; NAME/KEY: sig_peptide
; LOCATION: 244..309
; US-09-058-263-1

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Alignment Scores:
Pred. No.: 1,23e-21 Length: 2369
Score: 262.50 Matches: 65
Percent Similarity: 51.85% Conservative: 47
Best Local Similarity: 50.09% Mismatches: 75
Query Match: 19.33% Indels: 29
DB: 2 Gaps: 11

US-10-006-265-4 (1-252) x US-09-058-263-1 (1-2369)

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Qy 35 ProAlaLysProGluAenrIleSerCyValYrTrpYrArgLysAenrLeuThrCyThr 54
    |||||
Db 619 CCAGAAAAAAGCTTAAATTTGAGTTGCTGTGAACGAGGGAAGAAATGAGGTGTAG 678
Qy 55 TrpSerProGlyLysGluThrSerTrp---ThrGlnYrThrValLys-----Arg 70
    |||||
Db 679 TGGAGTGTGAAGGGAACACACTTGGAGCAAACTTCATTTAAATTCGAATGGGCA 738
Qy 71 ThrTrpAlaPheGlyGlu-----LysHisAsp-----AsnCyThrThrAsn 84
    |||||
Db 739 ACAACAGATTGCTGATGTGAAGCAAAAGCTGACACCCCACTCATGACGTGTGAT 798
Qy 85 SerSerThrSerGluAenrAlaSerCySerPhePheLeuProArgIleThrIlePro 104
    |||||
Db 799 TATTTCTACT-----GTGATTTTGTCT----- 819
Qy 105 AspaenrYrThrIleGluValGluAlaGluAenrGlyAspGlyValIleLeuSer---His 123
    |||||
Db 820 ---AACATTGAAGTCTGGGTAGAGAGAGAAATGCCCTTGGGAAGGTATCATCAGATCAT 876
Qy 124 MetThrYrTrpArgLeuGluAenrIleAlaLeuThrGluProProGlyIlePheArgVal 143
    |||||
Db 877 ATCAATTTTGATCCGTATATTAAGG---AAGCCCAATCCGCCATATTTATTCAGAG 933
Qy 144 LysProValIleGluIleLeuArgMetIleGluIleGluTrpIleLysProGluLeuAla 163
    |||||
Db 934 ATCAACTCAGAGAAATGCTGTAGTATCTTAAATTCACATGACCAACCAAGTATTAAAG 993
Qy 164 ProValSerSerAspLeuValYrThrIleuArgPheArgThrValAsnSerThrSerTrp 183
    |||||
Db 994 AGTGTATTAATA---CTAAATATATTAACATTCATATAGACCAAGATGCTCAACTTGG 1050
Qy 184 MetGluValAenrPheAlaLysAenrGlyAspGlyAsnGlnThrYrAsnLeuThrGly 203
    |||||
Db 1051 AGCCGAGATTCTCT---CTGAAGACACAGCATCCACCCGATCTTCATCTCCAGAC 1107
Qy 204 LeuGlnProPheThrGluTrpValIleAlaLeuArgCyAlaValIleGluSerLys--- 222
    |||||
Db 1108 CTTAAACCTTTTACAGAAATATGTGTTTAGGATTCGCTGATATGAAGAAAGATGTAAGGGA 1167
Qy 223 PheTrpSerAspTrpSerGlnGluLysMetGlyMetThrGluGlu 238
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Db 1168 TACTGAGTACTGAGTGAAGACGAAGGATCACCATTATGAAGAT 1215

RESULT 7

US-09-059-099-1

/ Sequence 1, Application US/09059099

/ Patent No. 5925740

/ GENERAL INFORMATION:

/ APPLICANT: Mosley, Bruce

/ APPLICANT: Cosman, David J.

/ TITLE OF INVENTION: Receptor for Oncostatin M

/ NUMBER OF SEQUENCES: 11

/ CORRESPONDENCE ADDRESS:

/ ADDRESSEE: Immunex Corporation

/ STREET: 51 University Street

/ CITY: Seattle

/ STATE: WA

/ COUNTRY: USA

/ ZIP: 98101

/ COMPUTER READABLE FORM:

/ MEDIUM TYPE: Floppy disk

/ COMPUTER: Apple Macintosh

/ OPERATING SYSTEM: Apple 7.1

/ SOFTWARE: Microsoft Word, Version 5.1a

/ CURRENT APPLICATION DATA:

/ APPLICATION NUMBER: US/09/059,099

/ FILING DATE:

/ CLASSIFICATION:

/ PRIOR APPLICATION DATA:

/ APPLICATION NUMBER: US/08/308,881

/ FILING DATE: 12-SEP-1994

/ APPLICATION NUMBER: US 08/249,553

/ FILING DATE: 26-MAY-1994

/ ATTORNEY/AGENT INFORMATION:

/ NAME: Seese, Kathryn A.

/ REGISTRATION NUMBER: 32,172

/ REFERENCE/DOCKET NUMBER: 2614-A

/ TELECOMMUNICATION INFORMATION:

/ TELEPHONE: (206) 587-0430

/ TELEFAX: (206) 233-0644

/ TELEX: 756822

/ INFORMATION FOR SEQ ID NO: 1:

/ SEQUENCE CHARACTERISTICS:

/ LENGTH: 2369 base pairs

/ TYPE: nucleic acid

/ STRANDEDNESS: single

/ TOPOLOGY: linear

/ MOLECULE TYPE: cDNA to mRNA

/ HYPOTHETICAL: NO

/ ANTI-SENSE: NO

/ FRAGMENT TYPE: N-terminal

/ ORIGINAL SOURCE:

/ TISSUE TYPE: human placenta

/ IMMEDIATE SOURCE:

/ CLONE: B10G/PDC303

/ FEATURE:

/ NAME/KEY: CDS

/ LOCATION: 244..2369

/ FEATURE:

/ NAME/KEY: mat_peptide

/ LOCATION: 310..2369

/ FEATURE:

/ NAME/KEY: sig_peptide

/ LOCATION: 244..309

US-09-059-099-1

Alignment Scores:

Pred. No.: 1.23e-21

Score: 262.50

Percent Similarity: 51.85%

Best Local Similarity: 30.09%

Query Match: 19.33%

DB: 2

Length: 2369

Matches: 65

Conservative: 47

Mismatches: 75

Indels: 29

Gaps: 11

US-10-006-265-4 (1-252) x US-09-059-099-1 (1-2369)

QY 35 ProAlaLysProGluAsnLLeSerCysValTYRTRYrArgLysAsnLeuThrCysThr 54

Db 619 CCAGAAAACCTTAAATTTGAGTTGATGGAACGAGGAGGAAATGAGTGTGAG 678

QY 55 TPSeSerProGlyLysGluThrSerTYr---ThrGlnTYrThValLys-----Arg 70

Db 679 TGGGATGCTGGAAGAAACACCTTGAGACAACTTAAACTGAAATGGGCA 738

QY 71 ThrTYrAlaPheGlyGlu-----LysHisAsp-----AsnCysThrThraSn 84

Db 739 ACACACAAAGTTGCTGATGCAAGCAAAACGTGACCCCACTTCATGCACTGTGAT 798

QY 85 SerSerThrSerGluAsnArgAlaSerCysSerPhePheLeuProArgLethrIlePro 104

Db 799 TATTTCTACT-----GTTGATTTTGTG----- 819

QY 105 AspAsnTYrThrIleGluValGluAlaGluAsnGlyAspGlyValIleLysSer---His 123

Db 820 ---AACATTGAAGTCTGGGTAGAGAGCAAGAAATGCCCTTGGGAAGGTTATCATCATCAT 876

QY 124 MetThrTYrTYrArgLysGluAsnIleAlaLysThrGluProProLysIlePheArgVal 143

Db 877 ATCAATTTTGATCTCTGATATATAAGTG---AAGCCCAATCCCAACATATTATATCATG 933

QY 144 LysProValLeuGlyrIleLysArgMetIleGlnIleGluTrpIleLysProGluLeuAla 163

Db 934 ATCAACTCAGAGAACTGTCTAGTACTTAAATTGACATGACCAACCAAGTATTAAG 993

QY 164 ProValSerSerAspLeuLysTYrThrLeuArgPheArgThrValAsnSerThrSerTrp 183

Db 994 AGTGTTATATA---CTAAATATTAACATTCATATATAGAACCAAGATGCCCAACTTG 1050

QY 184 MetGluValAsnPheAlaLysAsnArgLysAspLysAsnGlnThrTYrAsnLeuThrGly 203

Db 1051 AGCCAGATTCCT---CCTGAAAGACACAGCATCCACCCGATCTTCATTCAGTGTCCAAAG 1107

QY 204 LeuGlnProPheThrGluTYrValIleAlaLeuArgCysAlaValLysGluSerLys--- 222

Db 1108 CTTAAACCTTTTACAAATATATGTTTACGATTCGCTGATGAAGAAATGTTAAGGGA 1167

QY 223 PheTrpSerAspTrpSerGlnGluLysMetGlyMetThrGluGluGlu 238

Db 1168 TACTGAGTACTGAGTGAAGACGAAGGATCACCATTATGAAGAT 1215

RESULT 8

US-09-058-264-1

/ Sequence 1, Application US/09058264

/ Patent No. 6010886

/ GENERAL INFORMATION:

/ APPLICANT: Mosley, Bruce

/ APPLICANT: Cosman, David J.

/ TITLE OF INVENTION: Receptor for Oncostatin M

/ NUMBER OF SEQUENCES: 11

/ CORRESPONDENCE ADDRESS:

/ ADDRESSEE: Immunex Corporation

/ STREET: 51 University Street

/ CITY: Seattle

/ STATE: WA

/ COUNTRY: USA

/ ZIP: 98101

/ COMPUTER READABLE FORM:

/ MEDIUM TYPE: Floppy disk

/ COMPUTER: Apple Macintosh

/ OPERATING SYSTEM: Apple 7.1

/ SOFTWARE: Microsoft Word, Version 5.1a

/ CURRENT APPLICATION DATA:

/ APPLICATION NUMBER: US/09/058,264

/ FILING DATE:

/ CLASSIFICATION:

/ PRIOR APPLICATION DATA:

Alignment Scores:	
Pred. No.:	1,236-21
Score:	262.50
Percent Similarity:	51.85%
Best Local Similarity:	30.09%
Query Match:	19.33%
DB:	3
Length:	2369
Matches:	65
Conservative:	47
Mismatches:	75
Indels:	29
Gaps:	11

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[illegible]

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? CITY: Seattle
? STATE: WA
? COUNTRY: USA
? ZIP: 98101
? COMPUTER READABLE FORM:
? MEDIUM TYPE: floppy disk
? COMPUTER: IBM PC
? OPERATING SYSTEM: PC-DOS/MS-DOS
? SOFTWARE: PatentIn Release #1, Version #1.30
? CURRENT APPLICATION DATA:
? APPLICATION NUMBER: PCT/US95/06530
? FILING DATE:
? CLASSIFICATION:
? PRIOR APPLICATION DATA:
? APPLICATION NUMBER: US 08/308,881
? FILING DATE: 09-SEP-1994
? APPLICATION NUMBER: US 08/249,553
? FILING DATE: 26-MAY-1994
? ATTORNEY/AGENT INFORMATION:
? NAME: Anderson, Kathryn A.
? REGISTRATION NUMBER: 32,172
? REFERENCE/DOCKET NUMBER: 2614-WO
? TELECOMMUNICATION INFORMATION:
? TELEPHONE: (206) 587-0430
? TELEFAX: (206) 233-0644
? TELEX: 756822
? INFORMATION FOR SEQ ID NO: 1:
? SEQUENCE CHARACTERISTICS:
? LENGTH: 2369 base pairs
? TYPE: nucleic acid
? STRANDEDNESS: single
? TOPOLOGY: linear
? MOLECULE TYPE: cDNA to mRNA
? HYPOTHEICAL: NO
? ANTI-SENSE: NO
? FRAGMENT TYPE: N-terminal
? ORIGINAL SOURCE:
? TISSUE TYPE: human placenta
? IMMEDIATE SOURCE:
? CLONE: B10G/pDC303
? FEATURE:
? NAME/KEY: CDS
? LOCATION: 244..2369
? FEATURE:
? NAME/KEY: mat_peptide
? LOCATION: 310..2369
? FEATURE:
? NAME/KEY: sig_peptide
? LOCATION: 244..309
PCT-US95-06530-1
Alignment Scores:
Pred. No.: 1,23e-21 Length: 2369
Score: 262.50 Matches: 65
Percent Similarity: 51.85% Conservative: 47
Best Local Similarity: 30.09% Mismatches: 75
Query Match: 19.33% Indels: 29
DB: 5 Gaps: 11
US-10-006-265-4 (1-252) x PCT-US95-06530-1 (1-2369)
QY ProAlaIySPProGIuaSnIISeScCyValTYrTYrTYrArgLyASnDeurhCYsrThr 54
||| |||||||:::||:::||::|||::|||::|||::|||::|||::|||::|||
Db CGAGAAAACCTAAATAATTGAATTCGACTGTGGAGCAGGGGAGAAGAAATGAGCTGTAG 678
55 TPeSerProGIlyLyeGIuThSeTyT---ThrgInTYrThVaLLys-----Arg 70
||| |||||||:::||:::||| | ||| ||| ||| ||| ||| ||| ||| |||
Db TGGAGTGCGTAGAAGGAAACAACACTTGAGACAAACTCACTTAATCTGATGGCGCA 738
71 ThTrYrAlaPhneGIyGLU-----LYshIsAp-----AsnCyrThrTrIRan 84
||| |||||||:::||:::||| | ||| ||| ||| ||| ||| ||| ||| |||
Db ACACACAGATTGCATGTGGACAAAGCAAACGTGACACCACCCACCATCATGCACTGTTGAT 798
739 ACACACAGATTGCATGTGGACAAAGCAAACGTGACACCACCCACCATCATGCACTGTTGAT 798

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Qy      85 SerSerThrSerGluAsnArgAlaSerCysSerPhePheLeuProArgIleThrIlePro 104
      |||
Db      799 TATTTCTACT-----GTTGATTTTGTG----- 819
Qy      105 AspAsnTyrThrIleGluValGluAlaGluAsnGlyAspGlyValIleLeuSer---His 123
      |||
Db      820 ---AACATTGAAGCTGGGTGAGAACAGAGATGCGCTTGGGAGAGTTACATCATGATCAT 876
Qy      124 MetThrTyrTrpArgLeuGluAsnIleAlaLeuThrGluProProGlyIlePheArgVal 143
      |||
Db      877 ATCAATTTTGATCCGTGATATTAAGTG---AAGCCCAATCCGCACTAATTTATTCAGTGG 933
Qy      144 LysProValLeuGlyIleLeuArgMetIleGlnIleGluTrpIleLeuProGluLeuAla 163
      |||
Db      934 ATCAACTGAGAGAACTGCTAGTATCTTAAATTTGACATGACCAACCAAGTATTAG 993
Qy      164 ProValSerSerAspLeuLeuTyrThrLeuArgPheArgThrValAsnSerThrSerTrp 183
      |||
Db      994 AGTGTATTATATA---CTAAATATATACATTCATATATAGACCAAGATGCGCTCAACTGG 1050
Qy      184 MetGluValAsnPheAlaLysAsnArgLysAspLysAsnGlnThrTyrAsnLeuThrGly 203
      |||
Db      1051 AGCCAGATTCTCT---CTGAAGACACACAGCATCCACCCGATCTTCACTGCTCCAGAC 1107
Qy      204 LeuGlnProPheThrGluTyrValIleAlaLeuArgCysAlaValIleGluSerLys--- 222
      |||
Db      1108 CTTAAACCTTTTACGATATATGTGTTAGCATTCCTCTATGAAAGAAAGTCTTAAGGA 1167
Qy      223 PheTyrSerAspTrpSerGlnGluLysMetGlyMetThrGluGlu 238
      |||
Db      1168 TACTGAGTACTGAGTGAAGAACCAAGTGGATCACTATGAAGAT 1215

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RESULT 11

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US-08-825-558-5
: Sequence 5, Application US/08825558
: Patent No. 5965724
: GENERAL INFORMATION:
: APPLICANT: SHARKEY, ANDREW
: APPLICANT: SMITH, STEPHEN K.
: APPLICANT: DELLOW, KIMBERLEY A.
: TITLE OF INVENTION: Gp 130 Lacking the Transmembrane Domain
: NUMBER OF SEQUENCES: 14
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: STERN, KESSLER, GOLDSTEIN & FOX
: STREET: 1100 NEW YORK AVENUE
: CITY: WASHINGTON
: STATE: DC
: COUNTRY: USA
: ZIP: 20005
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patentin Release #1.0, Version #1.30
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/825,558
: FILING DATE: 19-MAR-1997
: CLASSIFICATION: 536
: ATTORNEY/AGENT INFORMATION:
: NAME: ESMOND, ROBERT W.
: REGISTRATION NUMBER: 32,893
: REFERENCE/DOCKET NUMBER: 0623.0530001
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (202)371-2600
: TELEFAX: (202)371-2540
: INFORMATION FOR SEQ ID NO: 5:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 2754 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: both
: TOPOLOGY: linear
: MOLECULE TYPE: cDNA
: FEATURE:

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: NAME/KEY: CDS
: LOCATION: 1..2754
US-08-825-558-5
Alignment Scores:
Pred. No.: 1.56e-21 Length: 2754
Score: 262.50 Matches: 65
Percent Similarity: 51.85% Conserved: 47
Best Local Similarity: 30.09% Mismatches: 75
Query Match: 19.33% Indels: 29
Gaps: 11

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US-10-006-265-4 (1-252) x US-08-825-558-5 (1-2754)

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Qy      35 ProAlaLysProGluAsnIleSerCysValTyrTyrTrpArgLysAsnLeuThrCysThr 54
      |||
Db      376 CCAAAAAAAGCTTAAATTTGATTTGATTTGACAGAGGAGAAATGAGGTGAC 435
Qy      55 TrpSerProGlyLysGluThrSerTyr---ThrGlnTyrThrValLys-----Arg 70
      |||
Db      436 TGGGATGTGTGAAGGAAACACACTTGAGACCAACTTAAATCTGAATGGCA 495
Qy      71 ThrTyrAlaPheGlyGlu-----LysHisAsp-----AsnCysThrThrAsn 84
      |||
Db      496 ACACACAAGTTTGCTGATTCAGAACAAAGCAACCCGACCTCATGACGTTGAT 555
Qy      85 SerSerThrSerGluAsnArgAlaSerCysSerPhePheLeuProArgIleThrIlePro 104
      |||
Db      556 TATTTCTACT-----GTTGATTTTGTG----- 576
Qy      105 AspAsnTyrThrIleGluValGluAlaGluAsnGlyAspGlyValIleLeuSer---His 123
      |||
Db      577 ---AACATTGAAGCTGGGTGAGAACAGAGATGCGCTTGGGAGAGTTACATCATGATCAT 633
Qy      124 MetThrTyrTrpArgLeuGluAsnIleAlaLeuThrGluProProGlyIlePheArgVal 143
      |||
Db      634 ATCAATTTTGATCCGTGATATTAAGTG---AAGCCCAATCCGCACTAATTTATTCAGTG 690
Qy      144 LysProValLeuGlyIleLeuArgMetIleGlnIleGluTrpIleLeuProGluLeuAla 163
      |||
Db      691 ATCAACTGAGAGAACTGCTAGTATCTTAAATTTGACATGACCAACCAAGTATTAG 750
Qy      164 ProValSerSerAspLeuLysTyrThrLeuArgPheArgThrValAsnSerThrSerTrp 183
      |||
Db      751 AGTGTATTATATA---CTAAATATATACATTCATATATAGACCAAGATGCGCTCAACTGG 807
Qy      184 MetGluValAsnPheAlaLysAsnArgLysAspLysAsnGlnThrTyrAsnLeuThrGly 203
      |||
Db      808 AGCCAGATTCTCT---CTGAAGACACAGCATCCACCCGATCTTCACTGCTCCAGAC 864
Qy      204 LeuGlnProPheThrGluTyrValIleAlaLeuArgCysAlaValIleGluSerLys--- 222
      |||
Db      865 CTTAAACCTTTTACGATATATGTGTTAGGATTCGCTGATGAAAGAAAGTGTTAAGGA 924
Qy      223 PheTyrSerAspTrpSerGlnGluLysMetGlyMetThrGluGlu 238
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Db      925 TACTGAGTACTGAGTGAAGAACCAAGTGGATCACTATGAAGAT 972

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RESULT 12

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US-09-312-611-5
: Sequence 5, Application US/09312611
: Patent No. 6380160
: GENERAL INFORMATION:
: APPLICANT: SHARKEY, ANDREW
: APPLICANT: SMITH, STEPHEN K.
: APPLICANT: DELLOW, KIMBERLEY A.
: TITLE OF INVENTION: Gp130 Lacking the Transmembrane Domain
: NUMBER OF SEQUENCES: 14
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: STERN, KESSLER, GOLDSTEIN & FOX
: STREET: 1100 NEW YORK AVENUE
: CITY: WASHINGTON
: STATE: DC

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Db 751 ACACACAGTTTGTGATTGCAAAAGCAACCCGACCTCATGACTGTGAT 810
Qy 85 SerSerThrSerGluAsnArgAlaSerCysSerPhePheLeuProArgIleThrIlePro 104
Db 811 TATCTTACT-----GTGATTTTGTGTC----- 831
Qy 105 AspAsnTyrThrIleGluValGluAlaGluAsnGlyAspGlyValIleLeuSer---His 123
Db 832 ---AACATTGAAGTCTGGGTAGACAGAGATGCCCTTGGAGAGTTACATCAGATCAT 888
Qy 124 MetThrTyrTrpArgLeuGluAsnIleAlaIleValThrGluProProIleValIlePheArgVal 143
Db 889 ATCAATTGATCCCTGATATTAAGTG---AAGCCCAATCCGCCCATATTATTCAGTG 945
Qy 144 LysProValIleGluIleLeuValArgMetIleGlnIleGluTrpIleLeuProGluLeuAla 163
Db 946 ATCAACTGAGAGAACTGTCTAGTATCTTAAATATGACATGACCAACCAAGTATTAG 1005
Qy 164 ProValSerSerAspLeuIleTyrThrLeuArgPheArgThrValAsnSerThrSerTrp 183
Db 1006 AGTGTTATATA---CTAAATATATACATTCATATAGACCAAGATGCCCTCAACTGG 1062
Qy 184 MetGluValAsnPheAlaIleValAsnArgIleValAspIleValAsnGlnThrTyrAsnLeuThrGly 203
Db 1063 AGCCAGATTCT---CTGAAGACACAGCATCCCGCATCTTCACTGCTCCAGAC 1119
Qy 204 LeuGlnProPheThrGluTyrValIleAlaLeuAlaGlyGlyAlaValIleGluSerIle--- 222
Db 1120 CTTAAACCTTTTACGAATATGTGTAGGATTCCTGTATGAGAAAGATGTGAAGGA 1179
Qy 223 PheTrpSerAspTrpSerGlnGluIleValMetGlyMetThrGluGlu 238
Db 1180 TACTGAGTGACTGAGTGAAGCAAGTGGATCCTATGAAGAT 1227

RESULT 14
; Sequence 4, Application US/09439856
; Patent No. 6410009
; GENERAL INFORMATION:
; APPLICANT: Galun, Ethan
; APPLICANT: Nahot, Orit
; APPLICANT: Blum, Herbert E.
; TITLE OF INVENTION: A Pharmaceutical Composition for Treating
; TITLE OF INVENTION: Hepatitis B Virus (HBV) Infection
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Davidson, Davidson and Kappel, LLC
; STREET: 1140 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: MS-DOS EDITOR
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/439, 856
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/795,473
; FILING DATE: 11-FEB-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Davidson, Clifford M.
; REGISTRATION NUMBER: 32,728
; REFERENCE/DOCKET NUMBER: 963,1007
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212)-997-1028
; TELEFAX: (212)-997-1037
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:

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; LENGTH: 3085 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: unknown
; US-09-439-856-4

Alignment Scores:
Pred. No.: 1,87e-21 Length: 3085
Score: 262.50 Matches: 65
Percent Similarity: 51.85% Conservative: 47
Best Local Similarity: 30.09% Mismatches: 75
Query Match: 19.33% Indels: 29
DB: 3 Gaps: 11

US-10-006-265-4 (1-252) x US-09-439-856-4 (1-3085)
Qy 35 ProValSerProGluAsnIleSerCysValTyrTyrArgIleValAsnLeuThrCysThr 54
Db 631 CGAGAAAACCTAAATAATTTGATGATTTGATGAGACGAGGAGAAATAAGAGTGAG 690
Qy 55 TrpSerProGlyIleGluThrSerTyr---ThrGlnTyrThrValIle---Arg 70
Db 691 TGGGATGGTGGAGAGGAAACACTTGGAGACAACTTCACTTAAATCTGAATGGGCA 750
Qy 71 ThrTyrAlaPheGlyGlu-----LysHisAsp-----AsnCysThrThrAsn 84
Db 751 ACACACAGTTTGTGATTGCAAAAGCAACCCGACCTCATGACTGTGAT 810
Qy 85 SerSerThrSerGluAsnArgAlaSerCysSerPhePheLeuProArgIleThrIlePro 104
Db 811 TATCTTACT-----GTGATTTTGTGTC----- 831
Qy 105 AspAsnTyrThrIleGluValGluAlaGluAsnGlyAspGlyValIleLeuSer---His 123
Db 832 ---AACATTGAAGTCTGGGTAGACAGAGATGCCCTTGGAGAGTTACATCAGATCAT 888
Qy 124 MetThrTyrTrpArgLeuGluAsnIleAlaIleValThrGluProProIleValIlePheArgVal 143
Db 889 ATCAATTGATCCCTGATATTAAGTG---AAGCCCAATCCGCCCATATTATTCAGTG 945
Qy 144 LysProValIleGluIleLeuValArgMetIleGlnIleGluTrpIleLeuProGluLeuAla 163
Db 946 ATCAACTGAGAGAACTGTCTAGTATCTTAAATATGACATGACCAACCAAGTATTAG 1005
Qy 164 ProValSerSerAspLeuIleTyrThrLeuArgPheArgThrValAsnSerThrSerTrp 183
Db 1006 AGTGTTATATA---CTAAATATATACATTCATATAGACCAAGATGCCCTCAACTGG 1062
Qy 184 MetGluValAsnPheAlaIleValAsnArgIleValAspIleValAsnGlnThrTyrAsnLeuThrGly 203
Db 1063 AGCCAGATTCT---CTGAAGACACAGCATCCCGCATCTTCACTGCTCCAGAC 1119
Qy 204 LeuGlnProPheThrGluTyrValIleAlaLeuAlaGlyGlyAlaValIleGluSerIle--- 222
Db 1120 CTTAAACCTTTTACGAATATGTGTAGGATTCCTGTATGAGAAAGATGTGAAGGA 1179
Qy 223 PheTrpSerAspTrpSerGlnGluIleValMetGlyMetThrGluGlu 238
Db 1180 TACTGAGTGACTGAGTGAAGCAAGTGGATCCTATGAAGAT 1227

RESULT 15
US-09-023-655-1131
; Sequence 1131, Application US/09023655
; Patent No. 6607879
; GENERAL INFORMATION:
; APPLICANT: Cocks, Benjamin G.
; APPLICANT: Susan G. Stuart
; APPLICANT: Jeffrey J. Seilhamer
; TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF BLOOD CELL GENE
; TITLE OF INVENTION: EXPRESSION
; NUMBER OF SEQUENCES: 1508
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: INCYTE PHARMACEUTICALS, INC.

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/ STREET: 3174 PORTER DRIVE
/ CITY: PALO ALTO
/ STATE: CALIFORNIA
/ COUNTRY: USA
/ ZIP: 94304
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/09/023,655
/ FILING DATE: HEREWITH
/ CLASSIFICATION:
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER:
/ FILING DATE:
/ CLASSIFICATION:
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Zeller, Karen J.
/ REGISTRATION NUMBER: 37,071
/ REFERENCE/DOCKET NUMBER: PA-0001 US
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (650) 855-0555
/ TELEFAX: (650) 845-4166
/ INFORMATION FOR SEQ ID NO: 1131:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 3085 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ IMMEDIATE SOURCE:
/ LIBRARY: GENBANK
/ CLONE: g186353
/ US-09-023-655-1131

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Alignment Scores:
Pred. No.: 1.87e-21 Length: 3085
Score: 262.50 Matches: 65
Percent Similarity: 51.85% Conservative: 47
Best Local Similarity: 30.09% Mismatches: 75
Query Match: 19.33% Indels: 29
DB: Gaps: 11

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US-10-006-265-4 (1-252) x US-09-023-655-1131 (1-3085)

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QY 35 ProAlaLysProGluAsnIleSerCysValTyrTyrArgLysAsnLeuThrCysThr 54
DB 631 CCAGAAAACCTTAAATTTGAGTTCATGTGACACGAGGGAAGAAATGAGTGTGAG 690
QY 55 TrpSerProGluLysGluThrSerTyr---ThrGlnTyrThrValLys-----Arg 70
DB 691 TGGGATGGTGGAGGAAACACCTTGAGACAACTTCACCTTAAATCTGAATGGCA 750
QY 71 ThrTyrAlaPheGluGlu-----LysHisAsp-----AsnCysThrThrAsn 84
DB 751 ACAACACAGTTTCTGATTCGAAGCAAAACGACACCCCACTCATGCTGTTGAT 810
QY 85 SerSerThrSerGluAsnArgAlaSerCysSerPhePheLeuProArgIleThrIlePro 104
DB 811 TATTTACT-----GTGATTTGTC----- 831
QY 105 AspAsnTyrThrIleGluValGluAlaGluAsnGlyAspGlyValIleLysSer---His 123
DB 832 ---AACATTGAAGTCTGGGAGAGAGAGATGCCCTTGGGAAGTTACATCAGATCAT 888
QY 124 MetThrTyrTrpArgLeuGluAsnIleAlaLysThrGluProProLysIlePheArgVal 143
DB 889 ATCAATTTTATCTCTGATATTAAGTG---AAGCCCAATCCGCCACATATTTATCAGTG 945
QY 144 LysProValLeuGlyIleLysArgMetIleGlnIleGluTrpIleLysProGluLeuAla 163
DB 946 ATCAACTCAGAGAACTGCTAGATCTTAAATTTGACATGACCAACCAAGTATTAAG 1005

```

```

QY 164 ProValSerSerAspLeuLysTyrThrLeuArgPheArgThrValAsnSerThrSerTrp 183
DB 1006 AGTGTTATATAA---CTAAATATTAACATTCATATATAGACCAAGATGCCCACTTG 1062
QY 184 MetGluValAsnPheAlaLysAsnArgLysAspLysAsnGlnThrTyrAsnLeuThrGly 203
DB 1063 AGCCAGATTCCCT---CTGAAAGACACAGCATCCACCCGATCTTCATTCCTGCCAAGAC 1119
QY 204 LeuGlnProPheThrGluTyrValIleAlaLeuArgCysAlaValLysGluSerLys--- 222
DB 1120 CTAAACCTTTTACAGAAATATGTGTTAGGATTCGCTGATATGAAGAGATGTATAGGGA 1179
QY 223 PheTrpSerAspTrpSerGlnGluLysMetGlyMetThrGluGluGlu 238
DB 1180 TACTGAGTGACTGGAGTGAAGACCAAGTGGGATCACCATTAGAAAT 1227

```

Search completed: February 23, 2005, 19:36:05
Job time : 126.023 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: February 23, 2005, 09:15:27 ; Search time 392.322 Seconds
(without alignments)
3796.488 Million cell updates/sec

Title: US-10-006-265-4

Perfect score: 1358
Sequence: 1 MKLSPQPSCVNLGMWMTMAL.....GMEEBEGLPAIVLSTIV 252

Scoring table:
BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Zgapop 6.0 , Zgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 538458 seqs, 2955248155 residues

Total number of hits satisfying chosen parameters: 10768316

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:
-MODEL=frame+_p2n.model -DEV=xlh
-Q=/cgn2_1/USPRO.spool/US10006265/runat.18022005.094659.22236/app.query.fasta_1.2069
-DB=Published Applications NA -OPT=fastlap -SUFFIX=rnpb -MINMATCH=0.1
-LOOPCL=0 -LOOEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62
-TRANS=human40.cdi -LIST=45 -DOALIGN=200 -THR_SCORE=pct -THR_MAX=100
-THR_MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=pct -NORM=ext -HEAPSIZE=500 -MINLEN=0
-MAXLEN=2000000000 -USER=US10006265@cgn1.1.1175 @runat.18022005.094659.22236
-NCPU=6 -ICPU=3 -NO_WMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSELOCK=100
-LONGLOG -DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5
-FGAPOP=6 -FGAREXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

Published Applications NA:*

- 1: /cgn2_6/ptodata/1/pubpna/US07_PUBCOMB.seq:*
- 2: /cgn2_6/ptodata/1/pubpna/PCT_NEW_PUB.seq:*
- 3: /cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq:*
- 4: /cgn2_6/ptodata/1/pubpna/US06_PUBCOMB.seq:*
- 5: /cgn2_6/ptodata/1/pubpna/US07_NEW_PUB.seq:*
- 6: /cgn2_6/ptodata/1/pubpna/PCTUS_PUBCOMB.seq:*
- 7: /cgn2_6/ptodata/1/pubpna/US08_NEW_PUB.seq:*
- 8: /cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq:*
- 9: /cgn2_6/ptodata/1/pubpna/US09_PUBCOMB.seq:*
- 10: /cgn2_6/ptodata/1/pubpna/US09_PUBCOMB.seq:*
- 11: /cgn2_6/ptodata/1/pubpna/US09C_PUBCOMB.seq:*
- 12: /cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq:*
- 13: /cgn2_6/ptodata/1/pubpna/US10_PUBCOMB.seq:*
- 14: /cgn2_6/ptodata/1/pubpna/US10_PUBCOMB.seq:*
- 15: /cgn2_6/ptodata/1/pubpna/US10C_PUBCOMB.seq:*
- 16: /cgn2_6/ptodata/1/pubpna/US10C_PUBCOMB.seq:*
- 17: /cgn2_6/ptodata/1/pubpna/US10E_PUBCOMB.seq:*
- 18: /cgn2_6/ptodata/1/pubpna/US10F_PUBCOMB.seq:*
- 19: /cgn2_6/ptodata/1/pubpna/US10F_NEW_PUB.seq:*
- 20: /cgn2_6/ptodata/1/pubpna/US11_NEW_PUB.seq:*
- 21: /cgn2_6/ptodata/1/pubpna/US11_NEW_PUB.seq:*
- 22: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1358	100.0	2440	15 US-10-006-265-3	Sequence 3, Appl1
2	1343	98.9	1476	10 US-09-892-949-21	Sequence 21, Appl
3	1343	98.9	1476	17 US-10-351-157-114	Sequence 11, Appl
4	1343	98.9	1476	18 US-10-772-531-21	Sequence 21, Appl
5	1292	95.1	2119	15 US-10-006-265-16	Sequence 16, Appl
6	1292	95.1	2238	10 US-09-892-949-5	Sequence 5, Appl1
7	1292	95.1	2238	18 US-10-715-667-5	Sequence 5, Appl1
8	1292	95.1	2295	10 US-09-892-949-68	Sequence 68, Appl
9	1292	95.1	2295	17 US-10-351-157-38	Sequence 38, Appl
10	1292	95.1	2295	17 US-10-352-554-38	Sequence 38, Appl
11	1292	95.1	2295	18 US-10-772-531-68	Sequence 68, Appl
12	1292	95.1	2480	10 US-09-892-949-3	Sequence 3, Appl1
13	1292	95.1	2480	18 US-10-715-667-3	Sequence 3, Appl1
14	1292	95.1	2903	10 US-09-892-949-53	Sequence 53, Appl
15	1292	95.1	2903	17 US-10-351-157-4	Sequence 4, Appl1
16	1292	95.1	2903	17 US-10-352-554-4	Sequence 4, Appl1
17	1292	95.1	2903	18 US-10-772-531-53	Sequence 53, Appl
18	1292	95.1	2969	15 US-10-006-265-1	Sequence 1, Appl1
19	1282	94.4	1299	10 US-09-892-949-17	Sequence 17, Appl
20	1282	94.4	1299	17 US-10-351-157-112	Sequence 112, Appl
21	1282	94.4	1299	18 US-10-772-531-17	Sequence 17, Appl
22	1282	94.4	2402	10 US-09-892-949-1	Sequence 1, Appl1
23	1282	94.4	2402	17 US-10-351-157-110	Sequence 110, Appl
24	1282	94.4	2402	18 US-10-772-531-1	Sequence 1, Appl1
25	1282	94.4	2445	14 US-10-227-884-91	Sequence 91, Appl
26	1282	94.4	2445	14 US-10-330-163-91	Sequence 91, Appl
27	1282	94.4	2445	14 US-10-230-338-91	Sequence 91, Appl
28	1282	94.4	2445	14 US-10-218-631-91	Sequence 91, Appl
29	1282	94.4	2445	14 US-10-230-414-91	Sequence 91, Appl
30	1282	94.4	2445	14 US-10-232-224-91	Sequence 91, Appl
31	1282	94.4	2445	14 US-10-216-1594-91	Sequence 91, Appl
32	1282	94.4	2445	14 US-10-218-849-91	Sequence 91, Appl
33	1282	94.4	2445	14 US-10-227-873-91	Sequence 91, Appl
34	1282	94.4	2445	14 US-10-227-883-91	Sequence 91, Appl
35	1282	94.4	2445	14 US-10-219-076-91	Sequence 91, Appl
36	1282	94.4	2445	14 US-10-230-434-91	Sequence 91, Appl
37	1282	94.4	2445	14 US-10-219-003-91	Sequence 91, Appl
38	1282	94.4	2445	14 US-10-219-075-91	Sequence 91, Appl
39	1282	94.4	2445	14 US-10-219-464-91	Sequence 91, Appl
40	1282	94.4	2445	14 US-10-219-466-91	Sequence 91, Appl
41	1282	94.4	2445	14 US-10-219-479-91	Sequence 91, Appl
42	1282	94.4	2445	14 US-10-219-481-91	Sequence 91, Appl
43	1282	94.4	2445	14 US-10-230-260-91	Sequence 91, Appl
44	1282	94.4	2445	14 US-10-232-231-91	Sequence 91, Appl
45	1282	94.4	2445	14 US-10-232-233-91	Sequence 91, Appl

ALIGNMENTS

RESULT 1
US-10-006-265-3
Sequence 3, Application US/10006265
Publication No. US20030125520A1
GENERAL INFORMATION:
APPLICANT: Maeda, Masateugu
TITLE OF INVENTION: NOVEL HEMOPHILIN RECEPTOR PROTEIN, NR10
FILE REFERENCE: 06501-096001
CURRENT APPLICATION NUMBER: US/10/006.265
CURRENT FILING DATE: 2003-01-06
PRIOR APPLICATION NUMBER: PCT/JP00/03556
PRIOR FILING DATE: 2000-06-01
PRIOR APPLICATION NUMBER: JP 11/155797
PRIOR FILING DATE: 1999-06-02
PRIOR APPLICATION NUMBER: JP 11/217797
PRIOR FILING DATE: 1999-07-30
NUMBER OF SEQ ID NOS: 40
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 3

/ LENGTH: 2440
 / TYPE: DNA
 / ORGANISM: Homo sapiens
 / FEATURE:
 / NAME/KEY: CDS
 / LOCATION: (523)...(1278)
 / US-10-006-265-3

Alignment Scores:

Pred. No.:	135e-161	Length:	2440
Score:	1358.00	Matches:	252
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	15	Gaps:	0

US-10-006-265-4 (1-252) x US-10-006-265-3 (1-2440)

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QY 1 MetlyseuSerProGlnProSerCysValasnleuGlyMetMetTrpThrTrpAlaLeu 20
DB 523 ATGAAGCTCTCTCCAGCCTTCATGTGTAACTGGGGATGATGTGACCTGGCAGCTG 582
QY 21 TrpMetLeuProSerLeuGlySlysPheSerleuAlaAlaLeuProAlaLysProGluasn 40
DB 583 TGGATGCTCCCTCCACTGCAAAATTCAGCTGGCAGCTCTGCCACTAAGCTGAGAAC 642
QY 41 lIeSerCysValTyrTyrTyrArgLysAsnLeuThrCysThrTrpSerProGlyLysGlu 60
DB 643 ATTTCTGTGTCTACTACTATAGAAAAATTTTAACTGCACTTGGAGTCCAGAAAGAA 702
QY 61 ThrSerTyrTrgIntTyrThrValLysArgThrTyrAlaPheGlyLysLysAspAsn 80
DB 703 ACCAGTTATACCCAGTACACAGATTAGAGAACTTACGCTTGGAGAAAAACATGATTAAT 762
QY 81 CysThrThrAsnSerSerThrSerGluAsnArgAlaSerCysSerPhePheLeuProArg 100
DB 763 TGTACACCAAAATGTTCTACAAAGTAAATCGGCTTCGCTTTTCTTCCCAAGA 822
QY 101 lIeThrIleProAspAsnTyrThrIleGluValGluAlaGluAsnGlyAspGlyValIle 120
DB 823 ATACACATCCCAATTAATTTACCATTTGAGCTGAAAGCTGAAATGAGATGTGTAAAT 882
QY 121 LysSerHisMetThrTyrTrpArgLysGluAsnIleAlaLysThrGluProLysIle 140
DB 883 AAATCTCATATGACATATCGAGATTAGAGAACATAGCGAAACTGAAACCACTTAAGATT 942
QY 141 PheArgValLysProValLeuGlyIleLysArgMetIleGlnIleGluTrpIleLysPro 160
DB 943 TTCGGTGTAAACCAAGTTTGGGCATCAACGAATGATTCMAATGATGATGATMAAGCCT 1002
QY 161 GluLeuAlaProValSerSerAspLeuLysTyrThrLeuArgPheArgThrValAsnSer 180
DB 1003 GAGTTGGCCCTTTTCATCTCTGATTTAAATACACCTTCGATTCCAGACAGTCAACAGT 1062
QY 181 ThrSerTrpMetGluValAsnPheAlaLysAsnArgLysAspLysAsnGlnThrTyrAsn 200
DB 1063 ACCAGCTGATGAGTCAACCTTCGCTAAGAACGTAAGATTAATAAACCAACGTAACAG 1122
QY 201 LeuThrGlyLeuGlnProPheThrGluTyrValIleAlaLeuArgCysAlaValLysGlu 220
DB 1123 CTCACGCGGGCTGAGCCTTTTACAGAAATGTCTATGCTCTCGAGTGTGGCGTCAAGGAG 1182
QY 221 SerLysPheTrpSerAspTrpSerGlnGluLysMetGlyMetThrGluGluGluGlyLys 240
DB 1183 TCAAAGTTCTGGAGTGACTGAGACCAAGAAAAATGGAAATGACTGAAGAGAGGCGAAG 1242
QY 241 LeuLeuProAlaIleProValLeuSerThrLeuVal 252
DB 1243 CTACTCCCTGCGATTCCCGTCTGTACTCTGTG 1278

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RESULT 2
 US-09-892-949-21
 / Sequence 21, Application US/09892949

/ Publication No. US20030096339A1
 / GENERAL INFORMATION:
 / APPLICANT: Sprecher, Cindy A.
 / APPLICANT: Presnell, Scott R.
 / APPLICANT: Gao, Zeren
 / APPLICANT: Whitmore, Theodore E.
 / APPLICANT: Kuiper, Joseph L.
 / APPLICANT: Maurer, Mark F.
 / TITLE OF INVENTION: CYTOKINE RECEPTOR ZCYTOR17
 / FILE REFERENCE: 00-42
 / CURRENT APPLICATION NUMBER: US/09/892,949
 / CURRENT FILING DATE: 2001-06-26
 / PRIOR APPLICATION NUMBER: US 60/214,282
 / PRIOR FILING DATE: 2000-06-26
 / PRIOR APPLICATION NUMBER: US 60/214,955
 / PRIOR FILING DATE: 2000-06-29
 / PRIOR APPLICATION NUMBER: US 60/267,963
 / PRIOR FILING DATE: 2001-08-02
 / NUMBER OF SEQ ID NOS: 93
 / SOFTWARE: FastSeq for Windows Version 3.0
 / SEQ ID NO 21
 / LENGTH: 1476
 / TYPE: DNA
 / ORGANISM: Homo sapiens
 / FEATURE:
 / NAME/KEY: CDS
 / LOCATION: (162)...(878)
 / US-09-892-949-21

Alignment Scores:

Pred. No.:	5.02e-160	Length:	1476
Score:	1343.00	Matches:	249
Percent Similarity:	99.60%	Conservative:	0
Best Local Similarity:	99.60%	Mismatches:	1
Query Match:	98.90%	Indels:	0
DB:	10	Gaps:	0

US-10-006-265-4 (1-252) x US-09-892-949-21 (1-1476)

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QY 3 LeuSerProGlnProSerCysValasnleuGlyMetMetTrpThrTrpAlaLeuTrpMet 22
DB 129 CTCCTCCCGACCTTCATGTGTAACTGGGATGATGAGAACCTGGCAGCTGTGGATG 188
QY 23 LeuProSerLeuGlySlysPheSerleuAlaAlaLeuProAlaLysProGluAsnIleSer 42
DB 189 CTCCTCTACTGCAAAATTCAGCTGCGAGCTCTGCCAGCTAAGCTGAGAACATTTCC 248
QY 43 CysValTyrTyrTyrArgLysAsnLeuThrCysThrTrpSerProGlyLysGluThrSer 62
DB 249 TGTGTCTACTACTATAGAAAAATTTTAACTGCACTTGGAGTCCAGAAAGAAACCAAGT 308
QY 63 TyrThrGlnTyrThrValLysArgThrTyrAlaPheGlyLysLysAspAsnCysThr 82
DB 309 TATACCACTACACAGTTAAGAACTTACGCTTTTGGAGAAAAACATGATTAATGTACA 368
QY 83 ThrAsnSerSerThrSerGluAsnArgAlaSerCysSerPhePheLeuProArgIleThr 102
DB 369 ACCAATAGTCTTCAAGTAATAAATCGTCTGTCTCTTTTCTTCCAGAAATTAAG 428
QY 103 lIeProAspAsnTyrThrIleGluValGluAlaGluAsnGlyAspGlyValIleLysSer 122
DB 429 ATCCAGATAATTAATACATGAGTGGAACTGAAATGAGAGATGTAATTAATCT 488
QY 123 HisMetThrTyrTrpArgLysGluAsnIleAlaLysThrGluProProLysIlePheArg 142
DB 489 CATATGACATCTACTGAGATTAGAGAACATAGGAAAACTGAACCACTTAAGATTTTCCGT 548
QY 143 ValLysProValLeuGlyIleLysArgMetIleGlnIleGluTrpIleLysProGluLeu 162
DB 549 GTGAACCAAGTTTGGGATTCAAACGATGATTCAAATTTGAATGATTAAGCTGAGTTG 608
QY 163 AlaProValSerSerAspLeuLysTyrThrLeuArgPheArgThrValAsnSerThrSer 182

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Dh 609 GCGCGTGTTCATCTGATTTAAATAACACACTTCGATTGAGACAGTCAAGTACAGC 668
Qy 183 TTPMETGLUVALAENPHEALALYASNAARGLYSAPLYSANGINTHTYRASNLEUTHR 202
Dh 669 TGGATGGAAGTCACATTGGCTTAAAGACGTAAAGGATTAACAAACCTACCAACTCAGC 728
Qy 203 GLYLEUGINPPOPHETHRGUITYRVALILEALALEUAQCYSAALAVALLYGILUSERLYS 222
Dh 729 GGGCTGCAGCCCTTTTACGAATAATATCTCATAGCTCTGCATGTGCGGTCAAGAGTCAAG 788
Qy 223 PHEITPSEASPTPSPERGINGULYMERGLYMERHGIUGIUGIUGIULYSLLEU 242
Dh 789 TTCTGGAGTGACTGGAGCCAAAGAAAATGGGAATGACTGAGAGAAAGGCAAGTACTC 848
Qy 243 PROALALEPROVALLEUSERTHIRLEUVAL 252
Dh 849 CCTGCGATTCCCGTCTGCTGCTGTG 878

RESULT 3
US-10-351-157-114
; Sequence 114, Application US/10351157
; Publication No. US20030215838A1
; GENERAL INFORMATION:
; APPLICANT: Gao, Zeren
; APPLICANT: Sprecher, Cindy A.
; APPLICANT: Kujiper, Joseph L.
; APPLICANT: Dasovich, Maria M.
; APPLICANT: Grant, Francis J.
; APPLICANT: Presnell, Scott R.
; APPLICANT: Whitmore, Theodore E.
; APPLICANT: Hammond, Angela K.
; APPLICANT: No. US20030215838A1ak, Julia E.
; APPLICANT: Gross, Jane A.
; APPLICANT: Dillon, Stacey R.
; TITLE OF INVENTION: CYTOKINE RECEPTOR ZCYTOR17 MULTIMERS
; FILE REFERENCE: 02-02
; CURRENT APPLICATION NUMBER: US/10/351,157
; CURRENT FILING DATE: 2003-01-21
; PRIOR APPLICATION NUMBER: US 60/435,361
; PRIOR FILING DATE: 2002-12-19
; PRIOR APPLICATION NUMBER: US 60/389,108
; PRIOR FILING DATE: 2002-06-14
; PRIOR APPLICATION NUMBER: US 60/350,325
; PRIOR FILING DATE: 2002-01-18
; NUMBER OF SEQ ID NOS: 183
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 114
; LENGTH: 1476
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (162)...(878)
US-10-351-157-114

Alignment Scores:
Pred. No.: 5.02e-160 Length: 1476
Score: 1343.00 Matches: 249
Percent Similarity: 99.60% Conservative: 0
Best Local Similarity: 99.60% Mismatches: 1
Query Match: 98.90% Indels: 0
DB: 17 Gaps: 0

US-10-006-265-4 (1-252) x US-10-351-157-114 (1-1476)
Qy 3 LEUSERPROGINPPOSERCYSAVALASNLUGLYMERMETTPHRTTPALALEUTHR 22
Dh 129 CTCTCTCCCGAGCTTTCATGTGTTAACCTGGGAGTGAATGAGACCTGGGCACTGTGATG 188
Qy 23 LEUPROSERLEUCYLYSPHESEITLEUALAILEUPROVALYSPROGILASNLISER 42
Dh 189 CTCCCTCACTCTCAATTAATTCAGCCTGGCAGCTCTGCGCAGCTTAAGCTGAGACATTTCC 248
```

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Qy 43 CYSAVALTYRTYRTRYARGLYASNLLEUTHRCYSTRHTPSPERPROGILYVGLUTHSER 62
Dh 249 TGTGTCTACTCTATAGGAAAAATTTAACTTGCACTTGGAATCCAGGAAAGAAACCACT 308
Qy 63 TYRTHRGINTYRTHRVALYASRGTHRTRYALAEHGLYGLYULYSHIASPASNQYSTR 82
Dh 309 TATACCCAGTACACAGTTAAGAGAACTTACGCTTTTGGAGAAAAATGATTAATGTGACA 368
Qy 83 THRANSESEITPSPERGILUASNAARGALASERCYSESPHEPHELEUPROVALILETHR 102
Dh 369 ACCAATGTTCTTACAGGAAAAATCGCTTCGCTCTTTTCTTCCTCCAAAGATACG 428
Qy 103 ILEPROSPAENYTYRTHRIEGLUVALIGLULASNGILYASPGILYVALILEYSSER 122
Dh 429 ATCCAGATTAATTAACATTGAGGTGAGACCTGAAAATGGAGATGTTAATTAATCT 488
Qy 123 HISMETHTYRTRYPARGLEUGLUASNLLEALYSTRHGIUPROPROLYSILEPHEARG 142
Dh 489 CATATGACATACCTGAGATTAGAGACATAGCGAAAATGAAACCACTAAGATTTCCGT 548
Qy 143 VALYSPROVALILEUGLYILEYSPARGMETILEGINTLEGIUTPPIELYSPPROGILU 162
Dh 549 GTGAACCAAGTTTGGGCATCAACGAATGATTCMAATTGATGATTAACCTGAGTGG 608
Qy 163 ALAPROVALSEISERAPLEULYSTRTRYRTHLEUARPHEARGTTRVALASNSEITPSPER 182
Dh 609 GCGCTGTTCATCTGATTTAAATAACACACTTGATTCAGGACAGTCAACAGTACAGC 668
Qy 183 TTPMETGLUVALAENPHEALALYASNAARGLYSAPLYSANGINTHTYRASNLEUTHR 202
Dh 669 TGGATGGAAGTCACATTGGCTTAAAGACGTAAAGATTAACAAACCAAGTCAACTCAGC 728
Qy 203 GLYLEUGINPPOPHETHRGUITYRVALILEALALEUAQCYSAALAVALLYGILUSERLYS 222
Dh 729 GGGCTGCAGCCCTTTTACGAATAATATCTCATAGCTCTGCATGTGCGTCAAGAGTCAAG 788
Qy 223 PHEITPSEASPTPSPERGINGULYMERGLYMERHGIUGIUGIUGIULYSLLEU 242
Dh 789 TTCTGGAGTGACTGGAGCCAAAGAAAATGGGAATGACTGAGAGAAAGGCAAGTACTC 848
Qy 243 PROALALEPROVALLEUSERTHIRLEUVAL 252
Dh 849 CCTGCGATTCCCGTCTGCTGCTGTG 878

RESULT 4
US-10-772-531-21
; Sequence 21, Application US/10772531
; Publication No. US20040142422A1
; GENERAL INFORMATION:
; APPLICANT: Sprecher, Cindy A.
; APPLICANT: Gao, Zeren
; APPLICANT: Presnell, Scott R.
; APPLICANT: Whitmore, Theodore E.
; APPLICANT: Kujiper, Joseph L.
; APPLICANT: Maurer, Mark F.
; TITLE OF INVENTION: CYTOKINE RECEPTOR ZCYTOR17
; FILE REFERENCE: 00-42
; CURRENT APPLICATION NUMBER: US/10/772,531
; CURRENT FILING DATE: 2004-02-05
; PRIOR APPLICATION NUMBER: US/09/892,949
; PRIOR FILING DATE: 2001-06-26
; PRIOR APPLICATION NUMBER: US 60/214,282
; PRIOR FILING DATE: 2000-06-26
; PRIOR APPLICATION NUMBER: US 60/214,955
; PRIOR FILING DATE: 2000-06-29
; PRIOR APPLICATION NUMBER: US 60/267,963
; PRIOR FILING DATE: 2001-08-02
; NUMBER OF SEQ ID NOS: 93
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 21
; LENGTH: 1476
; TYPE: DNA
; ORGANISM: Homo sapiens
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FEATURE:
; NAME/KEY: CDS
; LOCATION: (162)... (878)
US-10-772-531-21

Alignment Scores:

Pred. No.:	Length:	Matches:	Conservative:	Mismatches:	Indels:	Gaps:
5, 02e-160	1476	249	0	1	0	0
Score: 1343.00						
Percent Similarity: 99.60%						
Best Local Similarity: 99.60%						
Query Match: 98.90%						

US-10-006-265-4 (1-252) x US-10-772-531-21 (1-1476)

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QY      3 LeuSerProGlnProSerCysValaenLeuGlyMetMetTrpThrTrpAlaLeuTrpMet 22
DB      129 CTCTCTCCCGAGCTTCATGTGTAACTCGGGGATGATGTGAAGCTGGGCACTGTGGATG 188
QY      23 LeuProSerLeuCysIysPheSerLeuAlaLeuProAlaIysProGlnIysPheSer 42
DB      189 CTCCCTCACTCGCAAAATTCAGCTCGGAGCTCTGCCAGCTAAGCTGAGAACATTTCC 248
QY      43 CysValTyTyTyTyTyTyTyTyTyTyTyTyTyTyTyTyTyTyTyTyTyTyTyTyTyTyTy 62
DB      249 TGTGTACTACTATATAGAAAATTTAACTGCACTTGAGATCGAGAAAAGAACAG 308
QY      63 TyTyThGlnTyTyThTyTyTyTyTyTyTyTyTyTyTyTyTyTyTyTyTyTyTyTyTyTyTy 82
DB      309 TATACCAGTACACAGTTAAAGAACTTACGCTTTGGAGAAAACATGATTAATTGTACA 368
QY      83 ThrAsnSerSerThSerGluAsnArgAlaSerCysSerPhePheLeuProAlaIleThr 102
DB      369 ACCAATAGTTCTCAAGTGAATTCGTGCTGCTCTTTTCTTCCCAAGAAATACG 428
QY      103 IleProAspAsnTyThrIleGluValGluIleGluAsnGlyAspGlyValIleYsSer 122
DB      429 ATCCAGATATATATACATTGAGTGAAGCTGAAAGTGAAGATGATGTGTAATTAATCT 488
QY      123 HisMetThrTyTyThTyTyTyTyTyTyTyTyTyTyTyTyTyTyTyTyTyTyTyTyTyTyTy 142
DB      489 CATATACATACACTGAGATTAGAAACATAGCGAAAAATGAAACCATTAAGATTTTCCGT 548
QY      143 ValIysProValLeuGlyIleYsArgMetIleGlnIleGluTrpIleYsProGluLeu 162
DB      549 GTBAACCAAGTTTGGGCAATCAACGATGATTCAAATGATGATGATGATGATGATGATGATG 608
QY      163 AlaProValSerSerAspLeuTyTyTyTyTyTyTyTyTyTyTyTyTyTyTyTyTyTyTyTy 182
DB      609 GCGCCTGTTTCATCTGATTTAAATACACACTTCGATTGAGACAGTCAACAGTACAGC 668
QY      183 TrpMetGluValAsnPheAlaIysAsnArgIysAspIysAsnGlnIleThrTyTyAsnLeuThr 202
DB      669 TGGATGAAAGTCACTTCGCTAGAAACCGTAAAGATTAACCAACGTAACCTCACG 728
QY      203 GlyLeuGlnProPheThrGluTyTyTyTyTyTyTyTyTyTyTyTyTyTyTyTyTyTyTyTy 222
DB      729 GGGCTGAGCTTTTACAGAAATATGTCATAGCTCTGCGATGTCGCTGCAAGGAGTCAAG 788
QY      223 PheTrpSerAspTrpSerGlnIleYsMetGlyMetThrGluGluGluGluGluGluGlu 242
DB      789 TTCTGAGGTGACTGAGAGCAAGAAAAATGGAATGACTGAGAGAAAGCAAGTACTC 848
QY      243 ProAlaIleProValLeuSerThrLeuVal 252
DB      849 CTTGCGATTCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 878

```

RESULT 5

US-10-006-265-16
; Sequence 16, Application US/10006265
; Publication No. US20030125520A1
; GENERAL INFORMATION:
; APPLICANT: Maeda, Masaatsu

APPLICANT: Yaguchi, No. US20030125520A1ko
; TITLE OF INVENTION: NOVEL HEMOPOIETIN RECEPTOR PROTEIN, NR10
; FILE REFERENCE: 06501-096001
; CURRENT APPLICATION NUMBER: US/10/006,265
; CURRENT FILING DATE: 2003-01-06
; PRIOR APPLICATION NUMBER: PCT/JP00/03556
; PRIOR FILING DATE: 2000-06-01
; PRIOR APPLICATION NUMBER: JP 11/155797
; PRIOR FILING DATE: 1999-06-02
; PRIOR APPLICATION NUMBER: JP 11/217797
; PRIOR FILING DATE: 1999-07-30
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 16
; LENGTH: 2119
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (11)... (1996)
US-10-006-265-16

Alignment Scores:

Pred. No.:	Length:	Matches:	Conservative:	Mismatches:	Indels:	Gaps:
2, 73e-153	2119	238	0	0	0	0
Score: 1292.00						
Percent Similarity: 100.00%						
Best Local Similarity: 100.00%						
Query Match: 95.14%						

US-10-006-265-4 (1-252) x US-10-006-265-16 (1-2119)

```

QY      1 MetIysLeuSerProGlnProSerCysValaenLeuGlyMetMetTrpThrTrpAlaLeu 20
DB      11 ATGAAGCTCTCTCCCGAGCTTCATGTGTAACTCGGGGATGATGTGAAGCTGGGCACTG 70
QY      21 TrpMetLeuProSerLeuCysIysPheSerLeuAlaLeuProAlaIysProGlnIysPhe 40
DB      71 TGGATGTCCTCCCTCACTCGCAAAATTCAGCTCGGAGCTCTGCCAGCTAAGCTGAGAAC 130
QY      41 IleSerCysValTyTyTyTyTyTyTyTyTyTyTyTyTyTyTyTyTyTyTyTyTyTyTyTyTy 60
DB      131 ATTTCTGTGTCTACTACTATAGAAAATTTAACTGCACTTGAGATGATGATGATGATGATG 190
QY      61 ThrSerTyThGlnTyTyThTyTyTyTyTyTyTyTyTyTyTyTyTyTyTyTyTyTyTyTyTyTy 80
DB      191 ACCAGTTATACCACTGACATCACTTAAGACACTTCGCTTTGGAGAAAACATGATTAAT 250
QY      81 CysThrThAsnSerSerThSerGluAsnArgAlaSerCysSerPhePheLeuProArg 100
DB      251 TGTACACCAATAGTTCTACAGTGAATTCGTGCTGCTCTTTTCTTCCAGAGA 310
QY      101 IleThrIleProAspAsnTyThrIleGluValGluIleGluAsnGlyAspGlyValIle 120
DB      311 ATTAAGATCCAGAAATATATACATTGAGTGAAGCTGAAAGTGAAGATGATGATGATGATG 370
QY      121 LysSerHisMetThrTyTyThTyTyTyTyTyTyTyTyTyTyTyTyTyTyTyTyTyTyTyTy 140
DB      371 AAATCTATATACATCACTGAGATTAGAAACATAGCAACCACTGAAACCTTAAGATT 430
QY      141 PheArgValIysProValLeuGlyIleYsArgMetIleGlnIleGluTrpIleYsPro 160
DB      431 TTCCGTGTAAACCAAGTTTGGGCAATCAACGATGATTCAAATGATGATGATGATGATGATG 490
QY      161 GluLeuAlaProValSerSerAspLeuTyTyTyTyTyTyTyTyTyTyTyTyTyTyTyTyTyTy 180
DB      491 GAGTTGGCCCTGTTTCATCTGATTTAAATACACACTTCGATTGAGACAGTCAACACT 550
QY      181 ThrSerTrpMetGluValAsnPheAlaIysAsnArgIysAspIysAsnGlnIleThrTyTyAs 200
DB      551 ACCAGCTGATGATGATCACTTCGCTAAAGCCGTAAAGATTAACCAACGTAACGTAACG 610
QY      201 LeuThrGlyLeuGlnProPheThrGluTyTyTyTyTyTyTyTyTyTyTyTyTyTyTyTyTyTy 220

```


Db	481	GAGTTGGGCGCCCTGTTTCATCTGATTTAAATACACCTTCGATTCAGGACAGTCACACAGT	540
Qy	181	ThrsEtrPmEgLuVaLaAnPheAlaYsAsnArgLyAspLyAsnGlnTrhYrAsn	200
Db	541	ACCACCTGGATGGAGTGAACCTTCGGTATGAAACCGTAAGATATAAAAACCAACGATCAAC	600
Qy	201	LeuthrGlyLeuGlnProPheThrGluTrValIleAlaLeuArgCysAlaValLyGlu	220
Db	601	CTCACGGGGCTGCACGCTTTTACAGATATGTGCATATGCTCTCGATGTCGGTCAAGAG	660
Qy	221	SerLySphEtrPmEgAspTrPserGngLysMetGlyMetThrGlnGluGlu	238
Db	661	TCAAAGTCTGGAGTGACTGGAGCCAGAAAAAATGGGAATGATGAGAGAGA	714
RESULT 7			
US-10-715-667-5			
; Sequence 5, Application US/10715667			
; Publication No. US20040152161A1			
; GENERAL INFORMATION:			
; APPLICANT: Immunex Corporation			
; APPLICANT: Cosman, David J.			
; APPLICANT: Mosley, Bruce A.			
; APPLICANT: Bird, Timothy A.			
; APPLICANT: Dubose, Robert F.			
; APPLICANT: Wiley, Steven R.			
; TITLE OF INVENTION: HEMATOPOIETIN RECEPTORS HPR1 AND HPR2			
; FILE REFERENCE: 3160-B			
; CURRENT APPLICATION NUMBER: US/10/715, 667			
; CURRENT FILING DATE: 2003-11-14			
; PRIOR APPLICATION NUMBER: US/09/572, 708			
; PRIOR FILING DATE: 2001-10-05			
; NUMBER OF SEQ ID NOS: 29			
; SOFTWARE: PatentIn version 3.1			
; SEQ ID NO 5			
; LENGTH: 2238			
; TYPE: DNA			
; ORGANISM: Homo sapiens			
US-10-715-667-5			
Alignment Scores:			
Pred. No.: 2,986-153 Length: 2238			
Score: 1292.00 Matches: 238			
Percent Similarity: 100.00% Conservative: 0			
Best local Similarity: 100.00% Mismatches: 0			
Query Match: 95.14% Indels: 0			
DB: 18 Gaps: 0			
US-10-006-265-4 (1-252) x US-10-715-667-5 (1-2238)			
Qy	1	MethylsLeuSerProGlnProSerCysValAsnLeuGlyMetMetTrhTrpAlaLeu	20
Db	1	ATGAGGCTCTCTCCCAAGCCTTCATGTGTAACTCGGGGATATGTGACCTGGGCACTG	60
Qy	21	TrpMetLeuProSerLeuCysLySphSerLeuAlaAlaLeuProAlaLySProGlnAsn	40
Db	61	TGGAGTCCCTTCACCTCGCAAAATTCAGCGCTGCGACGCTCTCCAGCTAAAGCTGAAC	120
Qy	41	ILeserCysVallyrTrYrTrYrArgLyAsnLeuThrCysEtrTrPserProGlyLyGlu	60
Db	121	ATTTCCTGTGTCTACTACTATAGAAAAATTTAACCTCGACCTTGAGTCCAGAAAGGAA	180
Qy	61	ThrsEtrYrThnGlnTrhValLySArgTrhTrpAlaPheGlyGlyLySArgAspAsn	80
Db	181	ACCGATTATCCCACTACACAGTTAAGAACTTACGCTTTTGGAGAAAAACGTGTAAT	240
Qy	81	CysEtrThrAsnSerSerThrSerGluAsnArgAlaSerCysSerPhePheLeuProArg	100
Db	241	TGTCAACCACTAATGTTTCAACAAGTAANAATGTCGTCGTCTTTTTCCTTCCAAGA	300
Qy	101	ILeThrILePLeuAspAsnTrhTrpIleGluValGluAlaGlyAsnGlyAspGlyValIle	120
Db	301	ATAACGATCCCAAGTAATTTATACCTTAGGAGGAGCTGAAAAATGGAGATGTGTAAAT	360

```

QY 121 LysSerHisMetThrTyrTrpArgLeuGluAsnIleAlaIleThrGluProProlysisIle 140
Db 361 AATCTCATATGACATGACTGAGATTAGAGAACTAGCGAAACCTGAACCACTTAAGATT 420
QY 141 PheArgValIleProValIleuGlyIleIleArgMetIleGlnIleGluTrpIleIlePro 160
Db 421 TTCCTGTGTACTACTATGAGAAATTTAACTGCACTTGAGATCCAGAAAGGAA 180
QY 161 GluLeuAlaProValSerSerAspLeuLysTyrThrIleAspPheArgThrValIleAsnSer 180
Db 481 GAGTTGGCCCTGTTTCATCTGATTAAATACACCTTCGATTCCAGACAGTCAACAGT 540
QY 181 ThrSerTrpMetGluValAsnPheAlaIleAsnArgLysAspLysAsnGlnThrTyrAsn 200
Db 541 ACCAGCTGATGAGATGCAACTTCGTTAAGAACCGTAAGGATTAACCAACGTAACAAC 600
QY 201 LeuThrGlyLeuGlnProPheThrGluTyrValIleAlaIleuArgCysAlaValIleGlu 220
Db 601 CTCACGGGCTGACGCTTTTACAGAAATATGTCATAGCTCTGCGATGTGCGTCAAGAG 660
QY 221 SerLysPheTrpSerAspTrpSerGlnGluLysMetGluMetThrGluGluGlu 238
Db 661 TCAAACTTCTGAGTGACTGAGCCCAAGAAAATGGGAATGACTGAGGAGAGA 714

```

RESULT 8

```

US-09-892-949-68
; Sequence 68, Application US/09892949
; Publication No. US20030096339A1
; GENERAL INFORMATION:
; APPLICANT: Sprecher, Cindy A.
; APPLICANT: Presnell, Scott R.
; APPLICANT: Gao, Zeren
; APPLICANT: Whitmore, Theodore E.
; APPLICANT: Kuiper, Joseph L.
; TITLE OF INVENTION: CYTOKINE RECEPTOR ZCYTOR17
; FILE REFERENCE: 00-42
; CURRENT APPLICATION NUMBER: US/09/892,949
; CURRENT FILING DATE: 2001-06-26
; PRIOR APPLICATION NUMBER: US 60/214,282
; PRIOR FILING DATE: 2000-06-26
; PRIOR APPLICATION NUMBER: US 60/214,955
; PRIOR FILING DATE: 2000-06-29
; PRIOR APPLICATION NUMBER: US 60/267,963
; PRIOR FILING DATE: 2001-08-02
; NUMBER OF SEQ ID NOS: 93
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 68
; LENGTH: 2295
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Polynucleotide encoding human zcytor17-FC4 fusion
; NAME/KEY: CDS
; LOCATION: (1)...(2295)
US-09-892-949-68

```

Alignment Scores:

```

Pred. No.: 3,1e-153 Length: 2295
Score: 1292.00 Matches: 238
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 95.14% Indels: 0
DB: 10 Gaps: 0

```

US-10-006-265-4 (1-252) x US-09-892-949-68 (1-2295)

```

QY 1 MetLysLeuSerProGlnProSerCysValAsnLeuGlyMetMetTrpThrTrpAlaLeu 20
Db 1 ATGAACTCTCTCTCCCAAGCTTATATGTGTAACTGGGAGATGATGTGGACTTGGCACTG 60
QY 21 TrpMetLeuProSerLeuCysLysPheSerLeuAlaIleuProAlaIleProGluAsn 40

```

```

Db 61 TGAAGTCTCCCTTCACTGCAAAATTCAGCCCTGGAGAGCTTCAGCTAAGCTTGAGAAC 120
QY 41 IleSerCysValIleTyrTyrTrpArgLysAsnLeuThrCysThrTrpSerProGlyLysGlu 60
Db 121 ATTTCTGTGTACTACTATGAGAAATTTAACTGCACTTGAGATCCAGAAAGGAA 180
QY 61 ThrSerTyrThrGlnTyrThrValIleAspArgThrTyrAlaPheGlyGluLysHisAspAsn 80
Db 181 ACCAGTTATACCAGATGACAGATTAAGAACTTAACGCTTTTGGAGAAAAACATGATTAAT 240
QY 81 CysThrThrAsnSerSerThrSerGluAsnAlaGlaSerCysSerPhePheLeuProArg 100
Db 241 TGTACAAACCAATAGTCTTACCAAGTAAATCGTCTTCGTCTTTTCTTCCAAACA 300
QY 101 IleThrIleProAspAsnTyrThrIleGluValIleGluAlaGluAsnGlyLysGlyValIle 120
Db 301 ATTAAGATCCCAAGATTAATTAATTCATTGAGGTGAGAGCTGAAATAAGAGATGTATAT 360
QY 121 LysSerHisMetThrTyrTrpArgLeuGluAsnIleAlaIleThrGluProProlysisIle 140
Db 361 AATCTCATATGACATGACTGAGATTAGAGAACTAGCGAAACCTGAACCACTTAAGATT 420
QY 141 PheArgValIleProValIleuGlyIleIleArgMetIleGlnIleGluTrpIleIlePro 160
Db 421 TTCCTGTGTAAACCAAGTTTGGGCAATCAACCAATGATTCAATTCGAATGATTAAGCCT 480
QY 161 GluLeuAlaProValSerSerAspLeuLysTyrThrIleAspPheArgThrValIleAsnSer 180
Db 481 GAGTTGGCCCTGTTTCATCTGATTAAATACACCTTCGATTCCAGACAGTCAACAGT 540
QY 181 ThrSerTrpMetGluValAsnPheAlaIleAsnArgLysAspLysAsnGlnThrTyrAsn 200
Db 541 ACCAGCTGATGAGATGCAACTTCGTTAAGAACCGTAAGGATTAACCAACGTAACAAC 600
QY 201 LeuThrGlyLeuGlnProPheThrGluTyrValIleAlaIleuArgCysAlaValIleGlu 220
Db 601 CTCACGGGCTGACGCTTTTACAGAAATATGTCATAGCTCTGCGATGTGCGTCAAGAG 660
QY 221 SerLysPheTrpSerAspTrpSerGlnGluLysMetGluMetThrGluGluGlu 238
Db 661 TCAAACTTCTGAGTGACTGAGCCCAAGAAAATGGGAATGACTGAGGAGAGA 714

```

RESULT 9

```

US-10-351-157-38
; Sequence 38, Application US/10351157
; Publication No. US20030215838A1
; GENERAL INFORMATION:
; APPLICANT: Sprecher, Cindy A.
; APPLICANT: Gao, Zeren
; APPLICANT: Kuiper, Joseph L.
; APPLICANT: Dasovich, Maria M.
; APPLICANT: Grant, Francis J.
; APPLICANT: Presnell, Scott R.
; APPLICANT: Whitmore, Theodore E.
; APPLICANT: Hammond, Angela K.
; APPLICANT: No. US20030215838A1ak, Julia E.
; APPLICANT: Groes, Jane A.
; TITLE OF INVENTION: CYTOKINE RECEPTOR ZCYTOR17 MULTIMERS
; FILE REFERENCE: 02-02
; CURRENT APPLICATION NUMBER: US/10/351,157
; CURRENT FILING DATE: 2003-01-21
; PRIOR APPLICATION NUMBER: US 60/435,361
; PRIOR FILING DATE: 2002-12-19
; PRIOR APPLICATION NUMBER: US 60/389,108
; PRIOR FILING DATE: 2002-06-14
; PRIOR APPLICATION NUMBER: US 60/350,325
; PRIOR FILING DATE: 2002-01-18
; NUMBER OF SEQ ID NOS: 183
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 38
; LENGTH: 2295

```

```

; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: human zcytor17-Fc4 fusion polynucleotide
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1) ... (2295)
US-10-351-157-38

```

```

Alignment Scores:
Pred. No.: 3,1e-153 Length: 2295
Score: 1292.00 Matches: 238
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 95.14% Indels: 0
DB: 17 Gaps: 0

```

US-10-006-265-4 (1-252) x US-10-351-157-38 (1-2295)

```

Qy 1 MetLysLeuSerProGlnProSerCysValAsnLeuGlyMetMetTrpThrTrpAlaLeu 20
Db 1 ATGAAGCTCTCTCCCGACCTTCACTGTTAACTGGGGATGATGAGTGGACCTGGGCACTG 60
Qy 21 TrpMetLeuProSerLeuCysLysPheSerLeuAlaAlaLeuProAlaLysProGluAsn 40
Db 61 TGGATGCTCCCTCACTCTGCAAAATTCAGCTGGAGCTTGCCAGCTAAAGCTGAGAAC 120
Qy 41 LLeSerCysValLysTrpTrpArgLysAsnLeuThrCysThrTrpSerProGlyLysGlu 60
Db 121 ATTTCCTGTCTCTACTATAGCAAAATTTAACTCTGCACTGGAGTCCAGGAAGGAA 180
Qy 61 ThrSerTrpThrGlnTrpThrValLysArgThrTrpAlaPheGlyGlyLysHisAspAsn 80
Db 181 ACCGATTATACCCAGTACACAGTTAAGAACTTACGCTTTGGAGAAAACATGATATAT 240
Qy 81 CysThrThrAsnSerSerThrSerGluAsnArgLysSerCysSerPhePheLeuProArg 100
Db 241 TGTACACCAATAGTCTTCAAGTGAAGAAATGCTGCTCTCTCTTTTCTTCCCAAGA 300
Qy 101 LLeThrLLeProAspAsnTrpThrLLeGluValGluAlaGluAsnGlyAspGlyValLLe 120
Db 301 ATAAAGATCCAGATTAATTAATACCATTTGAGGTAAGCTGAAATGGAGATGTAATT 360
Qy 121 LysSerHisMetTrpTrpTrpArgLysAsnLLeAlaLysThrGluProProLysLLe 140
Db 361 AAATCTCATATGACATCTGAGAGATTAGAGAACTAGGAAACCTGAACCACTTAAGATT 420
Qy 141 PheArgValLysProValLLeGlyLLeLysArgMetLLeGlnLLeGluTrpLLeLysPro 160
Db 421 TTCCGTGTGAAACCAAGTTTGGGCATCAAAAGATGATTTCAATTTGAATGATTAAGCT 480
Qy 161 GluLeuAlaProValSerSerAspLeuLysTrpThrLeuArgPheArgThrValAsnSer 180
Db 481 GAGTGTGGCGCTGTTTCATCTGATTTAAATPACACACTTCGATTCAGGACGCTCAACAGT 540
Qy 181 ThrSerTrpMetGluValAsnPheAlaLysAsnArgLysAspLysAsnGlnThrTrpAsn 200
Db 541 ACCGATGAGAGGAAAGTCACTTGTCTAAGAACCGTAAAGATTAACCAACCTCAACAC 600
Qy 201 LeuThrGlyLeuGlnProPheThrGluTrpValLLeAlaLeuArgCysAlaValLLeGlu 220
Db 601 CTCACGGGGGCTGCAGCTTTTACAGATATATCTCACTGCTGCGATGTGGGTCAAGAG 660
Qy 221 SerLysPheTrpSerAspTrpSerGlnGluLysMetGlyMetThrGluGluGlu 238
Db 661 TCAAAAGTTCTGAGTGACTGGAGCCAAAGAAAATGGGAATGACTGAGGAAGAA 714

```

```

RESULT 10
US-10-352-554-38
; Sequence 38, Application US/10352554
; Publication No. US20030224487A1
; GENERAL INFORMATION:
; APPLICANT: Sprecher, Cindy A.

```

```

; APPLICANT: Kujiper, Joseph L.
; APPLICANT: Dasovich, Maria M.
; APPLICANT: Grant, Francis J.
; APPLICANT: Hammond, Angela K.
; APPLICANT: Novak, Julia E.
; APPLICANT: Gross, Jane A.
; APPLICANT: Dillon, Stacey R.
; TITLE OF INVENTION: NOVEL CYTOKINE ZCYTOR17 LIGAND
; FILE REFERENCE: 02-01
; CURRENT APPLICATION NUMBER: US/10/352,554
; PRIOR FILING DATE: 2003-01-21
; PRIOR APPLICATION NUMBER: US 60/350,325
; PRIOR FILING DATE: 2002-01-18
; PRIOR APPLICATION NUMBER: US 60/375,323
; PRIOR FILING DATE: 2002-04-25
; PRIOR APPLICATION NUMBER: US 60/435,315
; PRIOR FILING DATE: 2002-12-19
; NUMBER OF SEQ ID NOS: 168
; SOFTWARE: FASTSEQ for Windows Version 3.0
; SEQ ID NO 38
; LENGTH: 2295
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: human zcytor17-Fc4 fusion polynucleotide
; NAME/KEY: CDS
; LOCATION: (1) ... (2295)
US-10-352-554-38

```

Alignment Scores:

```

Pred. No.: 3,1e-153 Length: 2295
Score: 1292.00 Matches: 238
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 95.14% Indels: 0
DB: 17 Gaps: 0

```

US-10-006-265-4 (1-252) x US-10-352-554-38 (1-2295)

```

Qy 1 MetLysLeuSerProGlnProSerCysValAsnLeuGlyMetMetTrpThrTrpAlaLeu 20
Db 1 ATGAAGCTCTCTCCCGACCTTCACTGTTAACTGGGGATGATGAGTGGACCTGGGCACTG 60
Qy 21 TrpMetLeuProSerLeuCysLysPheSerLeuAlaAlaLeuProAlaLysProGluAsn 40
Db 61 TGGATGCTCCCTCACTCTGCAAAATTTAACTCTGCACTGGAGTCCAGCTAAAGCTGAGAAC 120
Qy 41 LLeSerCysValLysTrpTrpArgLysAsnLeuThrCysThrTrpSerProGlyLysGlu 60
Db 121 ATTTCCTGTCTCTACTATAGCAAAATTTAACTCTGCACTGGAGTCCAGGAAGGAA 180
Qy 61 ThrSerTrpThrGlnTrpThrValLysArgThrTrpAlaPheGlyGlyLysHisAspAsn 80
Db 181 ACCGATTATACCCAGTACACAGTTAAGAACTTACGCTTTGGAGAAAACATGATATAT 240
Qy 81 CysThrThrAsnSerSerThrSerGluAsnArgLysSerCysSerPhePheLeuProArg 100
Db 241 TGTACACCAATAGTCTTCAAGTGAAGAAATGCTGCTCTCTTTTCTTCCCAAGA 300
Qy 101 LLeThrLLeProAspAsnTrpThrLLeGluValGluAlaGluAsnGlyAspGlyValLLe 120
Db 301 ATAAAGATCCAGATTAATTAATACCATTTGAGGTAAGCTGAAATGGAGATGTAATT 360
Qy 121 LysSerHisMetTrpTrpTrpArgLysAsnLLeAlaLysThrGluProProLysLLe 140
Db 361 AAATCTCATATGACATCTGAGAGATTAGAGAACTAGCGAAATGCAACCACTTAAGATT 420
Qy 141 PheArgValLysProValLLeGlyLLeLysArgMetLLeGlnLLeGluTrpLLeLysPro 160
Db 421 TTCCGTGTGAAACCAAGTTTGGGCATCAAAAGATGATTTCAATTTGAATGATTAAGCT 480
Qy 161 GluLeuAlaProValSerSerAspLeuLysTrpThrLeuArgPheArgThrValAsnSer 180

```

```

Db      481 GAGTTGGCCCTGTTTCATCTGATTTAAATACACCTTCGATTCAGACAGTCACACAGT 540
Qy      181 ThrSerTrpMetGluValAsnPheAlaValAsnArgLysAspLysAsnGlnThrTyrAsn 200
Db      541 ACCAGCTGGATGAGAACTCACTTCGCTAAGAACCCGTAAAGATTAACCAACCGTAAAC 600
Qy      201 LeuThrGlyLeuGlnProPheThrGluTyrValIleAlaLeuArgCysAlaValLysGlu 220
Db      601 CTCACGGGGCTGCAGCCTTTTACAGAAATATGTCATAGCTCTGCGATGTGCGGTCAAGAG 660
Qy      221 SerLysPheTrpSerAspTrpSerGlnGluLysMetGlyMetThrGluGlu 238
Db      661 TCAAGTTCTGAGTGAAGTGAAGCCAAAGAAAATGGAATGACTGAGAGAAAGA 714

RESULT 11
US-10-772-531-68
; Sequence 68, Application US/10772531
; Publication No. US20040142422A1
; GENERAL INFORMATION:
; APPLICANT: Sprecher, Cindy A.
; APPLICANT: Preenell, Scott R.
; APPLICANT: Gao, Zeren
; APPLICANT: Whitmore, Theodore E.
; APPLICANT: Kuijper, Joseph L.
; APPLICANT: Maurer, Mark F.
; TITLE OF INVENTION: CYTOKINE RECEPTOR ZCYTOR17
; FILE REFERENCE: 00-42
; CURRENT APPLICATION NUMBER: US/10/772,531
; CURRENT FILING DATE: 2004-02-05
; PRIOR APPLICATION NUMBER: US/09/892,949
; PRIOR FILING DATE: 2001-06-26
; PRIOR APPLICATION NUMBER: US 60/214,282
; PRIOR FILING DATE: 2000-06-26
; PRIOR APPLICATION NUMBER: US 60/214,955
; PRIOR FILING DATE: 2000-06-29
; PRIOR APPLICATION NUMBER: US 60/267,963
; PRIOR FILING DATE: 2001-08-02
; NUMBER OF SEQ ID NOS: 93
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 68
; LENGTH: 2295
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Polynucleotide encoding human zcytor17-FC4 fusion
; NAME/KEY: CDS
; LOCATION: (1)...(2295)
US-10-772-531-68

Alignment Scores:
Pred. No.: 3,1e-153 Length: 2295
Score: 1292.00 Matches: 238
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 95.14% Indels: 0
DB: 18 Gaps: 0

US-10-006-265-4 (1-252) x US-10-772-531-68 (1-2295)
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Db      1 ATGAAGCTCTCTCCACGCTTCATGTGTTAACTGGGATGATGTGAACCTGGGACACTG 60
Qy      21 TrpMetLeuProSerLeuCysLysPheSerLeuAlaIleLeuProAlaLysProGluAsn 40
Db      61 TGGATGCTCCCTTCACCTGCAAAATTCAGCTGGAGCTGCTGCACTAAGCTGAGAAC 120
Qy      41 IleSerCysValIleTyrTyrArgLysAsnLeuThrCysThrTrpSerProGlyLysGlu 60
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Qy      61 ThrSerTyrThrGlnTyrThrValLysArgThrTyrAlaPheGlyGluLysHisAspAsn 80
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Qy      81 CysThrTrpAsnSerSerThrSerGluAsnArgAlaSerCysSerPhePheLeuProArg 100
Db      241 TGTACACCAATATGTTCTACAGAGTAAATCTGTGCTCTCTTTTCCCTCCAA 300
Qy      101 IleThrIleProAspAsnTyrThrIleGluValIleGluAlaGluAsnGlyValAspGlyValIle 120
Db      301 ATTAAGATCCAGATTAATTAATACATGAGTGAAGCTGAAATGAGATGCTGTAAT 360
Qy      121 LysSerHisMetThrTyrTrpArgLeuGluAsnIleAlaLysThrGluProProLysIle 140
Db      361 AATCTCATATGACATACATCGAGATTAAGAAACATATAGGAAATCGAACCATCAAGATT 420
Qy      141 PheArgValLysProValLeuGlyTylLysArgMetIleGlnIleGluTrpIleLysPro 160
Db      421 TTCCTGTGAAACCGAGTTTGGGCATCAACCAATGATTCAAATTGAATGAGTAAAGCCT 480
Qy      161 GluLeuAlaProValSerSerAspLeuLysTyrThrLeuArgPheArgThrValAsnSer 180
Db      481 GAGTTGGCGCTGTTTCATCTGATTTAAATACACACTTCGATTCAGACAGTCACACAGT 540
Qy      181 ThrSerTrpMetGluValAsnPheAlaLysAsnArgLysAspLysAsnGlnThrTyrAsn 200
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Qy      201 LeuThrGlyLeuGlnProPheThrGluTyrValIleAlaLeuArgCysAlaValLysGlu 220
Db      601 CTCACGGGGCTGCAGCCTTTTACAGAAATATGTCATAGCTCTGCGATGTGCGGTCAAGAG 660
Qy      221 SerLysPheTrpSerAspTrpSerGlnGluLysMetGlyMetThrGluGluGlu 238
Db      661 TCAAGTTCTGAGTGAAGTGAAGCCAAAGAAAATGGAATGACTGAGAGAAAGA 714

RESULT 12
US-09-972-708-3
; Sequence 3, Application US/09972708
; Publication No. US20030059871A1
; GENERAL INFORMATION:
; APPLICANT: Immunex Corporation
; APPLICANT: Cosman, David J.
; APPLICANT: Mosley, Bruce A.
; APPLICANT: Bird, Timothy A.
; APPLICANT: Dubose, Robert F.
; APPLICANT: Wiley, Steven R.
; TITLE OF INVENTION: HEMATOPOIETIN RECEPTORS HPRI AND HPR2
; FILE REFERENCE: 3160-B
; CURRENT APPLICATION NUMBER: US/09/972,708
; CURRENT FILING DATE: 2001-10-05
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: Patencin version 3.1
; SEQ ID NO 3
; LENGTH: 2480
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-972-708-3

Alignment Scores:
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Score: 1292.00 Matches: 238
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Best Local Similarity: 100.00% Mismatches: 0
Query Match: 95.14% Indels: 0
DB: 10 Gaps: 0

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QY <td>101</td> <td>ILethrIleProAspAsnTyrThrIleGluValGluAlaGluAsnGlyAspGlyValIle</td> <td>120</td> <td></td>	101	ILethrIleProAspAsnTyrThrIleGluValGluAlaGluAsnGlyAspGlyValIle	120	
Db <td>432</td> <td>ATTAAGATCCCAAGTAAATTAATTAACATTAAGCTGGAAGCTGAAAATGGAATGATGTAAAT</td> <td>4911</td> <td></td>	432	ATTAAGATCCCAAGTAAATTAATTAACATTAAGCTGGAAGCTGAAAATGGAATGATGTAAAT	4911	
QY <td>121</td> <td>LysSerHisMetThrTyrTrpArgLeuGluAsnIleAlaLysThrGluProProLysIle</td> <td>140</td> <td></td>	121	LysSerHisMetThrTyrTrpArgLeuGluAsnIleAlaLysThrGluProProLysIle	140	
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QY <td>141</td> <td>PheArgValLysProValLeuGlyIleLysArgMetIleGlnIleGluTrpIleLysPro</td> <td>160</td> <td></td>	141	PheArgValLysProValLeuGlyIleLysArgMetIleGlnIleGluTrpIleLysPro	160	
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QY <td>161</td> <td>GluLeuAlaProValSerSerAspLeuLysTyrThrLeuArgPheArgThrValAsnSer</td> <td>180</td> <td></td>	161	GluLeuAlaProValSerSerAspLeuLysTyrThrLeuArgPheArgThrValAsnSer	180	
Db <td>612</td> <td>GAGTTGGCCCTGTTTCATCTGATTTAAATATACACCTTCGATTCCAGACAGCTCAACAGT</td> <td>6711</td> <td></td>	612	GAGTTGGCCCTGTTTCATCTGATTTAAATATACACCTTCGATTCCAGACAGCTCAACAGT	6711	
QY <td>181</td> <td>ThrSerTrpMetGluValAsnPheAlaLysAsnArgLysAspLysAsnGlnThrTyrAsn</td> <td>200</td> <td></td>	181	ThrSerTrpMetGluValAsnPheAlaLysAsnArgLysAspLysAsnGlnThrTyrAsn	200	
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: Sequence 3, Application US/10715667				
: Publication No. US20040152161A1				
: GENERAL INFORMATION:				
: APPLICANT: Immunex Corporation				
: APPLICANT: Cosman, David J.				
: APPLICANT: Mosley, Bruce A.				
: APPLICANT: Bird, Timothy A.				
: APPLICANT: Dubose, Robert F.				
: TITLE OF INVENTION: HEMATOPOIETIN RECEPTORS HPR1 AND HPR2				
: FILE REFERENCE: 3160-B				
: CURRENT APPLICATION NUMBER: US/10/715,667				
: CURRENT FILING DATE: 2003-11-14				
: PRIOR APPLICATION NUMBER: US/09/972,708				
: PRIOR FILING DATE: 2001-10-05				
: NUMBER OF SEQ ID NOS: 29				
: SOFTWARE: PatentIn version 3.1				
: SEQ ID NO 3				
: LENGTH: 2480				
: TYPE: DNA				
: ORGANISM: Homo sapiens				
US-10-715-667-3				
Alignment Scores:				
Pred. No.:	3,496-153	Length:	2480	
Score:	1292.00	Matches:	238	
Percent Similarity:	100.00%	Conservative:	0	

Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	95.14%	Indels:	0
DB:	18	Gaps:	0
US-10-006-265-4 (1-252) x US-10-715-667-3 (1-2480)			
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DB	132 ATGAAGCTCTCCGCCAGCCTTCATGTGTAACTCGGGGATGATGTGGACTGGGCACTG	191	
QY	21 TTPMetLeuProSerLeuCysLysPheSerLeuAlaAlaLeuProAlaLysProGluAsn	40	
DB	132 TCGATGCTCCCTTACTCTGCAAAATTCACGCTTGCGAGCTCTGCCAGTAAGCTTGAGAC	251	
QY	41 ILeSerCysValTyrTyrTyrArgLysAsnLeuThrCysThrTrpSerProGlyLysGlu	60	
DB	252 ATTTCTGTGTCTACTACTATAGAAAAATTAACTGCACCTTGAGTCCAGAAAAAGAA	311	
QY	61 ThrSerTyrThrGlnTyrThrValLysArgThrTyrAlaPheGlyGlyLysHisAspAsn	80	
DB	312 ACCAGATTATCCCACTATACAGATTAAAGAACTTACGCTTTGGAAAAAACTGATTAAT	371	
QY	81 CysThrTrpAsnSerSerThrSerGluAsnArgAlaSerCysSerPheLeuProArg	100	
DB	372 TGTACACCAATATGTTCTTCAAGTGAATAATCGTGCTTGCTCTTTTCTTCCAGAA	431	
QY	101 ILeThrIleProAspAsnTyrThrIleGluValGluAlaGluAsnGlyLysGlyValIle	120	
DB	432 ATTAACGATCCCAATATTAATATACATTGAGGTGGAAGCTGGAATAATGAGATGCTGTAAT	491	
QY	121 LysSerHisMetThrTyrTrpArgLeuGluAsnIleAlaLysThrGluProProlGlyIle	140	
DB	492 AAATCTCATATGACATACACTGAGATTAGGAACATATGCAAAAACCTAACCACTAAGATT	551	
QY	141 PheArgValLysProValLeuGlyIleLysArgMetIleGlnIleGluTrpIleLysPro	160	
DB	552 TTCCTGTGAACCAAGTTTGGCAATCAACCAAGATTCCTAAATTGAATGAGATTAAGCCT	611	
QY	161 GluLeuAlaProValSerSerAspLeuLysTyrThrLeuArgPheArgThrValAsnSer	180	
DB	612 GAGTTGGGGCCGCTTTCATCTGATTTAAATACACACTTCGATTACGACAGTCAACGT	671	
QY	181 ThrSerTrpMetGluValAsnPheAlaLysAsnArgLysAspLysAsnGlnThrTyrAsn	200	
DB	672 ACCAGCTGATGAGATCAACTTCCTCTAAGAACCGTAAGATTAATAACCAACGTCAAC	731	
QY	201 LeuThrArgLysLeuGlnProPheThrGluTyrValIleAlaLeuArgCysAlaValLysGlu	220	
DB	732 CTCAAGGGGCGTCACGCTTTTACAAATATGTCAATAGCTCTCGAGTCCGGTCAAGAG	791	
QY	221 SerLysPheTrpSerAspTrpSerGlnGluLysMetGlyMetThrGluGluGlu	238	
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Sequence 53, Application US/09892949			
Publication No. US20030096339A1			
GENERAL INFORMATION:			
APPLICANT: Sprecher, Cindy A.			
APPLICANT: Presnell, Scott R.			
APPLICANT: Gao, Zeren			
APPLICANT: Whitmore, Theodore E.			
APPLICANT: Kuiper, Joseph L.			
APPLICANT: Maurer, Mark F.			
TITLE OF INVENTION: CYTOKINE RECEPTOR ZCYTOR17			
FILE REFERENCE: 00-42			
CURRENT APPLICATION NUMBER: US/09/892,949			
CURRENT FILING DATE: 2001-06-26			
PRIOR APPLICATION NUMBER: US 60/214,282			
PRIOR FILING DATE: 2000-06-26			
PRIOR APPLICATION NUMBER: US 60/214,955			
PRIOR FILING DATE: 2000-06-29			


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Job time : 400.322 secs

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GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Run on: February 23, 2005, 08:54:07 ; Search time 2316.44 Seconds
(without alignments)
4140.927 Million cell updates/sec

Title: US-10-006-265-4
Perfect score: 1358
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Scoring table: BLOSUM62
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Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 34239544 segs, 19032134700 residues
Total number of hits satisfying chosen parameters: 68479088

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Maximum DB seg length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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2: gb_est2.*
3: gb_hlc.*
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7: gb_est6.*
8: gb_gss1.*
9: gb_gss2.*
Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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4	345	25.4	459	8	A0022781 HS_2180 A
5	342	25.2	479	6	CA560924 K0279C07-
6	302	22.2	546	6	CA555774 K0202F08-
7	298.5	22.0	628	6	CB427282 K02850 MA
8	297	21.9	553	6	CA559989 K0286C03-
9	270.5	19.9	699	6	CB168262 HSF603268

10	270	19.9	518	6	CA561193 K0283F09-
11	270	19.9	523	6	CA559290 K0256G09-
12	265.5	19.6	1512	3	BC020454 Mus muscu
13	265	19.5	487	5	B0560019 H4061G10-
14	262.5	19.3	887	7	CF780723 AGENCOURT
15	262.5	19.3	5264	3	BC071555 Homo sapi
16	257	18.9	3055	3	AY310138 Rattus no
17	235	17.3	948	5	BU956443 AGENCOURT
18	228	16.8	1069	5	BM928529 AGENCOURT
19	221.5	16.3	9223	5	B0644443 AGENCOURT
20	215	15.8	876	5	B0646417 AGENCOURT
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22	207	15.2	761	7	CN265171 170004240
23	196	14.4	515	8	CC144782 NST002_Ba
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ALIGNMENTS

RESULT 1
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DEFINITION CF174021 637 bp mRNA linear EST 25-JUL-2003
ACCESSION CF174021
VERSION CF174021
KEYWORDS musculus cDNA clone NIA: B0932D09 IMAGE:30475340 5', mRNA sequence.
SOURCE CF174021.1 GI:33283570
ORGANISM Mus musculus (house mouse)
EST.
Mus musculus

REFERENCE Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
AUTHORS Piao, Y., Ko, N.T., Lim, M.K. and Ko, M.S.H.
TITLE Construction of long-transcript enriched cDNA libraries from
submicrogram amounts of total RNAs by a universal PCR amplification
method

JOURNAL Genome Res. 11 (9), 1553-1558 (2001)
MEDLINE 21429098
PUBMED 11544199
COMMENT Contact: Dawood B. Dudekula
Laboratory of Genetics
National Institute on Aging/National Institutes of Health
333 Cassell Drive, Suite 4000, Baltimore, MD 21224-6820, USA
Email: cdna@igsun-grc.nia.nih.gov
Plate: B0932 row: D column: 09
Seq primer: M13 Reversease
High quality sequence stop: 637
POLYA=No.

FEATURES
source 1. 637
/organism="Mus musculus"
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/dev_stage="Unfertilized Egg"
/lab_host="DH10B"
/clone_1ib="NIA Mouse Unfertilized Egg cDNA Library (Long
1)"
/notes="Vector: PCMV-SPORT6 (Invitrogen); Site 1: SalI;
Site 2: NotI. Mouse cDNA project by the Laboratory of
Genetics, National Institute on Aging (NIA), Intramural
Research Program, NIH (http://igsun.grc.nia.nih.gov/cDNA).
This is a long-transcript enriched cDNA library (Ref.
Genome Res. 11: 1553-1558 (2001). [PMID: 11544199]). Total
RNAs were extracted from a pool of 1488 unfertilized eggs.
Double-stranded cDNAs were synthesized with an Oligo(dT)
primer [Invitrogen:
5'-pGACTAGTCTAGATCGCGAGCGCGCCCTTTT-3'],
treated with T4 DNA polymerase, and purified by
ethanol-precipitation. The cDNAs were ligated to
Lone-linker L1-SalI, purified by phenol/chloroform, and
separated from free linkers by Centricon 100. Then, the
cDNAs were amplified by long-range high fidelity PCR using
Ex Taq polymerase (Takara) with a primer Sal4-S. The
products were purified by phenol/chloroform and Centricon
100. The cDNAs were digested with SalI and NotI enzymes
and cloned into SalI/NotI site of PCMV-SPORT6 plasmid
vector. The DH10B E. coli host was transformed with the
ligation mixture by the standard chemical method. The
average insert size is about 2.5 kb. The library was
constructed by Yulan Piao."

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ORIGIN

Alignment Scores:

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Pred. No.: 6,766-42 Length: 637
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Percent Similarity: 63.59% Conservative: 21
Best Local Similarity: 52.17% Mismatches: 54
Query Match: 34.50% Indels: 13
DB: 7 Gaps: 4

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US-10-006-265-4 (1-252) x CF174021 (1-637)

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QY 7 ProSerCyValAsnLeuGlyMetCysThrTrpAlaLeuTrpMetLeuProSerLeu 26
Db 119 CCTCGGCTGTGAACCGTGAATATGTGACCTTGGCACTGGGCACTTCCTTCCTC 178
QY 27 CySLyPheSerLeuAlaLeuProAlaLysProGluAsnLysSerCyValTyrTyr 46
Db 179 TGCAAATTCAGCTGCGACGCTGCGCACTPAACCAAGAAACATTCCTGCGCTTTAC 238
QY 47 TyrArgLysAsnLeuThrCysThrTrpSerProGlyLysGluThrSerTyrThrGlnTyr 66
Db 239 TTCGACAGAAATCTGACTGCTTGAGACCGAGAAAGGAAACCAATGATACCACTAT 298
QY 67 ThrValLysArgThrTyrAlaPheGlyGluLysHisAspAsnCySerThrThrAsnSer 86
Db 299 ATTGTACTTGACTTACTTACTCTATGAAAA-----AGCAAT 334
QY 87 ThrSerGluAsnArgLysSerCysSerPheLeuProArgLleThrIle-----Pro 104
Db 335 TATAGTACATATCTCAAGAGCTCATATTTCTTCCCGCTTCGTCGATATGCCCA 394
QY 105 AspAsnTyrThrLleGluValaGluAsnGlyAspGlyValLleLysSerHisMet 124
Db 395 GACATCTGCAGTGTGAAGTAAAGCTCAAAATGAGATGTGTAAGTAAATCTGACATC 454
QY 125 ThrTyrTrpArgLeuGluAsnLleAlaLysThrGluProProLysLlePheArgValys 144
Db 455 ACATATTTGGATTATATCTCATAGCAAAACCGAACCACTTAATTTTAAGTGAAT 514
QY 145 ProValLeuGlyLleLysArgMetLleGlnLleTrpLleLysProGluLeuAlaPro 164

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FEATURES

source

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Db 515 CCATTT-----TGATATAGAAATGTTCCAGATACAAATGG---AAACCGGTGAAAAAGACT 565
QY 165 ValSerSerAspLeuLysTyrThrLeuArgPheArgThrValAsnSerThrSerTrpMet 184
Db 566 CGTGGCTTTCCTTTGATATGATGATGCTTCGTTCAAGACTGTAAACGATGACCACTGACG 625
QY 185 GluValAsnPhe 188
Db 626 GAAGTCAATTTT 637

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RESULT 2
CF915066
LOCUS
DEFINITION
B0973F04-5 NIA Mouse Unfertilized Egg cDNA Library (Long 1) Mus
musculus cDNA clone NIA:B0973F04 IMAGE:30479295 5', mRNA sequence.
CF915066
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Mus musculus (house mouse)
MUS MUSCULUS
REFERENCE
AUTHORS
TITLE
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 651)
Piao, Y., Ko, N.-T., Lim, M.-K. and Ko, M.-S. H.
Construction of long-transcript enriched cDNA libraries from
submicrogram amounts of total RNAs by a universal PCR amplification
method
Genome Res. 11 (9), 1553-1558 (2001)
JOURNAL
MEDLINE
PUBMED
21429098
11544199
COMMENT
Contact: Dawood B. Dudekula
Laboratory of Genetics
National Institute on Aging/National Institutes of Health
333 Cassell Drive, Suite 4000, Baltimore, MD 21224-6820, USA
Email: cdna@igsun.grc.nia.nih.gov
Plate: B0973 Row: F Column: 04
Seq primer: M13 Reverse
High quality sequence stop: 651
POLVA=No.

Location/Qualifiers
1..651
/organism="Mus musculus"
/mol_type="mRNA"
/strain="C57BL/6J"
/db_xref="nlaEST:B0973F04-5"
/db_xref="taxon:10090"
/clone="NIA:B0973F04 IMAGE:30479295"
/dev_stage="Unfertilized Egg"
/lab_host="DH10B"
/clone_1ib="NIA Mouse Unfertilized Egg cDNA Library (Long
1)"
/notes="Vector: PCMV-SPORT6 (Invitrogen); Site 1: SalI;
Site 2: NotI. Mouse cDNA project by the Laboratory of
Genetics, National Institute on Aging (NIA), Intramural
Research Program, NIH (http://igsun.grc.nia.nih.gov/cDNA).
This is a long-transcript enriched cDNA library (Ref.
Genome Res. 11: 1553-1558 (2001). [PMID: 11544199]). Total
RNAs were extracted from a pool of 1488 unfertilized eggs.
Double-stranded cDNAs were synthesized with an Oligo(dT)
primer [Invitrogen:
5'-pGACTAGTCTAGATCGCGAGCGCGCCCTTTT-3'],
treated with T4 DNA polymerase, and purified by
ethanol-precipitation. The cDNAs were ligated to
Lone-linker L1-SalI, purified by phenol/chloroform, and
separated from free linkers by Centricon 100. Then, the
cDNAs were amplified by long-range high fidelity PCR using
Ex Taq polymerase (Takara) with a primer Sal4-S. The
products were purified by phenol/chloroform and Centricon
100. The cDNAs were digested with SalI and NotI enzymes
and cloned into SalI/NotI site of PCMV-SPORT6 plasmid
vector. The DH10B E. coli host was transformed with the
ligation mixture by the standard chemical method. The
average insert size is about 2.5 kb. The library was

ORIGIN constructed by Yulan Piao."

Alignment Scores:
 Pred. No.: 7.64e-34 Length: 651
 Score: 397.00 Matches: 79
 Percent Similarity: 64.90% Conservative: 19
 Best Local Similarity: 52.32% Mismatches: 41
 Query Match: 29.23% Indels: 12
 DB: 7 Gaps: 3

US-10-006-265-4 (1-252) x CP915066 (1-651)

Qy 6 GlnProSerCyValAsnLeuGlyMeMetTrpThrTrpAlaLeuTrpMetLeuProSer 25
 Db 229 CAGCCTCTGGGTGTGAACCGCTGAATATATGTGACCTTGGACCTGTGGCATTCTCTTC 288
 Qy 26 LeuCyAlpSerLeuAlaLeuProAlaLysProGluAsnLysSerCyValTyr 45
 Db 289 CTCGCAAAATTCAGCTGCGAGTCTGCGCACTAAGCCAGAGAACATTCTCGGCTCTT 348
 Qy 46 TyrTrpAlaGlyAsnLeuThrCySerThrTrpSerProGlyLysGluThrSerTyrThrGln 65
 Db 349 TACTTCGACAGAAATCTGACTTGCACCTTGGAGACCAAGAAAGAACCAATGATACAGC 408
 Qy 66 TyrThrValLysArgThrTyrAlaPheGlyGlyLysIleAspAsnCySerThrTrpAsnSer 85
 Db 409 TACATTGTGACTTGTGACTTACTCTATGAGAAA-----AGC 444
 Qy 86 SerThrSerGluAsnArgAlaSerCySerPhePheLeuProArgIleThrIle----- 103
 Db 445 AATTATAGTGACAAATGCTACAGAGGCTTCATATCTTTCCCGTCTCGTGCATGCC 504
 Qy 104 ProAspAsnTyrThrIleGluValGluAlaGluAsnGlyAspGlyValIleLysSerHis 123
 Db 505 CCAGACATCTGCAGTGTGAAGTCAAGCTCAAAATGAGATGATTAAGTTAAATCTGAC 564
 Qy 124 MetThrTyrTrpArgLeuGluAsnIleAlaLysThrGluProProLysIlePheArgVal 143
 Db 565 ATCCACATATGGCATTTATCTCCATAGCAAAACCGAACCCTATATATTTAAGTGTG 624
 Qy 144 LysProValLeuGlyLysIleLysArgMetIleGln 154
 Db 625 AATCCAAT-----TGTAATGAAATGTTCAG 651

RESULT 3
 CAS61173 592 bp mRNA linear EST 19-NOV-2002
 LOCUS K0283D09-5N NIA Mouse Unfertilized Egg cDNA Library (Long) Mus
 DEFINITION muscular cDNA clone NIA:K0283D09 IMAGE:30052652 5', mRNA sequence.
 ACCESSION CAS61173.1 GI:25105828
 VERSION EST.
 KEYWORDS Mus musculus (house mouse)
 SOURCE Mus musculus
 ORGANISM Mus musculus; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 REFERENCE 1 (bases 1 to 592)
 AUTHORS Piao, Y., Kargul, G.J., Dudekula, D.B., Qian, Y., Luo, A., Steag, C.A., Martin, P., Alpa, K., Tanaka, T. and Ko, M.S.H.
 TITLE Systematic Analyses of NIA Mouse Unfertilized Egg cDNA Library (Long)
 JOURNAL Unpublished (2001)
 COMMENT Other_ests: K0283D09-3
 Contact: Dawood B. Dudekula
 Laboratory of Genetics
 National Institute on Aging/National Institutes of Health
 333 Cassell Drive, Suite 4000, Baltimore, MD 21224-6620, USA
 Email: cdna@igsun.grc.nia.nih.gov
 Plate: K0283 row: D column: 09
 Seq primer: M13 Reverse
 High quality sequence stop: 592
 POLYA=No.

FEATURES
 source

Location/Qualifiers

1..592
 /organism="Mus musculus"
 /mol_type="mRNA"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /db_xref="taxon:10090"
 /clone="NIA:K0283D09 IMAGE:30052652"
 /tissue_type="Unfertilized Egg"
 /lab_host="DH10B"
 /clone_id="NIA Mouse Unfertilized Egg cDNA Library (Long)"

/note="Vector: pSPORT1 (Invitrogen); Site 1: SalI; Site 2: NotI. Mouse cDNA project by the Laboratory of Genetics, National Institute on Aging (NIA), Intramural Research Program, NIH (http://igsun.grc.nia.nih.gov/cDNA). This is a long-transcript enriched cDNA library (Ref. Genome Res. 11: 1553-1558 (2001). [PMID: 11544199]). Total RNAs were extracted from a pool of 148 unfertilized eggs. Double-stranded cDNAs were synthesized with an oligo(dT) primer [Invitrogen: 5'-pGACTAGTCTAGATCGGAGCGGCCCTTTTCTTTT-3'], treated with T4 DNA polymerase, and purified by ethanol-precipitation. The cDNAs were ligated to lone-linker lB-Sal4, purified by phenol/chloroform, and separated from free linkers by Centricon 100. Then, the cDNAs were amplified by long-range high fidelity PCR using Ex Taq polymerase (Takara) with a primer Sal4-S. The products were purified by phenol/chloroform and Centricon 100. The cDNAs were digested with SalI and NotI enzymes and cloned into SalI/NotI site of pSPORT1 plasmid vector. The DH10B E. coli host was transformed with the ligation mixture by the standard chemical method. The average insert size is about 2.5 Kb. The library was constructed by Yulan Piao (NIA)."

ORIGIN

Alignment Scores:

Pred. No.: 2.79e-28 Length: 592
 Score: 347.00 Matches: 67
 Percent Similarity: 65.89% Conservative: 18
 Best Local Similarity: 51.94% Mismatches: 34
 Query Match: 25.55% Indels: 10
 DB: 6 Gaps: 2

US-10-006-265-4 (1-252) x CAS61173 (1-592)

Qy 6 GlnProSerCyValAsnLeuGlyMeMetTrpThrTrpAlaLeuTrpMetLeuProSer 25
 Db 229 CAGCCTCTGGGTGTGAACCGCTGAATATATGTGACCTTGGACCTGTGGCATTCTCTTC 288
 Qy 26 LeuCyAlpSerLeuAlaLeuProAlaLysProGluAsnLysSerCyValTyr 45
 Db 289 CTCGCAAAATTCAGCTGCGAGTCTGCGCACTAAGCCAGAGAACATTCTCGGCTCTT 348
 Qy 46 TyrTrpAlaGlyAsnLeuThrCySerThrTrpSerProGlyLysGluThrSerTyrThrGln 65
 Db 349 TACTTCGACAGAAATCTGACTTGCACCTTGGAGACCAAGAAAGAACCAATGATACAGC 408
 Qy 66 TyrThrValLysArgThrTyrAlaPheGlyGlyLysIleAspAsnCySerThrTrpAsnSer 85
 Db 409 TACATTGTGACTTGTGACTTACTCTATGAGAAA-----AGC 444
 Qy 86 SerThrSerGluAsnArgAlaSerCySerPhePheLeuProArgIleThrIle----- 103
 Db 445 AATTATAGTGACAAATGCTACAGAGGCTTCATATCTTTCCCGTCTCGTGCATGCC 504
 Qy 104 ProAspAsnTyrThrIleGluValGluAlaGluAsnGlyAspGlyValIleLysSerHis 123
 Db 505 CCAGACATCTGCAGTGTGAAGTCAAGCTCAAAATGAGATGATTAAGTTAAATCTGAC 564
 Qy 124 MetThrTyrTrpArgLeuGluAsnIle 132
 Db 132

Db 565 ATCACAATTGGCATTTAATCTCCATA 591

RESULT 4
LOCUS A0022781 459 bp DNA linear GSS 16-JUN-1998
DEFINITION HS_2180_A2.B11.MR.CIT.Approved.Human.Genomic.Sperm.Library.D.Homo.sapiens.genomic.clone.Plate=2180.Col=22.Row=C,genomic.survey.sequence.

ACCESSION A0022781
VERSION A0022781
KEYWORDS GSS.
SOURCE Homo.sapiens (human)
ORGANISM Homo.sapiens

REFERENCE
AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 459)
Keller,A., Shaker,R., Furlong,D., Young,D., Zhao,S., Adams,W.D. and Hood,L.
Sequence-tagged connectors: A sequence approach to mapping and scanning the human genome
Proc. Natl. Acad. Sci. U.S.A. 96 (17), 9739-9744 (1999)

JOURNAL MEDLINE 99380589
PUBMED 10449764
COMMENT Contact: Mahairas GG, Wallace JC, Hood L
High Throughput Sequencing Center
University of Washington
401 Queen Anne Avenue North, Seattle, WA 98109, USA
Tel: (206) 616-3618
Fax: (206) 616-3887
Email: jwallace@u.washington.edu
Sequence Tagged Connector
Plate: 2180 row: C column: 22
Class: BAC ends
High quality sequence stop: 459.

FEATURES
source
1..459
Location/Qualifiers
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
/clone="plate=2180.Col=22.Row=C"
/sex="male"
/clone_lib="CIT.Approved.Human.Genomic.Sperm.Library.D"
/note="Organ: Sperm; Vector: pBelOBAC11; BAC Clones in E-Coli DH10B"

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Alignment Scores:
Pred. No.: 3,24e-28 Length: 459
Score: 345.00 Matches: 68
Percent Similarity: 90.79% Conservative: 1
Best Local Similarity: 89.47% Mismatches: 7
Query Match: 25.41% Indels: 0
Gaps: 0

US-10-006-265-4 (1-252) x A0022781 (1-459)

QY 177 ThrValAsnSerThrsertPmetGluValAsnPheAlaLysAsnArgLysAspLysAsn 196
Db |||:|||||
190 ACATATGCTCTGTTCTTAGATGAGAGTCACTGCTPAGAACCGTAAGGTTAAAC 249
QY 197 GlnThrTyAsnLeuThrGlyLeuGlnProPheThrGluTyValAlaAlaLeuArgCys 216
Db |||:|||||
250 CAAACGTACACCTCACGGGGCTGCACACTTNTACAGATATGTCTAGCTCGCATGT 309
QY 217 AlaValLysGluSerLysPheTTPSerAAPTTPSerGlnGluLysMetGlyMetThrGlu 236
Db |||:|||||
310 GCGGTCAAGGAGCAAGTCTGAGTGACTGAGCCAGAAAAATGGGAATGACTGAG 369
QY 237 GlnGlnGlyLysLeuLeuProAlaIleProValLeuSerThrLeuVal 252
Db |||:|||||
370 GAAGANCGAAGCTACTCTCGATTCGCCGTCTGCTGCTGAG 417

RESULT 5
LOCUS CA560924 479 bp mRNA linear EST 19-NOV-2002
DEFINITION K0279C07-SN.NIA.Mouse.Unfertilized.Egg.cDNA.library.(long).Mus.musculus.cDNA.clone.NIA:K0279C07.IMGs:30052254.5,mRNA.sequence.

ACCESSION CA560924
VERSION CA560924
KEYWORDS EST.
SOURCE Mus.musculus (house mouse)
ORGANISM Mus.musculus

REFERENCE
AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 479)
Piao,Y., Kargul,G.J., Dudekula,D.B., Qian,Y., Luo,A., Steagy,C.A., Martin,P., Alba,R., Tanaka,T. and Ko,M.S.H.
Systematic Analyses of NIA Mouse Unfertilized Egg cDNA Library (Long)
Unpublished (2001)
Other ESTs: K0279C07-3
Contact: Dawood B. Dudekula
Laboratory of Genetics
National Institute on Aging/National Institutes of Health
333 Cassell Drive, Suite 4000, Baltimore, MD 21224-6820, USA
Email: cdna@igsun.grc.nia.nih.gov
Plate: K0279 row: C column: 07
Seq primer: M13 Reverse
High quality sequence stop: 479
POLYA-No.

FEATURES
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1..479
Location/Qualifiers
/organism="Mus musculus"
/mol_type="mRNA"
/strain="C57BL/6J"
/db_xref="taabST:K0279C07-SN"
/db_xref="taxon:10090"
/clone="NIA:K0279C07.IMGs:30052254"
/tissue_type="Unfertilized Egg"
/lab_host="DH10B"
/clone_lib="NIA.Mouse.Unfertilized.Egg.cDNA.library (long)"
/note="Vector: pSPORT1 (Invitrogen); Site.1: SalI; Site.2: NotI; Mouse cDNA project by the Laboratory of Genetics, National Institute on Aging (NIA), Intramural Research Program, NIH (http://igsun-grc.nia.nih.gov/cdna). This is a long-transcript enriched cDNA library (Ref. Genome Res. 11: 1553-1558 (2001). [PMID: 11544191]). Total RNAs were extracted from a pool of 1488 unfertilized eggs. Double-stranded cDNAs were synthesized with an Oligo(dT) primer (Invitrogen): 5'-pGACTAGTTCATGATCGGAGCGCGCCCTTTT-3', treated with T4 DNA polymerase, and purified by ethanol-precipitation. The cDNAs were ligated to lona-linker L1-SalI, purified by phenol/chloroform, and separated from free linkers by Centricon 100. Then, the cDNAs were amplified by long-range high fidelity PCR using Ex Tag polymerase (Takara) with a primer SalI-S. The products were purified by phenol/chloroform and Centricon 100. The cDNAs were digested with SalI and NotI enzymes and cloned into SalI/NotI site of pSPORT1 plasmid vector. The DH10B E. coli host was transformed with the ligation mixture by the standard chemical method. The average insert size is about 2.5 kb. The library was constructed by Yulan Piao (NIA)."

ORIGIN
Alignment Scores:
Pred. No.: 7.49e-28 Length: 479
Score: 342.00 Matches: 66
Percent Similarity: 65.62% Conservative: 18
Best Local Similarity: 51.56% Mismatches: 34
Query Match: 25.16% Indels: 10
Gaps: 2

US-10-006-265-4 (1-252) x CA560924 (1-479)

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Qy 7 ProserCysValanLeuGlyMetMetTrpThrPalaleuTrpMetLeuProSerIeu 26
Db 119 CCTGGGTGTGAACGCTGGAATATGTGACCTTGGACATGTGGCATTCCTTCTC 178
Qy 27 CysLysPheSerLeuAlaAlaLeuProAlaLysProGluAniLeuSerCysValTrpTyr 46
Db 179 TGCMAATTCACCTGCGCAGCTCTGCGCACTTAAGCCAGAAACATTTCTGCGCTTTTAC 238
Qy 47 TyrArgLysAenLeuThrCysThrTrpSerProGlyLysGluThrSerTyrThrGlnTyr 66
Db 239 TTCACAGAAATTCGACTTGCACCTTGGAGACAGAAAGAAACCAATGATACCAAGCAT 298
Qy 67 ThrValLysArgThrTyrAlaPheGlyGluLysHisAbaPancCysThrThrasnSer 86
Db 299 ATTGTGCTTGTGACTTACTCTATGAAAA-----AGCAAT 334
Qy 87 ThrSerGluAenArgAlaSerCysSerPhePheLeuProArgIleThrIle-----Pro 104
Db 335 TATAGTACAAATGCTACAGAGGCTTCAATATCTTTTCCCGTCTGCGCATGCCCCCA 394
Qy 105 AspaPantYrThrIleGluValGluAlaGluAniLysArgLysValIleLysSerHisMet 124
Db 395 GACATCTGCAGCTGTGAAGTCAAGCTCAAAATGAGATGTGAAGTAAATTCGACATC 454
Qy 125 ThrTyrTrpArgLeuGluAniLe 132
Db 455 ACATATTGGCATTTAATCTCCATA 478

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RESULT 6

CA555774

LOCUS CA555774 546 bp mRNA linear EST 19-NOV-2002
 DEFINITION K0202F08-5N NIA Mouse Unfertilized Egg cDNA Library (Long) Mus
 musculus cDNA clone NIA:K0202F08 IMAGE:30044899 5', mRNA sequence.

ACCESSION CA555774

VERSION CA555774.1 GI:25100137

SOURCE EST.

ORGANISM Mus musculus (house mouse)

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 546)

AUTHORS Piao, Y., Kangul, G.D., Dudekula, D.B., Qian, Y., Luo, A., Stagg, C.A.,
 Martin, P., Alba, K., Tanaka, T. and Ko, M.S.H.
 Systematic Analyses of NIA Mouse Unfertilized Egg cDNA Library
 (Long)

TITLE Unpublished (2001)

JOURNAL Other_ESTs: K0202F08-3

COMMENT Contact: Dawood B. Dudekula

Laboratory of Genetics
 National Institute on Aging/National Institutes of Health
 333 Cassell Drive, Suite 4000, Baltimore, MD 21224-6820, USA
 Email: cdna@gsun-grc.nia.nih.gov
 Plate: K0202 row: F column: 08

Seq primer: M13 Reversee

High quality sequence stop: 546

POLYA=No.

Location/Qualifiers

1. 546

/organism="Mus musculus"

/mol_type="mRNA"

/strain="C57BL/6J"

/db_xref="taxon:10090"

/clone="NIA:K0202F08 IMAGE:30044899"

/issue_type="Unfertilized Egg"

/lab_host="DH10B"

/clone_id="NIA Mouse Unfertilized Egg cDNA Library
 (Long)"

REFERENCE: pSPORN1 (Invitrogen); Site 1: Sali; Site 2:
 NotI; Mouse cDNA project by the Laboratory of Genetics,
 National Institute on Aging (NIA), Intramural Research

Program, NIH (<http://lgsun-grc.nia.nih.gov/cDNA>). This is
 a long-transcript enriched cDNA library (Ref. Genome Res.
 11: 1553-1558 (2001)). (PMID: 115441991). Total RNAs were
 extracted from a pool of 148 unfertilized eggs.
 Double-stranded cDNAs were synthesized with an Oligo(dT)
 primer (Invitrogen):
 5'-pGACTAGTCTAGATCGAGCGCGCCCTTTTCTTTT-3',
 treated with T4 DNA polymerase, and purified by
 ethanol-precipitation. The cDNAs were ligated to
 Lome-linker L1-SalI, purified by phenol/chloroform, and
 separated from free linkers by Centricon 100. Then, the
 cDNAs were amplified by long-range high fidelity PCR using
 Ex Tag polymerase (Takara) with a primer SalI-5'. The
 products were purified by phenol/chloroform and Centricon
 100. The cDNAs were digested with SalI and NotI enzymes
 and cloned into Sali/NotI site of pSPORN1 plasmid vector.
 The DH10B E. coli host was transformed with the ligation
 mixture by the standard chemical method. The average
 insert size is about 2.5 kb. The library was constructed
 by Yulan Piao (NIA)."

ORIGIN

Alignment Scores:
 Pred. No.: 2,856-23 Length: 546
 Score: 302.00 Matches: 59
 Percent Similarity: 64.91% Conservative: 15
 Best Local Similarity: 51.75% Mismatches: 30
 Query Match: 22.24% Indels: 10
 DB: 6 Gaps: 2

US-10-006-265-4 (1-252) x CA555774 (1-546)

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Qy 6 GlnProSerCysValanLeuGlyMetMetTrpThrPalaleuTrpMetLeuProSer 25
Db 229 CAGCCTGTGGGTGTGAACGCTGGAATATGTGACCTTGGACATGTGGCATTCCTTTC 288
Qy 26 LeuCysLysPheSerLeuAlaAlaLeuProAlaLysProGluAniLeuSerCysValTyr 45
Db 289 CTGCAAAATTCACCTGCGCAGCTCTCCAGCTTAAGCAGAAACATTTCTGCGCTTT 348
Qy 46 TyrTrpArgLysAenLeuThrCysThrTrpSerProGlyLysGluThrSerTyrThrGln 65
Db 349 TACTTCGACAGAAATTCGACTTGCACCTTGGAGACCAGAAAGAAACCAATGATACCAAGC 408
Qy 66 TyrThrValLysArgThrTyrAlaPheGlyGluLysHisAbaPancCysThrThrasnSer 85
Db 409 TACATTTGACTTGTGACTTACTCTATGAAAA-----AGC 444
Qy 86 SerThrSerGluAenArgAlaSerCysSerPhePheLeuProArgIleThrIle----- 103
Db 445 AATTATAGTACAAATGCTACAGAGGCTTCAATATCTTTTCCCGTCTGCGCATGCCCC 504
Qy 104 ProAspaPantYrThrIleGluValGluAlaGluAniLysArgLysValIleLysSerHisMet 117
Db 505 CCAGACATCTGCAGCTGTGAAGTCAAGCTCAAAATGAGAT 546

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RESULT 7

CB427282

LOCUS CB427282 628 bp mRNA linear EST 25-MAR-2003
 DEFINITION 602850 MARC 6BOV Bos taurus cDNA 5', mRNA sequence.

ACCESSION CB427282

VERSION CB427282.1 GI:29200175

KEYWORDS EST.

SOURCE Bos taurus (cow)

ORGANISM Bos taurus

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 Bovinae; Bos.

1 (bases 1 to 628)

AUTHORS Smith, T.P.L., Roberts, A.J., Echeverkamp, S.E., Chitko-McKown, C.G.,
 Wray, J.E. and Keele, J.W.

TITLE A second set of bovine ESTs from pooled-tissue normalized libraries

JOURNAL Unpublished (2003)

Score: 297.00 Matches: 59
 Percent Similarity: 64.35% Conservative: 15
 Best Local Similarity: 51.30% Mismatches: 31
 Query Match: 21.87% Indels: 10
 DB: 6 Gaps: 2

US-10-006-265-4 (1-252) x CAS59989 (1-553)

QY 6 GlnProSerCysValaenLeuGlyMetMetTrpThrTrpAlaLeuTrpMetLeuProSer 25
 Db 229 CAGCCTCTGGGTGGTGAACGCTGGAAATATGTGGACCTTGGCACTGTGGCAATCTCTTTC 288
 QY 26 LeuCysIysPheSerLeuAlaAlaLeuProAlaIysProGluAenIleSerCysValTyr 45
 Db 289 CTCGCAAAATTCACCTCGGAGCTGCTCCGACTAGCCAGACAGAAACCAATTCCTAGCTCTT 348
 QY 46 TyrTyrArgIysAenLeuThrCysThrTrpSerProGlyIysGluThrSerTyrTrpGln 65
 Db 349 TACTTCGACAGAAATTCGACTTGCACCTTGAGACCAAGAAAGAAACCAATGATACCAAGC 408
 QY 66 TyrThrValIysArgThrTyrAlaPheGlyGluIysHisAenCysThrThrAenSer 85
 Db 409 TACATTTGTGACTTGTACTTCTCTATGAGAAA-----AGC 444
 QY 86 SerThrSerGluAenArgAlaSerCysSerPhePheLeuProArgIleThrIle----- 103
 Db 445 AATTATATGTGACATTCGTACAGAGCTTCATATCTTTCCCGTTCTCTGTGCAATGCC 504
 QY 104 ProApananTyrThrIleGluValGluAlaGluAenGlyAenGly 118
 Db 505 CCAGACATCTGCAGTGTGAAAGTACAAGCTCAAAATGAGATGGT 549

RESULT 9

CB168262/c 699 bp mRNA linear EST 30-JAN-2003
 LOCUS HSF603268406.R1 CSEQFXN4 small intestine Bos taurus cDNA, mRNA
 DEFINITION sequence.

ACCESSION CB168262
 VERSION CB168262.1 GI:28154387
 KEYWORDS EST.
 SOURCE Bos taurus (cow)
 ORGANISM Bos taurus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 Bovinae; Bos.

REFERENCE 1 (bases 1 to 699)
 AUTHORS Adelson, D.L. and Gill, C.A.
 TITLE Bovine ESTs (Adelson and Gill)
 JOURNAL Unpublished (2003)
 COMMENT Contact: David L. Adelson
 Animal Breeding and Genetics
 Texas A&M University
 Animal Science Dept., TAMU-2471, College Station, TX 77843-2471,
 USA

FEATURES
 Source Tel: 9798455216
 Fax: 9798455670
 Email: david.adelson@tamu.edu.
 Location/Qualifiers

1..699
 /organism="Bos taurus"
 /mol_type="mRNA"
 /db_xref="taxon:9913"
 /clone_type="small intestine"
 /note="Organ: small intestine; Vector: pBluescript SK+;
 Site 1: NCI; Site 2: EcorI; sequence 5' of the insert
 (5'-NNN...NNNinsert)
 GCGAATTGAGCTCACCACCGCGCGCGCGCTGAG. Sequence 3' of
 the insert (AAGATTCGATATCAAGCTTATTCATACCGTGCAGCTGAG.
 normalized RD 2 library, sequenced 3' with M13R primer."

ORIGIN

Alignment Scores:

Pred. No.: 1,41e-19 Length: 699
 Score: 270.50 Matches: 67
 Percent Similarity: 53.11% Conservative: 44
 Best Local Similarity: 32.06% Mismatches: 87
 Query Match: 19.92% Indels: 12
 DB: 6 Gaps: 9

US-10-006-265-4 (1-252) x CB168262 (1-699)

QY 35 ProAlaIysPheGluAenIleSerCysValTyrTyrTrpArgIysAenLeuThrCysThr 54
 Db 627 CCTGAAAAAACCCTAAATAATTTGAGTTGATGCTGAATGAGAAAGAAATATGATGTCAG 568
 QY 55 TrpSerProGlyIysGluThrSerTyr---ThrGlnTyrThrValIysArgThrTyrAla 73
 Db 567 TGGGATCCTGGAAAGGAAACATACCTGGAAACCAATCACTTTAAATCTGAGCTGAGCA 508
 QY 74 PheGlyIysIysHisAenCysThrThrAenSerThrSerGluAenArgAlaSer 93
 Db 507 ---ACAGAGAAAGTTGATGATGTAAAGCAAAAGTACACCC-----ACCTCA 460
 QY 94 CysSerPhePheLeuProArgIleThrIleProApananTyrThrIleGluValGluAla 113
 Db 459 TGCACGTGTGATATCTCTCCCTGTATTTGTC---AACATGGAAGCTGGGTGAGAGCA 403
 QY 114 GluAenGlyAenGlyValIleIysSer---HisMetThrTyrTrpArgIysAenIle 132
 Db 402 GAGATGCCCTTGGGAAAGTTTACTCTCAATCATATTCATATTTGATCCTGTAGATTAAG 343
 QY 133 AlaIysThrGluProProIysIlePheArgValIysProValIleGlyIleIysArgMet 152
 Db 342 ---AAGCTCAATCCACACCATATTTTATCACTCAACAGTTCAAGAACTGCTAGATTT 286
 QY 153 IleGlnIleGluTyrIleIysProGluLeuAlaProValIysSerAenPheLeuTyrThr 172
 Db 285 TTAAATATGACATGACATGATTCACGTTTAAAGATTATTAACA---CTGAATATATGAC 229
 QY 173 LeuArgPheArgThrValAenSerThrSerTyrMetGluValAenPheAlaIysAenArg 192
 Db 228 ATTCATATATGAGAACCAAGATGCTCAACTGGAAACAGGTTCT---CCTGAATATACA 172
 QY 193 LysAenPysAenGlnTyrThrAenLeuThrGlyLeuGlnProPheThrGluTyrValIle 212
 Db 171 TCATCTACCCGATTTTATTCACCTTCAGAGCTTAAACCTTTTACAGA-TATGTGTTT 113
 QY 213 AlaLeuArgCysAlaValIysGluSerIys---PheTrpSerAenTrpSerGlnIlyls 231
 Db 112 AGATTCGTTGTGTGAAGAAAGATGTAAGATATTGAGTACTGAGTGAAGAAAGCA 53
 QY 232 MetGlyMetThrGluGluGlyIys 240
 Db 52 AGTGTATCATATGATGAAGATGTAAG 26

RESULT 10

CAS61193 518 bp mRNA linear EST 19-NOV-2002
 LOCUS K0283F09-5N NIA Mouse Unfertilized Egg cDNA library (Long) Mus
 DEFINITION musculus cDNA clone NIA:K0283F09 IMAGE:30052676 5', mRNA sequence.

ACCESSION CAS61193
 VERSION CAS61193.1 GI:25105848
 KEYWORDS EST.
 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 518)
 AUTHORS Piao, Y., Kargul, G.J., Dudekula, D.B., Qian, Y., Luo, A., Seagg, C.A.,
 Martin, P., Alba, K., Tanaka, T. and Ko, M.S.H.
 TITLE Systematic Analyses of NIA Mouse Unfertilized Egg cDNA Library
 (Long)

JOURNAL Unpublished (2001)
 COMMENT Other ESTs: K0283F09-3
 Contact: Dawood B. Dudekula

US-10-006-265-4 (1-252) x CA559290 (1-523)

Qy 6 GlnProSerCysValAsnLeuGlyMetMetTrpThrTrpAlaLeuTrpMetLeuProSer 25
 Db 229 CAGCCTCGGTGGTGGACGCTGGAAATATGAGACCTTGGACATCTGTGGCAATCTCTTTC 288

Qy 26 LeuCysLysPheSerLeuAlaAlaLeuProAlaLysProGluAsnIleSerCysValTyr 45
 Db 289 CTCGCAAAATTCACGCTGGACGCTGCTGCCACTAAGCCAGAGAACATTTCTGCTCTT 348

Qy 46 TyrTrArgLysAsnLeuThrCysThrTrpSerProGlyLysGluThrSerTyrTrgln 65
 Db 349 TACTTCGACAGAAATCGACTTGCATTCGACGACAGAGAGAGAAACCAATGATATCCAGC 408

Qy 66 TyrThrValLysAsnGlyTrpAlaPheGlyGluLysHisAspAsnCysThrThrAsnSer 85
 Db 409 TACATTTGTGACTTGTACTTACTCTCTATGTGAAA-----AGC 444

Qy 86 SerThrSerGluAsnArgAlaSerCysSerPhePheLeuProArg 100
 Db 445 AATTATAGTGCATTCCTACAGAGCTTCAATATCTTCCCGCT 489

RESULT 12
 LOCUS BC020454
 DEFINITION Mus musculus interleukin 6 signal transducer, mRNA (CDNA clone IMAGE:3598166).

ACCESSION BC020454
 VERSION BC020454.1 GI:18045025
 KEYWORDS Mus musculus (house mouse)
 SOURCE Mus musculus
 ORGANISM Mus musculus

REFERENCE 1
 AUTHORS Strausberg, R.L., Feingold, E.A., Grouse, L.H., Dergs, J.G., Altschuler, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D., Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J.J., Heien, F., Dapkin, M., Soares, M.B., Bonaldi, M.F., Cabavant, T.L., Scheetz, T.E., Brownstein, M.J., Usdin, T.B., Tothiyaki, S., Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J., Abramson, R.D., Mullany, S.J., Boeck, S.A., McEwan, P.J., McKernan, K.D., Malek, J.A., Gunaratne, P.H., Richards, S., Morley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W., Viallon, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A., Fahey, J.J., Helton, E., Kettman, M., Madan, A., Rodriguez, S., Sanchez, A., Whitting, M., Madan, A., Young, A.C., Shevchenko, Y., Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D., Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M., Butlerfield, Y.S., Krzywinski, M.I., Skalska, U., Smalhus, D.E., Schenck, A., Schein, J.E., Jones, S.J., and Marra, M.A.
 Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences
 Proc Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)

TITLE JOURNAL MEDLINE
 PUBMED 12477932
 REFERENCE 2 (bases 1 to 1512)
 AUTHORS Strausberg, R.
 TITLE Direct Submission
 JOURNAL Submitted (03-JUN-2002) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA

REMARK NIH-MGC Project URL: <http://mgc.nci.nih.gov>
 Contact: MGC help desk
 Email: gcgaps-remail.nih.gov
 Tissue Procurement: Jeffrey Green M.D.
 cDNA Library Preparation: Life Technologies, Inc.
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (ILML)
 DNA Sequencing by: Baylor College of Medicine Human Genome

Sequencing Center
 Center code: BCM-HGSC
 Web site: <http://www.hgsc.bcm.tmc.edu/cdna/>
 Contact: amgdbcm.tmc.edu
 Gunaratne, P.H., Garcia, A.M., Lu, X., Hulyk, S.W., Louised, H., Kowis, C.R., Sneed, A.J., Martin, R.G., Muzny, D.M., Nambavali, A.N., Gibbs, R.A.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/ILML at: <http://image.llnl.gov>
 Series: IRAC Plate: 16 Row: K Column: 14
 This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 6754337
 This clone has the following problem: no poly-a-tail.

FEATURES
 source
 location/qualifiers
 1..1512
 /organism="Mus musculus"
 /mol_type="mRNA"
 /strain="FVB/N"
 /db_xref="taxon:10090"
 /clone="IMAGE:3598166"
 /tissue_type="mammary tumor, C3(1)-Tag model, infiltrating ductal carcinoma, 5 month old virgin mouse."
 /clone_id="NCI CGAP_Mam6"
 /lab_host="DH10B"
 /note="Vector: pCMV-SPORT6"

ORIGIN
 Alignment Scores:
 Pred. No.: 1,57e-18 Length: 1512
 Score: 265.50 Matches: 65
 Percent Similarity: 52.88% Conservative: 45
 Best Local Similarity: 31.25% Mismatches: 83
 Query Match: 19.55% Indels: 15
 DB: 3 Gaps: 9

US-10-006-265-4 (1-252) x BC020454 (1-1512)

Qy 35 ProAlaLysProGluAsnIleSerCysValTyrTyrArgLysAsnLeuThrCysThr 54
 Db 613 CCACATTAACCTTACAAATTTGACTTGTGATGATGAGGAGGAGAAATATCTGTCCAG 672

Qy 55 TrpSerProGlyLysGluThrSerTyr---ThrGlnTyrThrValLysArgThrTyrAla 73
 Db 673 TGGACCCCGGAGAGGAGACTTACTTGAACCAACTACCTTGAATTCAGAGTGGCA 732

Qy 74 PheGlyGluLysHisAspAsnCysThrThrAsnSerSerThrSerGluAsnArgAlaSer 93
 Db 733 ---ACAGAAAGTTTCCGTGATGTCAGTCAAGATGAGCACT-----TCA 774

Qy 94 CysSerPhe---PheLeuProArgIleThrIleProAspAsnTyrThrIleGluValGlu 112
 Db 775 TGTATGTCAGCTACAGCCACCACTTATATGTC-----AACATTGAAGTCTGGTGAA 828

Qy 113 AlaGluAsnGlyAspGlyValIleLysSerHisMetThrTyrTrpArgLeuGluAsnIle 132
 Db 829 GCAGAGATGCCCTTGGAGAGCTCTCTCAGAGCTTATCAATTTTGAACCCCGGATPAA 888

Qy 133 AlaLysThrGluProProlLysIlePheArgValLysProValLeuGlyIleLysArgMet 152
 Db 889 GTGAAACCCACCCACCATTAATTAATTCAGTGACCAACTCAGAGAAATTCAGATATA 948

Qy 153 IleGlnIleGluTrpIleLysProGluLeuAlaProValSerSerAspLeuLysTyrThr 172
 Db 949 TTAAGCTATCATGAGTGCAGTTCAGGCTGGCGGTCTT---TTAGATCTTAAAGTCTGAC 1005

Qy 173 LeuArgPheArgThrValAsnSerThrSerTrpMetGluValAsnPheAlaLysAsnArg 192
 Db 1006 ATCCAAATATAGAGCAAAAGATGCTTCACTTGAATCCAGGCTCTT---GAAGATACA 1062

Qy 193 LysAspLysAsnGlnTyrThrValLeuThrGlyLeuGlnProPheThrGlyTyrValIle 212
 Db 1063 ATGCTCTCGAAGCTTCTTCACTGTCAGAGACCTCAAGCTTTTACAGATATGCTTT 1122

QY 213 AIAleuArgCyAlaValIysGluSer-----LysPheTrpSerAspTrpSerGlnGlu 230
 Db 1123 AAGATCCGG---TCCATTAAAGACACTGGGAAGCGCTACTGAGTACTGAGTGAAGAG 1179
 QY 231 LysMetGlyMetThrGlnGluGlu 238
 Db 1180 GCTAGTGGAGCACATACAGAGAC 1203

RESULT 13
 BOS60019 487 bp mRNA linear EST 20-JUN-2002
 LOCUS H4061G10-5 NIA Mouse 7.4K cDNA Clone Set Mus musculus cDNA clone
 DEFINITION H4061G10 5', mRNA sequence.
 ACCESSION BOS60019
 VERSION BOS60019.1 GI:21460904
 KEYWORDS EST.
 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 487)
 VanBuren,V., Pao,Y., Dudekula,D.B., Qian,Y., Carter,M.G.,
 Martin,P.R., Steag,C.A., Baesey,U., Alba,K., Hamatani,T.,
 Kargul,G.U., Luo,A.G., Kelso,J., Hide,W. and Ko,M.S.H.
 Assembly, verification, and initial annotation of NIA 7.4K mouse
 cDNA clone set
 Genome Res. 12 (12), 1999-2003 (2002)
 MEDLINE 22354164
 PUBMED 12466305
 COMMENT Other ESTs: H4061G10-3
 Contact: Yong Qian
 Laboratory of Genetics
 National Institute on Aging/National Institutes of Health
 333 Cassell Drive, Suite 3000, Baltimore, MD 21224-6820, USA
 Email: cna@igsun.grc.nia.nih.gov
 This clone set has been freely distributed to the community. Please
 visit http://igsun.grc.nia.nih.gov/cDNA/NIA_7_4K.html for details.
 Plate: H4061 row: G column: 10
 Seq primer: -21M13 Reverse
 High quality sequence stop: 487
 POLY=A=No.

FEATURES
 source Location/Qualifiers
 1..487
 /organism="Mus musculus"
 /mol_type="mRNA"
 /strain="C57BL/6"
 /db_xref="taxon:10090"
 /db_xref="taxon:10090"
 /clone="H4061G10"
 /sex="mixed"
 /dev_stage="mixed"
 /lab_host="DH10B"
 /clone_lib="NIA Mouse 7.4K cDNA Clone Set"
 /note="Vector: pSPORT1; Site 1: SalI; Site 2: NotI; This
 clone is among a rearranged set of 7,407 clones from more
 than 20 cDNA libraries."

ORIGIN
 Alignment Scores:
 Pred. No.: 3,49e-19 Length: 487
 Score: 265.00 Matches: 50
 Percent Similarity: 64.89% Conservative: 11
 Best Local Similarity: 53.19% Mismatches: 25
 Query Match: 19.51% Indels: 8
 DB: 5 Gaps: 1

US-10-006-265-4 (1-252) x BOS60019 (1-487)

QY 6 GlnProSerCysValAsnLeuGlyMetMetTrpThrTrpAlaLeuTrpMetLeuProSer 25
 Db 229 CAGCCTCGGTGTGTGAACCTGGAAATATATGTGAGCCTTGCGACACTGTGGCATTCCTTTC 288

QY 26 LeuCyAlsPheSerLeuAlaAlaLeuProAlaLysProGluAsnLysSerCysValTyr 45
 Db 289 CTTGTGAATTCAGCTGGACGCTCTCCGCACTTAAGCCAGAGAACTTTCGCGCTTT 348
 QY 46 TyrTyrArgLysAsnLeuThrCysThrTrpSerProGlyLysGluThrSerTyrThrGln 65
 Db 349 TACTTCGACAGAAATCTGACTTGACCTTGAGACAGAGAGAAACCAATATACACAC 408
 QY 66 TyrThrValLysArgThrTyrAlaPheGlyGluLysHisAspAsnCyThrThrAsnSer 85
 Db 409 TACATTGTGACTTTCGACTTCTCTATGAAAA-----AAC 444
 QY 86 SerThrSerGluAsnArgAlaSerCysSerPhePheLeuPro 99
 Db 445 AATTATAGTACAAATGCTACAGAGGCTTCATATCTTTTCCC 486

RESULT 14
 CF780723 887 bp mRNA linear EST 20-OCT-2003
 LOCUS AGENCOURT 15873120 NIH MGC 219 Homo sapiens cDNA clone
 DEFINITION IMAGE:30523682 5', mRNA sequence.
 ACCESSION CF780723
 VERSION CF780723.1 GI:37740344
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
 1 (bases 1 to 887)
 NIH-MGC <http://mhc.nci.nih.gov/>.
 National Institutes of Health, Mammalian Gene Collection (MGC)
 Unpublished (1999)
 COMMENT Contact: Daniela S. Gerhard, Ph.D.
 Office of Cancer Genomics / NIH
 National Cancer Institute / NIH
 Bldg. 31 Rm10A07 Bethesda, MD 20892
 Email: cga@b3-remail.nih.gov
 Tissue Procurement: James Martin, University of Iowa
 cDNA Library Preparation: M. Bento Soares, University of Iowa
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Agencourt Bioscience Corporation
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
 Plate: NDAW602 row: a column: 03
 High quality sequence stop: 683.

FEATURES
 source Location/Qualifiers
 1..887
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:30523682"
 /tissue_type="Pooled Chondrosarcoma Tumor cells"
 /lab_host="DH10B (T1 phage-resistant)"
 /clone_lib="NIH MGC 219"
 /note="Vector: pYX-AecI; Site 1: EcoRI; Site 2: NotI;
 library is oligo-dT primed and directionally cloned
 Denatured RNA was size fractionated on a 1% agarose gel.
 First strand cDNA synthesis was primed with oligo-dT
 primer containing a Not I site. Double strand cDNA was
 size selected according to mRNA size fraction, ligated with
 EcoR I adaptor, digested with Not I and then cloned
 directionally into pYX-AecI vector. Average insert size
 0.5-1kb. Adaptors 5'(AATTCGACACAGG)3' and 5'd
 (CCTCGTGGCG)3'. 3' linker sequence - GGCGCGCTGAGAGCC T18.
 Sequencing primers 3'end: T3 promoter primer 5'd
 (AATTAACCTCCTTAAGGGA)3', 5' End: T7 promoter primer 5'd
 (TAATACGACCTCATTAAGG)3'. Library was constructed in the
 laboratory of M. Bento Soares. Average insert size 2-3kb.
 Note: this is a NIH_MGC library."

ORIGIN
 Alignment Scores:

Pred. No.:	1,586-18	Length:	887
Score:	262.50	Matches:	65
Percent Similarity:	51.85%	Conservative:	47
Best Local Similarity:	30.09%	Mismatches:	75
Query Match:	19.33%	Indels:	29
DB:	7	Gaps:	11

US-10-006-265-4 (1-252) x CF780723 (1-887)

QY	35	PROALALYSPROGLUASNLLESERYVALTYRTRYRGLYASNLTHRCYSYTHR	54
DB	85 <td>CCAGAAAAACCTTAAATTTGAGTTGATCGAAGAGGGAGAAATAGAGTGTGAG</td> <td>144</td>	CCAGAAAAACCTTAAATTTGAGTTGATCGAAGAGGGAGAAATAGAGTGTGAG	144
QY	55 <td>TRPSERPROGLYVGLIUTHSERTRY---THRGINTYRTHVALYV-----ARG</td> <td>70</td>	TRPSERPROGLYVGLIUTHSERTRY---THRGINTYRTHVALYV-----ARG	70
DB	145 <td>TGGATGTGTGAAGGAAACACACTTGAGACAACTTCACTTAAATCTGMAATGGCA</td> <td>204</td>	TGGATGTGTGAAGGAAACACACTTGAGACAACTTCACTTAAATCTGMAATGGCA	204
QY	71 <td>THRTYRALPHEGLYGLU-----LYSHLSAEP-----ASACYSYTHRTHASN</td> <td>84</td>	THRTYRALPHEGLYGLU-----LYSHLSAEP-----ASACYSYTHRTHASN	84
DB	205 <td>ACACACAAAGTTTGCATTTGCAACCAAAACCTGCACCCCACTTCATGCATTTGAT</td> <td>264</td>	ACACACAAAGTTTGCATTTGCAACCAAAACCTGCACCCCACTTCATGCATTTGAT	264
QY	85 <td>SERSETHRSERGLUASNAHGLASERCYSERPEHELEUPROARGILETHRIEPRO</td> <td>104</td>	SERSETHRSERGLUASNAHGLASERCYSERPEHELEUPROARGILETHRIEPRO	104
DB	265 <td>TATTTACT-----GCTATTTTGTG-----</td> <td>285</td>	TATTTACT-----GCTATTTTGTG-----	285
QY	105 <td>ASPARTYRTHRIEGLUVALGLUAGLUANGLYASPGLYVALILEYLSER---HIS</td> <td>123</td>	ASPARTYRTHRIEGLUVALGLUAGLUANGLYASPGLYVALILEYLSER---HIS	123
DB	286 <td>--AACATTTGAAGCTGTGGTGTGAAACAGAGATGCTTGGGAGAGTTACATCAATCAT</td> <td>342</td>	--AACATTTGAAGCTGTGGTGTGAAACAGAGATGCTTGGGAGAGTTACATCAATCAT	342
QY	124 <td>METHTRYTRTPARGLEUGLUSNLLEALALYSETHRGUINPROPOLYALIEPHERVAL</td> <td>143</td>	METHTRYTRTPARGLEUGLUSNLLEALALYSETHRGUINPROPOLYALIEPHERVAL	143
DB	343 <td>ATCAATTTTGATCTCTGATATPAAAGTG--AAGCCCAATTCGCCACATPAAATTTATCACTG</td> <td>399</td>	ATCAATTTTGATCTCTGATATPAAAGTG--AAGCCCAATTCGCCACATPAAATTTATCACTG	399
QY	144 <td>LYSPROVALLEUGLYLILEYASRGWETILEGLINLEGLUTRIPLELSPROGLIUDUALA</td> <td>163</td>	LYSPROVALLEUGLYLILEYASRGWETILEGLINLEGLUTRIPLELSPROGLIUDUALA	163
DB	400 <td>ATCAACCTGAGAGAACTGCTAGATCTTAAATTTGACATGAGACCAACCAAGATTAAAG</td> <td>459</td>	ATCAACCTGAGAGAACTGCTAGATCTTAAATTTGACATGAGACCAACCAAGATTAAAG	459
QY	164 <td>PROVALSERSEAPLEULYSTRYTHRIEUDARGPHEARTGTHVALASNERTHSERTRP</td> <td>183</td>	PROVALSERSEAPLEULYSTRYTHRIEUDARGPHEARTGTHVALASNERTHSERTRP	183
DB	460 <td>AGTGTATPAAATA--CTAAATATATCAATTCATATATAGACCAAAAGATGCTCAACTGG</td> <td>516</td>	AGTGTATPAAATA--CTAAATATATCAATTCATATATAGACCAAAAGATGCTCAACTGG	516
QY	184 <td>METGLUVALAANPHEALILEYASNAHGLYASAPLYSAENGINTHYRASHLEUTHRLY</td> <td>203</td>	METGLUVALAANPHEALILEYASNAHGLYASAPLYSAENGINTHYRASHLEUTHRLY	203
DB	517 <td>AGCCAGATTCCT--CCTGAAGACACACACATCCACCCGATCTTCATCTGTCCAGAC</td> <td>573</td>	AGCCAGATTCCT--CCTGAAGACACACACATCCACCCGATCTTCATCTGTCCAGAC	573
QY	204 <td>LEUGINPROPHETHRGUITYRVALILEALALEUARGYSALAVAILYGLUSERLYS---</td> <td>222</td>	LEUGINPROPHETHRGUITYRVALILEALALEUARGYSALAVAILYGLUSERLYS---	222
DB	574 <td>CTTAAACCTTTTACGATATGTGTGTTAGCATTCCTGTATGAGAAAGATGCTAAAGGA</td> <td>633</td>	CTTAAACCTTTTACGATATGTGTGTTAGCATTCCTGTATGAGAAAGATGCTAAAGGA	633
QY	223 <td>PHETPSERAPETPSERGINGLULYSWETGLYMETHRGJUGLUGLU</td> <td>238</td>	PHETPSERAPETPSERGINGLULYSWETGLYMETHRGJUGLUGLU	238
DB	634 <td>TACTGAGTAGTACTGAGTAGAAGCAAGTGGGATCACTATGAAGAT</td> <td>681</td>	TACTGAGTAGTACTGAGTAGAAGCAAGTGGGATCACTATGAAGAT	681

RESULT 15
BC071555
LOCUS
DEFINITION
Homo sapiens CDNA clone IMAGE:4374041, containing frame-shift error.
ACCESSION
VERSION
KEYWORDS
BC071555.1 GI:47938807
SOURCE
ORGANISM
Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 5264)
Straubery,R.L., Collins,F.S., Wagner,L., Shemen,C.M., Schuler,G.D., Klausner,R.D., Collins,F.S., Wagner,L., Shemen,C.M., Schuler,G.D., Altschul,S.F., Zeeberg,B., Butow,K.H., Schaefer,C.F., Bhat,N.K., Hopkins,R.F., Jordan,H., Moore,T., Max,S.I., Wang,J., Hsieh,F., Ditschenko,L., Marusina,K., Farmer,A.A., Rubin,G.M., Hong,L., Stepicron,M., Soares,M.B., Bonaldo,M.F., Casavant,T.L., Schaefer,T.E., Brownstein,M.J., Udell,T.B., Toshitaki,S.,

TITLE	Abramson,R.D., Mullighy,S.J., Bosak,S.A., McEwan,P.J., McKernan,K.U., Malek,J.A., Gunaratne,P.H., Richards,S., Worley,K.C., Hale,S., Garcia,A.M., Gay,L.J., Huily,S.W., Villalon,D.K., Muzny,D.M., Sodergren,E.J., Lu,X., Gibbs,R.A., Fahay,J., Helton,E., Kettelman,M., Madan,A., Rodriguez,S., Sanchez,A., Whiting,M., Madan,A., Young,A.C., Shevchenko,Y., Boulford,G.G., Blakesley,R.W., Touchman,J.W., Green,E.D., Dickson,M.C., Rodriguez,A.C., Grimwood,J., Schmeitz,U., Myers,R.M., Butterfield,Y.S., Krzywinski,M.I., Skalska,U., Smalish,D.E., Schnerch,A., Schein,J.B., Jones,S.J. and Martin,M.A. Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences <i>Proc. Natl. Acad. Sci. U.S.A.</i> 99 (26), 16899-16903 (2002)
JOURNAL	12471932
PUBMED	2 (bases 1 to 5264)
REFERENCE	Strausberg,R. Direct Submission
AUTHORS	Submitted (01-JUN-2004) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA
TITLE	NIH-MGC Project URL: http://mgc.nci.nih.gov Contact: MGC help desk Email: cgsbdb-re@mail.nih.gov Tissue procurement: Miklos Palcovits, M.D., Ph.D. CDNA library preparation: Michael J. Brownstein (NHGRI) & Shiraki Toehiyuki and Piero Carninci (RIKEN) CDNA library Arrayed by: The I.M.A.G.E Consortium (LNL) DNA Sequencing by: Sequencing Group at the Stanford Human Genome Center, Stanford University School of Medicine, Stanford, CA 94305 Web site: http://www.sbgc.stanford.edu Contact: (Dickson, Mark) mcd@pacifi.stanford.edu Dickson, M., Schmutz, J., Grimwood, J., Rodriguez, A., and Myers, R. M.
REMARK	Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNLT at: http://image.lnl.gov Series: IRAX Plate: 167 Row: a Column: 18 This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA g1: 28610146 This clone has the following problem: frame shifted.
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GenCore version 5.1.6
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Run on: February 23, 2005, 07:24:37 ; Search time 8369.27 Seconds
(without alignments)
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Post-processing: Minimum Match 0%
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Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	3528	100.0	2903	6	AX365201 Sequence
3	3528	100.0	2903	9	AY499342 Homo sapi
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RESULT 1	LOCUS	DEFINITION	ACCESSION	VERSION	KEYWORDS	SOURCE	ORGANISM	REFERENCE	AUTHORS	TITLE	JOURNAL	COMMENT	
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OS	Homo sapiens (human)	PN	WO 0075314-A/14	PD	14-DEC-2000	WO 2000JP003556	PR	02-JUN-1999 JP 99P	155797,30-JUL-1999 JP 99P	217797 PI	MASATSUGU MADA,NORIKO YAGUCHI	PC	C12N15/12,C12N5/10,C07K14/715,C07K16/28,C12P21/02,G01N33/53,
CC	G01N33/566	FT	Key	Location/Qualifiers	(11)..(1996).								

ALIGNMENTS

RESULT 1	LOCUS	DEFINITION	ACCESSION	VERSION	KEYWORDS	SOURCE	ORGANISM	REFERENCE	AUTHORS	TITLE	JOURNAL	COMMENT	
BD091877	Novel hemopoietin receptor protein, NR10.	BD091877.1 GI:22637488	WO 0075314-A/14.	Homo sapiens (human)	Homo sapiens	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.	1 (bases 1 to 2119)	Maeda,M. and Yaguchi,N.	Novel hemopoietin receptor protein, NR10	Patent: WO 0075314-A 14-DEC-2000;	CHIGAI RESEARCH INSTITUTE FOR MOLECULAR MEDICINE INC, MASATSUGU	MADA, NORIKO YAGUCHI	
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FEATURES

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US-10-006-265-17 (1-662) x BD091877 (1-2119)

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REFERENCE
AUTHORS Sprecher, C.A., Presnell, S.R., Gao, Z., Whitmore, T.E., Kuiper, J.L.
          and Maurer, M.F.
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REFERENCE 1 (bases 1 to 2903)
AUTHORS Dillon,S.R., Sprecher,C., Hammond,A., Bilsborough,J., Maurer,M.,
Resenfeld-Franklin,M., Presnell,S.R., Haugen,H.S., Harder,B.,
Harder,B., Johnston,J., Bort,S., Mudri,S., Kujiper,J.L.,
Bukowski,T., Shea,P., Dong,D.L., Dasovich,M., Grant,F.J.,
Lockwood,L., Levin,S.D., Leciel,C., Maggie,K., Day,H., Topouzis,S.,
Kramer,J., Kuestner,R., Chen,Z., Foster,D., Parrish-Novak,J. and
Gross,J.A.
Interleukin 3l, a cytokine produced by activated T cells, induces
dermatitis in mice
JOURNAL Nat. Immunol. 5 (7), 752-760 (2004)
PUBMED 15184896
REFERENCE 2 (bases 1 to 2903)

AUTHORS Dillon,S.R., Sprecher,C., Hammond,A., Resenfeld-Franklin,M.,
Presnell,S.R., Haugen,H., Bilsborough,J., Maurer,M., Harder,B.,
Johnston,J., Bort,S., Mudri,S., Kujiper,J., Bukowski,T., Shea,P.,
Dong,D., Dasovich,M., Lockwood,L., Levin,S., Leciel,C., Maggie,K.,
Kramer,J., Kuestner,R., Chen,Z., Foster,D., Parrish-Novak,J. and
Gross,J.A.
TITLE Direct Submission
JOURNAL Submitted (10-DEC-2003) Bioinformatics, ZymoGenetics, Inc., 1201
Eastlake Avenue East, Seattle, WA 98102, USA
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 and Maurer,M.F.
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 DEFINITION Sequence 5 from Patent WO0229060.
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 VERSION AX467335.1 GI:21900585
 KEYWORDS
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 Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
 REFERENCE 1 Cosman,D.J., Mosley,B.A., Bird,T.A., Dubose,R.F. and Wiley,S.R.
 Hematopoietic receptors hprt and hprt2

JOURNAL Patent: WO 0229060-A 5 11-APR-2002;
Immunex Corporation (US)
FEATURES Location/Qualifiers
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ORIGIN

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US-10-006-265-17 (1-662) x AX467335 (1-2238)

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DEFINITION complete cds, alternatively spliced.
ACCESSION AY499341
VERSION AY499341.1 GI:46276460

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REFERENCE
AUTHORS 1 (bases 1 to 2393)
Dillon,S.R., Sprecher,C., Hammond,A., Bilborough,J.,
Rosenfeld-Franklin,M., Presnell,S.R., Haugen,H.S., Maurer,M.,
Harder,B., Johnston,J., Bort,S., Mudri,S., Kuijper,J.L.,
Bukowski,T., Shea,P., Dong,D.L., Dasovich,M., Grant,F.J.,
Lockwood,L., Levin,S.D., Leciel,C., Maggie,K., Day,H., Topouzis,S.,
Kramer,J., Kuestner,R., Chen,Z., Foster,D., Parrish-Novak,J. and
Gross,J.A.

TITLE Interleukin 31, a cytokine produced by activated T cells, induces
dermatitis in mice
JOURNAL Nat. Immunol. 5 (7), 752-760 (2004)

REFERENCE
PUBMED 15184896
2 (bases 1 to 2393)
Dillon,S.R., Sprecher,C., Hammond,A., Rosenfeld-Franklin,M.,
Presnell,S.R., Haugen,H., Bilborough,J., Maurer,M., Harder,B.,
Johnston,J., Bort,S., Mudri,S., Kuijper,J., Bukowski,T., Shea,P.,
Dong,D., Dasovich,M., Lockwood,L., Levin,S., Leciel,C., Maggie,K.,
Kramer,J., Kuestner,R., Chen,Z., Foster,D., Parrish-Novak,J. and
Gross,J.A.

TITLE Direct Submission
JOURNAL Submitted (10-DEC-2003) Bioinformatics, ZymoGenetics, Inc., 1201
Eastlake Avenue East, Seattle, WA 98102, USA
FEATURES
source location/Qualifiers

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 DEFINITION Sequence 1 from Patent WO0200721.
 ACCESSION AX365149

VERSION AX365149.1 GI:18696908
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 SOURCE
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 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 REFERENCE
 1 Sprecher, C.A., Preenell, S.R., Gao, Z., Whitmore, T.E., Kujper, J.L.,
 and Maurer, M.F.
 Cytokine receptor zcytor17
 Patent: WO 020721-A 1 03-JAN-2002;
 JOURNAL ZymoGenetics, Inc. (US)
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 REFERENCE 1
 AUTHORS Cosman, D.J., Mosley, B.A., Bird, T.A., Dubose, R.F. and Wiley, S.R.
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 Immunex Corporation (US)
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 REFERENCE 1 (bases 1 to 2952)
 AUTHORS Maeda,M., Yasuchi,N. and Hasegawa,M.
 TITLE NR10 splicing variants
 JOURNAL Patent: WO 02077230-A 3 03-OCT-2002;
 CHUGAI PHARMACEUTICAL CO LTD,MASATSUGU MAEDA,NORIKO YASUCHI,
 MASAKAZU HASEGAWA
 OS Homo sapiens (human)
 PN WO 02077230-A/3
 PD 03-OCT-2002
 PF 22-MAR-2002 WO 2002JP002769

PR 26-MAR-2001 JP 01P 087298
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DB AAGTCTCCAGTGGCCACCTGAGGATTCAGCTAATTCAGAAATCATTTCAAGTCAAT 1089
QY 343 GluValMetGluAlaCysValAlaGluAspGlnLeuValValLysTrpGlnSerSerAla 362
DB GAGTCATACAGGCTCGCTGCTGAGAGACCACTAGTGTGAAGTGGCAAGCTCTGCT 1149
QY 363 LeuAspValAsnThrTrpMetIleGluTrpPheProAspValAspSerGluProThr 382
DB CTAGACGTGAACACTGATGATGAAATGTTCCGAGATGGACTCAGAGCCACACACC 1209
QY 383 LeuSerTrpGluSerValSerGlnAlaThrAsnTrpThrIleGlnGlnAspLysLeuLys 402
DB CTTCCTGGAAATCTGTGTCTCAGGACAGGACAGGACATGACATCAAGAAATTAATTA 1269
QY 403 ProPheTrpCysTyrAsnIleSerValTyrPrometLeuHisAspLysValGlyLysPro 422
DB CTTTGTGCTCTATTAACATCTCTGTGTATCCAATTTGCAATGACAAATTTGGCAGCA 1329
QY 423 TyrSerIleGlnAlaTyrAlaLysGluGlyValProSerGluGlyProGluTrpVal 442
DB TATTCATCAGGCTTATCCAAAGAGGCGTTCCATCAGAGTCCAGAGTCCAGAGGTTG 1389
QY 443 GluAsnIleGlyValLysThrValThrIleThrTrpLysGluIleProLysSerGluArg 462
DB GAGAACTTGGGCGTGAAGAGGTCAGATCAATGAAAGAGTTCCAAAGTGTGAGAA 1449
QY 463 LysGlyIleIleCysAsnTyrThrIlePheTyrGlnAlaGluGlyLysGlyPheSer 482
DB AAGGATATCATCTGCACTACACATCTTTTACCAAGCTGAAAGTGAAGATTTCTCC 1509
QY 483 LysThrValAsnSerSerIleLeuGlnTyrGlyLeuGluSerLeuLysArgLysThrSer 502
DB AAGACAGTCAATTCAGCATCTTTCAGTACGGGCTGAGTCCCTGAAACGAAAGACTCT 1569
QY 503 TyrIleValGlnValMetAlaSerThrSerAlaGlyGlyThrAsnGlyThrSerIleAsn 522
DB TACATTTGTCAGTCAATGCGACAGCAACAGTGTGGGGAAACCAACGAGCAATTAAT 1629
QY 523 PheLysThrLeuSerPheSerValPheGluIleIleLeuIleThrSerLeuIleGlyGly 542
DB TTCAAGACATTTGATTCATTCAGTGTCTTTGAGATTAATCTCATTAATCTCTGATGTGA 1689
QY 543 GlyLeuLeuIleLeuIleIleLeuThrValAlaTyrGlyLeuLysLysProAsnLysLeu 562
DB GGCTTTCTTATTCCTATTAATCCGACAGAGTGGCATATGCTCAAAAACCAACAATTTG 1749
QY 563 ThrHisLeuCysTrpProThrValProAsnProAlaGluSerSerIleAlaThrTrpHis 582
DB ACTCATCTGTGTGGCCACCGTTCACCACTGTGGAAGAGATTAACCAATGCAATGGCA 1809
QY 583 GlyAspAspPheLysAspLysLeuAsnLeuLysGluSerAspAspSerValAsnTrpGlu 602
DB GAGGATGATTTTCAAGATTAAGCTTAACCTGAAAGAACTGTGATGATCTGTGAACACAGA 1869
QY 603 AspArgIleLeuLysProCysSerThrProSerAspLysLeuValIleAspLysLeuVal 622

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Db      1870 GACAGGATCTTAAACCATGTTCCACCCCGAGTGCAAGTGGATGACAGTGGTG 1929
Qy      623 ValanphegiAasnValleuGInguIlePheThraSpGluAlaYrThrGlyGIngu 642
Db      1930 GTGAACCTTGGGAATGTTCTCCAGAAATTTTTCACAGATGAAGCAGAACGGGTGAGAA 1989
Qy      643 AasnleuGlyGlyGluYrAasnGlyThraGlyIleuSerSerCyPro 659
Db      1990 AACAAATTAGAGGGGAAAGATGG-----TATGTGACCTGCCCC 2031

RESULT 13
BD178871
LOCUS      BD178871          5271 bp      DNA      linear      PAT 16-APR-2003
DEFINITION NR10 splicing variants.
ACCESSION  BD178871
VERSION    BD178871.1 GI:30016138
KEYWORDS   WO 02077230-A/2.
SOURCE     Homo sapiens (human)
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE  1 (bases 1 to 5271)
AUTHORS   Maeda, M., Yaguchi, N. and Hasegawa, M.
TITLE     NR10 splicing variants
JOURNAL    Parent: WO 02077230-A 2 03-OCT-2002;
           CHUGAI PHARMACEUTICAL CO LTD, MASATSUGU MAEDA, NORIKO YAGUCHI,
           MASAKAZU HASEGAWA
COMMENT    OS Homo sapiens (human)
           PN WO 02077230-A/2
           PD 03-OCT-2002
           PR 22-MAR-2002 WO 2002JP002769
           PI 26-MAR-2001 JP 01P 087298
           PT MASATSUGU MAEDA, NORIKO YAGUCHI, MASAKAZU HASEGAWA PC
           CI2N1/12, C07K14/715, C07K16/28, CI2N1/15, CI2N1/19, CI2N1/21, PC
           CI2N5/10,
           PC C12P21/02, G01N33/15, G01N33/50, G01N33/53
           FH NR10 splicing variants
           FT CDS
           Location/Qualifiers
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             /db_xref="taxon:9606"

ORIGIN
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Pred. No.:      1,26-299      Length:      5271
Score:          3465.50      Matches:      651
Percent Similarity: 99.24%      Conservative: 1
Best Local Similarity: 99.09%      Mismatches: 2
Query Match:    98.23%      Indels:      3
DB:             6      Gaps:      1

US-10-006-265-17 (1-662) x BD178871 (1-5271)
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Qy      23 LeuProSerLeuCyGlySpPheSerLeuAlaAlaLeuProAlaLysProGluAasnIleSer 42
Db      130 CTCCTCCCGACGCTTCAAAATTCAGCTGGCACTTGGCAGCTTAAGCTTGAGAAATTTCC 189
Qy      43 CyValIlyrYrYrYrAsglyAasnleuThrCySerThrTPSerProGlyLysGlyLysSer 62
Db      190 TGTGTCTACTACTATAGAAAATTTTAACCTGCACCTGCACTGCAAGAAAGAAACCGT 249
Qy      63 TyrThrGlnTyrThrValLysAsglyThrTyrAlaPheGlyGlyLysLysAasnCySerThr 82
Db      250 TATACCCAGTACAGAGTTAAGAACTTAACGCTTTGGAGAAAACATGATTAATTGTACA 309

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Qy      83 ThrAasnSerThrSerGluAasnArgAlaSerCySerPhePheLeuProArgIleThr 102
Db      310 ACCAATAGTTCTACAGAGGAAATCGTCTTCGTCTTTTCTTCTTCCCAAGAAATACG 369
Qy      103 IleProAasnTyrThrIleGlyValGluAlaGluAasnGlyAasnGlyValIleYsSer 122
Db      370 ATCCAGATTAATTATACCATGAGGTGGAACTGAAAATGAGATGGGTATTAATCT 429
Qy      123 HisMetThrTyrTPThraGlyLeuAasnIleAlaLysThrGluProProLysIlePheArg 142
Db      430 CATATGACATCTAGAGATTAGAAACATACCGAAACCTGAACCACTTAAGATTTTCCGT 489
Qy      143 ValLysProValleuGlyIleLysArgMetIleGlnIleGluTyrIleLysProGluLeu 162
Db      490 GTGAACCAAGTTTGGGCATCAACAGATGATTTAAATTTGAATGATTAAGCTTGAGTTG 549
Qy      163 AlaProValSerSerAasnLysTyrThrLeuArgPheArgThrValAasnSerThrSer 182
Db      550 GCGCTGTTTCATCTGATGATTTAAATVACACACTTCGATTCAAGACAGTCAACAGTACAGC 609
Qy      183 TPMetGluValAasnPheAlaLysAasnArgLysAasnGlyAasnGlnThrTyrAasnLeuThr 202
Db      610 TGATGTGAAGTCAACTTCGCTTAAGAACCGTAAAGATTAACCAACGTAACACTCAGC 669
Qy      203 GlyLeuGlnProPheThrGluTyrValIleAlaLeuArgCyValAlaValLysGluSerLys 222
Db      670 GGGCTGACGCTTTTACGATATGCTCATACTCTTCGATGTGCGCTCAAGAGTCAAG 729
Qy      223 PheTyrSerAasnTPSerGlnGluLysMetGlyMetThrGluGluGluAlaProCyGly 242
Db      730 TTTCTGAGTGTACTGGAGCCAAAGAAAATGGGAATGACTGAGAAAGACCTCATGTGGC 789
Qy      243 LeuGluLeuTPThraGlyValLysProAlaGluAlaAasnGlyAasnGlyProValArgLeu 262
Db      790 CTGAACATGTGGAAAGCTCGAAACCAAGCTGAGCGGATGAAAGAGCCAGTGGGTGG 849
Qy      263 LeuTPThraLysValAasnGlyValAProValleuGluLysThrLeuGlyTyrAasnIleTP 282
Db      850 TTATGAGAAAGGCAAGAGAGGCCCTTCTTAAGAAACACTTGGCTACACATATGG 909
Qy      283 TyrTyrProGlnSerAasnThrAasnLeuThrGluThrMetAasnThrAasnGlnLeu 302
Db      910 TACTATCAGAAACCAACACTTAACCTCAAGAAACATTAACACTTAACACAGACTT 969
Qy      303 GluLeuHisLeuGlyGlyGluSerPheThrValSerMetIleSerTyrAasnSerLeuGly 322
Db      970 GAACCTGATCTGGAGGCGAGAGCTTTGGGTCTATGATTTCTTAAATCTCTTGGG 1029
Qy      323 LysSerProValAlaThrLeuArgIleProAlaIleGlnGluLysSerPheGlnCyAla 342
Db      1030 AAGTCTCAGTGGCCACCTGAGGATTCAGCTAATTCAGAAATCAATTCAGTGCATT 1089
Qy      343 GluValMetGlnAlaCyValAlaGluAasnLeuValLysTyrTPGlnSerSerAla 362
Db      1090 GAGGTATGCAAGCGCTCGTGTCTGAGAGCACAGCTAATGTGGAGAGTGGCAAGCTCTGCT 1149
Qy      363 LeuAasnValAasnThrTPMetIleGluTyrPheProAasnValAasnSerGluProThr 382
Db      1150 CTAAACCTGAACACTTGAATGATTAATGATTTCCGATGTGGACTCAGAGCCACACACC 1209
Qy      383 LeuSerTPGlnSerValSerGlnAlaThrAasnThrIleGlnGlnAasnLysLeuLys 402
Db      1210 CTTTCTGGGAATGTGTCTCAGGCGCACAGAACCTGAGCGAATTCAGAAATTAATAA 1269
Qy      403 ProPheTPCySerAasnIleSerValTyrProMetLeuHisAasnLysValGlyLysPro 422
Db      1270 CTTTCTGGGTGATTAACATCTGTGTATCAATGTGATGACAAAGTTGGAGACCA 1329
Qy      423 TyrSerIleGlnAlaTyrAlaLysGlyValProSerGluGlyProGluThrLysVal 442
Db      1330 TATTTCATCCAGGCTTAATGCAAGAGGCTTCCATCAAGAGTCTTGAGAACCAAGTGT 1389
Qy      443 GluAasnIleGlyValLysThrValThrIleThrTPryGluIleProLysSerGluArg 462

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Db 1450 AAGGGATCATCTTGCAACTACACCATCTTTTACCAAGCTGAAGGTGAAAGAAATCTCC 1509
QY 483 LysThrValAsnSerSerIleLeuGlnYrGlyLeuGluSerLeuYrAspYrGlyThrSer 502
Db 1510 AAGACAGTCATTTCCAGCATCTTGAGTACGGCTGGAGTCCCTGAAGCAAGAAAGACTCT 1569
QY 503 TyrIleValGlnValMetAlaSerThrSerAlaGlyGlyYrThrAsnGlyYrThrSerIleAsn 522
Db 1570 TACATTGTTCAGGTCAATGGCCACACAGGTGCTGGGGGAAACCAACGGACCAACATTAAT 1629
QY 523 PheLysThrLeuSerPheSerValPheGluIleIleLeuIleIleThrSerLeuIleGlyGly 542
Db 1630 TTCAAGCATGTTCATTCAGTTCGTTCCTTGAGATTATCTCTCAATACCTCTCTGATTGGTGA 1689
QY 543 GlyLeuLeuIleLeuIleIleLeuThrValAlaYrGlyLeuYrAspYrProAsnYrSLeu 562
Db 1690 GGCCTTCTTATCTCATTTATCTGACAGTGGCATATGCTCAAAAAACCAACAATTTG 1749
QY 563 ThrIleLeuCysTrpProThrValProAsnProAlaGluSerSerIleAlaThrTrpHis 582
Db 1750 ACTCATCTGTGTGGCCACCGTTCCACCTGTGAAAGTATAGCCACATGGCAT 1809
QY 583 GlyAspAspPheLysAspLysLeuAsnLeuLeuYrGluSerAspAspSerValAsnTrpGlu 602
Db 1810 GAGATGATTTCAAGGATTAAGTAACTGTAAGAGATCTGATGATCTGTGAACACAGAA 1869
QY 603 AspArgIleLeuYrProCysSerThrProSerAspLysLeuValIleAspLysLeuVal 622
Db 1870 GACAGATCTTAAACCATGTTCCACCCGACGTGACAAAGTTGGTGAATGCAAGTTGGTG 1929
QY 623 ValAsnPheGlyAsnValLeuGlnGluIlePheThrAspGluAlaArgThrGlyGlnGlu 642
Db 1930 GTCAACTTTGGGATGTCTGCAAGAAATTTTCAAGATGAACCCAGAACGGGTCAAGAA 1989
QY 643 AsnAspLeuGlyGlyGlyLysAsnGlyYrThrArgIleLeuSerSerCysPro 659
Db 1990 AACCAATTTAGAGAGGAAAGAAATGGG-----TATGTGACCTGCCCC 2031

RESULT 14
BD178873 3072 bp DNA linear PAT 16-Apr-2003
LOCUS NR10 splicing variants.
DEFINITION BD178873.1 GI:30016140
ACCESSION BD178873.1
VERSION WO 02077230-A/4.
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 3072)
AUTHORS Maeda,M., Yaguchi,N. and Hasegawa,M.
TITLE NR10 splicing variants
JOURNAL Patient: WO 02077230-A 4 03-OCT-2002;
CHUGAI PHARMACEUTICAL CO LTD, MASATSUGU MAEDA, NORIKO YAGUCHI,
MASAKAZU HASEGAWA
COMMENT OS Homo sapiens (human)
PN WO 02077230-A/4
PD 03-OCT-2002
PF 22-MAR-2002 WO 2002JP002769
PR 26-MAR-2001 JP 01P 087298
PI MASATSUGU MAEDA, NORIKO YAGUCHI, MASAKAZU HASEGAWA PC
C12N15/12, C07K14/715, C07K16/28, C12N1/15, C12N1/19, C12N1/21, PC
C12N5/10,
PC C12P21/02, G01N33/15, G01N33/50, G01N33/53
CC NR10 splicing variants
FH Key Location/Qualifiers
FT CDS Location/Qualifiers
(7)..(1887)).

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/organism="Homo sapiens"
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ORIGIN

Alignment Scores:
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Score: 3435.50 Matches: 651
Percent Similarity: 93.548 Conservative: 1
Best Local Similarity: 93.408 Mismatches: 2
Query Match: 97.388 Indels: 43
DB: 6 Gaps: 2

US-10-006-265-17 (1-662) x BD178873 (1-3072)

QY 3 LeuSerProGlnProSerCysValAsnLeuGluYrMetTrpThrTrpAlaLeuTrpMet 22
Db 70 CTCTCTCCACCTTCATGTGTAACTGGGAGATGATGTGACCTGGGCACCTGGATG 129
QY 23 LeuProSerLeuCysLeysPheSerLeuAlaAlaLeuProAlaLysProGluAsnIleSer 42
Db 130 CTCCTCTCACTGTGCAAAATTCAGCTGCGAGCTCTGCCAGCTTAAGCTTGAACAATTCC 189
QY 43 CysValYrTrpYrTrpArgLysAsnLeuThrCysThrTrpSerProGlyLysGluThrSer 62
Db 190 TGTGTCTACTACTATATGAAAAATTTAACTGCACCTTGAGTCCAGAAAGAAACAGT 249
QY 63 TyrThrGlnTyrThrValLysArgThrYrAlaPheGlyLysLysHisAspAsnCysThr 82
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QY 83 ThrAsnSerSerThrSerGluAsnArgAlaSerCysSerPhePheLeuProArgIleThr 102
Db 310 ACCAATAGTTTCAACAAGTAAATCTGCTGTGTGCTCTTTTCTTCCACAAGAAATAAG 369
QY 103 IleProAspAsnYrThrIleGluValGluAlaGluAsnGlyAspGlyValIleYrSer 122
Db 370 ATCCCACTAATTAATATACATTGAGGTGAAGCTGAAGAAATGAGATGTAAATTAATCT 429
QY 123 HisMetThrTrpTrpArgLeuGluAsnIleAlaLysThrGluProProLysIlePheArg 142
Db 430 CATATGACATACTGAGATTAAGAAACATAGCAAAATGAAACCATTAATTTCCGT 489
QY 143 ValLysProValLeuGlyIleLysArgMetIleGlnIleGluTrpIleLysProGluLeu 162
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QY 163 AlaProValSerSerAspLeuYrYrThrLeuArgPheArgThrValAsnSerThrSer 182
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QY 203 GlyLeuGlnProPheThrGlnYrValIleAlaLeuArgCysAlaValLysGluSerLys 222
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QY 223 PheTrpSerAspTrpSerGlnGluYrMetGlyMetThrGluGluGluAlaProCysGly 242
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QY 243 LeuGluLeuTrpArgValLeuLysProAlaGluAlaAspGlyArgArgProValAlaGluLeu 262
Db 790 CTGGAACTGTGAGATCTCTGAACCAAGCTGAGCGGATGAGAAAGGCGCAGTGGTGG 849
QY 263 LeuTrpLysLeuAlaArgGlyAlaProValLeuGluLysThrLeuGlyYrThrAsnIleTrp 282
Db 850 TTATGAGAAAGAGCAAGAGAGGCCCAATCTTATGAGAAAACACTTGGCTACACATATGG 909
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Db 910 TACTATCCAGAAAGCAACACTACCTCAACAGAAACAACTACCTACCTACAGACGCTT 969
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Db 970 GAACGTGCATCTGGGAGCGAGAGCTTTTGGGTCTATGATTTCTTATATATCTCTGGG 1029
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Db 1390 GAGAACATTTGCGGAAACGCTCAGATCACTGAGAAAGATTCACCAAGAGTGAAGA 1449
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Qy 483 LysThrValAsnSerSerileleuglnTyrGlyleugluserleuysArgLysThrSer 502
Db 1510 AAGACAGTCAATTCAGCATCTTGCAAGTACGGCTCGAGTCCCTGAAAGCAAAAGCTCT 1569
Qy 503 TyrIleValGlnValMetAlaSerTherSerAlaGlyLysThrAsnGlyThrSerIleAsn 522
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Qy 523 PheLysThrLeuSerPheSerValPheGluIleIleleuIleThrSerleuIleGly 542
Db 1630 TTCAAGACATTTGCTAGTCTTGAATTAATCTCATTAATCTCTGATTTGGTGA 1689
Qy 543 GtyleuLeuIleleuIleIleleuThrValAlaTyrGlyLeuLysLysProAsnLysleu 562
Db 1690 GGCCTTCTTATTCATCATATCTGACAGTGCATATGCTCAAAAAACCAACAATTTG 1749
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Db 1750 ACTCATCTGTTGGCCACCGTTCACCAACCTGCTGAAGATAGTACCAACATGGCAT 1809
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Qy 603 AspArgIleleuLysProCySerThrProSerAspLysLysValIleAspLysleuVal 622

Db 1990 GACAGATCTTAACAACATGTTCCACCCCGAGTACAGAGTTGTGATTTGACAGTTGGTG 2049
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Db 2050 GTGAACCTTTGGGAATGTTCTCCAAAGAAATTTTCAACATGAGCAGACGAGCTGAGAA 2109
Qy 643 AsnAsnleuGlyGlyGlyLysAsnGlyThrArgIleleuSerSerCyPro 659
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LOCUS AF486620
DEFINITION Homo sapiens gp130-like monocyte receptor mRNA, complete cds.
ACCESSION AF486620
VERSION AF486620.1 GI:20563276
KEYWORDS
SOURCE
ORGANISM Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE
AUTHORS Ghilardi, N., Li, J., Hongo, J. A., Yi, S., Gurney, A. and de
Savage, F. J.
TITLE A novel type I cytokine receptor is expressed on monocytes, signals
proliferation, and activates STAT-3 and STAT-5
JOURNAL J. Biol. Chem. 277 (19), 16831-16836 (2002)
MEDLINE 11877449
PUBMED 11877449
REFERENCE 2 (bases 1 to 2199)
AUTHORS Ghilardi, N., Li, J., Hongo, J. A., Yi, S., Gurney, A. and de
Savage, F. J.
TITLE Direct Submission
SUBMITTED (21-FEB-2002) Molecular Oncology, Genentech, 1 DNA Way,
South San Francisco, CA 94080, USA
FEATURES
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ALIGNMENT Scores:
Pred. No.: 8.58e-295 Length: 2199
Score: 3405.50 Matches: 640
Percent Similarity: 99.23% Conservative: 1
Best Local Similarity: 99.07% Mismatches: 2
Query Match: 96.53% Indels: 3
DB: 9 Gaps: 1
US-10-006-265-17 (1-662) x AF486620 (1-2199)
Qy 14 MetMettrpThrTrpAlaLeuTrpMetLeuProSerleuCybLysPheSerleuAlaLa 33

```

Db      1 ATGATGTGAGACCTGGGACAGTGGATGCTCCCTTCACTGCAAAATTCAGCCCTGGAGCT 60
Qy      34 LeuProAlaIySerProGluIuSenIleSerCyValTyrTyrTrpArgIyAsnLeuThrCyS 53
Db      61 CTGGCAGCTAGAGCTTAGAACATTTCTGTGTCTACTACTATAGAAAAATTTAACTGTG 120
Qy      54 ThrTrpSerProGluIySerGluThrSerTyrThrGlnTyrValIyAsnArgThrTyrAla 73
Db      121 ACTTGAGTCCAGGAAAGGAAACAGATTATCCAGTAGCAACATTAAAGAACATTACGCT 180
Qy      74 PheGlyGluIySerIleAspAsnCyThrThrAsnSerSerThiSerGluAsnArgIleSer 93
Db      181 TTTGGAGAAACATATATATTGTAACCAATAGTCTTCAAGTGAATTCGTGCTTCG 240
Qy      94 CySerPhePheLeuProArgIleThrIleProAspAsnTyrThrIleGluValIyGluAla 113
Db      241 TGCTCTTTTTCCTTCCAGAAATACGATCCAGATTAATTATACCATGAGGTGGAAAGCT 300
Qy      114 GluAsnGlyAspGlyValIleIySerSerIleMetThrTyrTrpArgLeuGluAsnIleAla 133
Db      301 GAAATTCGAGATGTGTAAATTAATCTCATATGACATCTCGAGATTAGAGAACATAGCG 360
Qy      134 IySerThrGluProProIySerIlePheArgValIySerProValIyGluIyIleIySerMetIle 153
Db      361 AAAAAGTGAACCACTTAAGATTTTCCGTGTGAAACCAAGTTTGGGCAATCAAAACGAATGATT 420
Qy      154 GlnIleGluThrIleIySerProGluIuSenAlaProValSerSerAspLeuIySerThrIleu 173
Db      421 CAATTTGAATGGATTAAGACCTGAGTGGCGCTGTTCATCTGATTTAAATAACACACTT 480
Qy      174 ArgPheArgThrValAsnSerThrSerTrpMetGluValAsnPheAlaIyAsnArgIyS 193
Db      481 CGATTCAAGACATCACTAACAGTACACAGTGGATGGAAAGTCAACTTCGTTAAGAACCGTAG 540
Qy      194 AspIyAsnGlnThrTyrAsnLeuThrGlyLeuGlnProPheThrGluTyrValIleAla 213
Db      541 GATAAAAACCAACGTAACACTCACGGGGCTGCAAGCTTTTACAGAAATGTGCATAGCT 600
Qy      214 LeuArgCyAlaIleValIySerIySerIySerPheTrpSerAspTrpSerGlnIyIySerMetGly 233
Db      601 CTGGCAGATGTGGGTCAAGAGGTCAAGATTCTGAGGTGACCTGAGCCCAAGAAAAATGGGA 660
Qy      234 MetThrGluGluIuSenAlaProCySerGlyLeuGluIuSenTrpArgValIyLeuIySerProAlaGlu 253
Db      661 ATGATCGAGGAAGAGAGCTCATGTGGCTGGAACTGTGGAGATCTCTGAAGAACAGCTGAG 720
Qy      254 AlaAspGlyArgArgProValIleGluLeuTyrIySerIleAlaArgGlyAlaProValIleu 273
Db      721 GCGGATGGAAGAGGCGCAGTGGCTGTGTTATGGAAGAGGCAAGAGAGCCCAAGTCTTA 780
Qy      274 GluIySerThrLeuGlyTyrAsnIleTyrIyTrpProGluSerAsnThrAsnLeuThrGlu 293
Db      781 GAAATAAACCTTGTGCTACCAATATGTGTAATCCAGAAAGCAACTTAACCTCACAGAA 840
Qy      294 ThrMetAsnThrThrAsnGlnIleuGluLeuIleuGlyIyGluIySerPheTrpVal 313
Db      841 ACAATGAACACTTAACCAAGAGCTTGAACCTGCATCTGGGAGCCAGAGAGCTTTGGGTG 900
Qy      314 SerMetIleSerTyrAsnSerLeuGlyIySerProValIleAlaThrLeuArgIleProAla 333
Db      901 TCTATGATTTCTTATATATCTCTTGGGAGTCTCCAGTGGCCACCCGAGAGATTCCAGCT 960
Qy      334 IleGlnIyIySerPheGlnIySerIleGluValMetGlnAlaCyValAlaGluAspGln 353
Db      961 ATTCAAGAAAAACATTTCACTGCTCATTTGAGAGTCAAGCGCTGCTGTGAGAGCAG 1020
Qy      354 LeuValIyIySerTrpGlnSerSerAlaLeuAspValAsnThrTrpMetIleGluTyrPhe 373
Db      1021 CTAGTGTGAGAGGCGAAAGCTCTGCTCTAGACGTGAACCTTGGATGATGAAATGTTT 1080
Qy      374 ProAspValAspSerGluProThrThrLeuSerTrpGluSerValSerGlnAlaThrAsn 393

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Db      1081 CCGAGTGTGACTCAGAGCCCAACCCCTTCTCGGAATCTGTGTTCAGGCCCAAGAC 1140
Qy      394 TrpThrIleGlnIleAspIySerLeuIySerProPheTrpCyThrAsnIleSerValTyrPro 413
Db      1141 TGGACATCAGCAAGATTAATTTAAACCTTTCTGGTGTATTAACATCTCTGTGTATCCA 1200
Qy      414 MetLeuIleAspIySerValIyGluProTyrSerIleGlnAlaTyrAlaIySerGluIyVal 433
Db      1201 ATGTTGCATGACAAAGATTGGCAGCCATATTCATCCACAGCTTAATGCCAAAGAGGCGTT 1260
Qy      434 ProSerGluGlyProGluThrIySerValIyGluAsnIleGlyValIySerThrValThrIleThr 453
Db      1261 CCATCGAAGGTCCTGAGACCAAGGTGAGAACATTTGGGTAAAGCGGTCAAGATCA 1320
Qy      454 TrpIySerGluIleProIySerSerGluArgIySerIleIleCyAsnTyrThrIlePheTyr 473
Db      1321 TGGAAAGAAATTTCCAGAGTAGAGAAAGGGGATCATGTGCAATCAACCATCTTTTAC 1380
Qy      474 GlnAlaGluGlyIySerGlyPheSerIyThrValAsnSerSerIleLeuGlnTyrGly 493
Db      1381 CAAGCTGAAGGTGGAAGAAAGATTTCCAGACAGTCAATTCAGCATCTTGCAGTAGCGC 1440
Qy      494 LeuGluSerLeuIySerGlyIySerTyrIleValGlnValMetAlaSerThrSerAla 513
Db      1441 CTGGAGTCCCTTAACGAAAGACCTTTACATTTGTTCAGGTATGGCCAGCACAGTGTCT 1500
Qy      514 GlyIyThrAsnGlyThrSerIleAsnPheIySerThrLeuSerPheSerValPheGluIle 533
Db      1501 GGGGAAACCAAGGAGCAACGATTAATTTCAAGACATTTGTCACTTCAGTCTTTTGAGATT 1560
Qy      534 IleLeuIleThrSerLeuIleGlyIyGlyLeuLeuIleLeuIleIleLeuThrValAla 553
Db      1561 ATCCTCATTAATCTCTGATGTGTGAGGCTTTCTTATCTCATTAATCTGACAGTGCA 1620
Qy      554 TyrGlyLeuIySerProAsnIySerLeuThrIleuCySerTrpProThrValProAsnPro 573
Db      1621 TATGTCTCAAAAAACCAACAAATTTGACTCATCTGTGTGGCCCAACCGTTCCCAACCTT 1680
Qy      574 AlaGluSerSerIleAlaThrTrpIleGlyIyAspAspPheIyAspIySerLeuAsnLeuIyS 593
Db      1681 GCTGAAGATGATATAGCCATAGCATGAGATGATTTCAAGATTAAGCTTAACCTGAAG 1740
Qy      594 GluSerAspAspSerValAsnThrGluAspArgIleLeuIySerProCySerThrProSer 613
Db      1741 GAGTCTGATGACTCTGTGAACACAGAAAGCAGGATCTTAAACCATGTTCCACCCCAAGT 1800
Qy      614 AspIySerLeuValIleAspIySerLeuValIleAsnPheGlyAsnValIleuGlnIyIlePhe 633
Db      1801 GACAAATTGTGTATTTGACAAAGTTGTGTGAACTTTGGGAAATGTTCTGCAAGAAATTTTTC 1860
Qy      634 ThrAspGluAlaArgThrGlyGlnIleuAsnAsnLeuGlyIyGlyIyIyAsnGlyIyThrArg 653
Db      1861 ACAGATGAAGCCAGAACGGGTCAAGAAACAAATTTTGGAGGGGAAAGAAATGGG----- 1914
Qy      654 IleLeuSerSerCyAspPro 659
Db      1915 ---TATGTGACCTGCCCC 1929

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Search completed: February 23, 2005, 15:25:27
 Job time : 8440.27 secs

GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Run on: February 23, 2005, 05:20:17; Search time 977.782 Seconds

(without alignments)
4007.918 Million cell updates/sec

Title: US-10-006-265-17

Perfect score: 3528
Sequence: 1 MKLSPQSPSCVNLGMMTWAL.....NNLGKKNKTRILSSCPSTI 662

Scoring table:

BLOSUM62	
Xgapop 10.0, Xgapext 0.5	
Ygapop 10.0, Ygapext 0.5	
Fgapop 6.0, Fgapext 7.0	
Delop 6.0, Delext 7.0	

Searched: 4390206 seqs, 2959870667 residues

Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

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-Q=/cgn2.1/USPRO.spool/US10006265/runat.18022005.094657.22172/app.query.fasta_1.2069
-DB=N Geneseq.16Dec04 -QWMT=fastap -SUFFIX=ring -MINMATCH=0.1 -LOOFCI=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=blonum62 -TRANS=human40.cdi
-LIST=45 -DOCALLIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15
-MODE=LOCAL -OUTFMT=pco -NORW=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000
-USER=US10006265.qcgn.1_1098 @runat.18022005.094657.22172 -MCPU=6 -ICPU=3
-NO MMAP -LARGESUBSTRY -NEG_SCORES=0 -WAIT -DSPLOCK=100 -LONGLOG
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database: N_Geneseq.16Dec04:*

1: Geneseqn1980s:*\n2: Geneseqn1990s:*\n3: Geneseqn2000s:*\n4: Geneseqn2001as:*\n5: Geneseqn2001bs:*\n6: Geneseqn2002as:*\n7: Geneseqn2002bs:*\n8: Geneseqn2003as:*\n9: Geneseqn2003bs:*\n10: Geneseqn2003cs:*\n11: Geneseqn2003ds:*\n12: Geneseqn2004as:*\n13: Geneseqn2004bs:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result	No.	Score	Query	Match	Length	ID	Description
1	3528	100.0	2119	4	AAC92350		Aac92350 Human hae
2	3528	100.0	2903	6	ABA93808		Ab93808 Human zcy
3	3528	100.0	2903	10	ADD68146		Add68146 Human zcy
4	3528	100.0	2903	11	ADL26569		Adl26569 Human cyt
5	3518	99.7	2529	6	ABA93803		Ab93803 Human zcy

6	3518	99.7	2529	11	ADL26671		Adl26671 Human cyt
7	3518	99.7	4315	8	ABO83363		Ab83363 Human NRI
8	3512	99.5	2969	4	AAC92337		Aac92337 Human hae
9	3465.5	98.2	2386	6	ABA93767		Ab93767 Human zcy
10	3465.5	98.2	2402	11	ADL26673		Adl26673 Human cyt
11	3465.5	98.2	2480	6	AAD38772		Aad38772 Human hae
12	3465.5	98.2	2481	10	ACF36434		Acf36434 Human typ
13	3465.5	98.2	2952	8	ABO83365		Ab83365 Human NRI
14	3465.5	98.2	5271	8	ABO83364		Ab83364 Human NRI
15	3435.5	97.4	3072	8	ABO83366		Ab83366 Human NRI
16	3276	92.9	2858	8	ABO83368		Ab83368 Human NRI
17	3263	92.5	2870	8	ABO83367		Ab83367 Human NRI
18	3096	87.8	2776	8	ABO83369		Ab83369 Human NRI
19	3072	87.1	2108	10	ADL21969		Adl21969 Novel hum
20	2888	81.9	1986	6	ABA93809		Ab93809 Human zcy
21	2888	81.9	1986	11	ADL26685		Adl26685 Human cyt
22	2853	80.9	2295	6	ABA93821		Ab93821 Human zcy
23	2853	80.9	2295	10	ADD68179		Add68179 Human cyt
24	2853	80.9	2295	11	ADL26602		Adl26602 Human zcy
25	2836	80.4	1947	6	ABA93804		Ab93804 Human zcy
26	2836	80.4	1947	11	ADL26684		Adl26684 Human cyt
27	2806.5	79.5	2196	6	ABA93768		Ab93768 Human zcy
28	2806.5	79.5	2196	11	ADL26683		Adl26683 Human cyt
29	2782	78.9	1557	10	ADD68201		Add68201 Human zcy
30	2782	78.9	1557	11	ADL26633		Adl26633 Human cyt
31	2606	73.9	2445	6	ABK33581		Abk33581 CDNA enco
32	2606	73.9	2445	6	ABL88257		Ab188257 Human PRO
33	2606	73.9	2445	6	ABL95746		Ab195746 Human ang
34	2606	73.9	2445	8	ACA68542		Ac68542 Novel hum
35	2606	73.9	2445	9	ABT44271		Abt44271 Human PRO
36	2606	73.9	2445	9	ABT44554		Abt44554 Human PRO
37	2606	73.9	2445	9	ACD82221		Ac82221 Human sec
38	2606	73.9	2445	9	ABT43927		Abt43927 Human mem
39	2606	73.9	2445	9	ADB83581		Ad83581 Novel hum
40	2606	73.9	2445	9	ADB80687		Ad80687 Novel hum
41	2606	73.9	2445	9	ADB73228		Ad73228 Novel hum
42	2606	73.9	2445	9	ADB78310		Ad78310 Novel hum
43	2606	73.9	2445	10	ADB84958		Ad84958 Human PRO
44	2606	73.9	2445	10	ADB78064		Ad78064 Novel hum
45	2606	73.9	2445	10	ADB87130		Ad87130 Human PRO

ALIGNMENTS

RESULT 1	
AAC92350	
ID	AAC92350 standard; CDNA; 2119 BP.
XX	
AC	AAC92350;
XX	
DT	26-MAR-2001 (first entry)
XX	
DE	Human haemopoietin receptor protein NR10.3 encoding CDNA SEQ ID NO:16.
XX	
KW	Human; haemopoietin receptor; NR10.1; NR10.2; NR10.3; NR10;
KW	immunoregulation; haematopoietic cell regulation; transmembrane;
KW	immune disorder; haematopoietic disorder; autoimmune disease; allergy;
KW	metal allergy; pollen allergy; ss.
XX	
OS	Homo sapiens.
XX	
PN	WO200075314-A1.
XX	
PD	14-DEC-2000.
XX	
PF	01-JUN-2000; 2000WO-JP003556.
XX	
PR	02-JUN-1999; 99JP-00155797.
XX	
PR	30-JUN-1999; 99JP-00217797.
XX	
PA	(CHUG-1) CHUGAI RES INST MOLECULAR MEDICINE INC.
XX	
PI	Maeda M, Yaguchi N;

XX WPI: 2001-061720/07.
 DR P-PsDB; AAB51244.
 XX Hematopoietin receptor protein NR10 for screening potential ligands for
 PT treatment of immune and hematopoietic disorders such as autoimmune
 PT diseases and allergies.
 XX
 PS Claim 1; Fig 13-14; 127pp: Japanese.
 XX
 CC The present sequence encodes a human haemopoietin receptor protein
 CC (NR10), specifically designated NR10.3. NR10 occurs as a transmembrane
 CC protein and a soluble protein. NR10 is a haemopoietin receptor molecule
 CC which participates in immunoregulation and haematopoietic cell regulation
 CC in vivo, and is useful in searching for haematopoietic factors capable of
 CC binding to the receptor. NR10 can be used for the identification of
 CC substances for the treatment and prevention of immune and haematopoietic
 CC disorders including autoimmune diseases and allergies such as metal and
 CC pollen allergy
 CC
 SQ Sequence 2119 BP; 643 A; 459 C; 504 G; 513 T; 0 U; 0 Other:
 Alignment Scores:
 Pred. No.: 0 Length: 2119
 Score: 3528.00 Matches: 662
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: Gaps: 0
 US-10-006-265-17 (1-662) x AAC92350 (1-2119)
 QY 1 MetLysLeuSerProGlnProSerCysValAsnLeuGlyMetMetTrpThrTPAlaLeu 20
 Db 11 ATAAGGCTCTCTCCAGCCTTCAATGATGATGAGATGATGAGATGAGATGAGATGAGATG 70
 QY 21 TrpMetLeuProSerLeuCysLysPheSerLeuAlaLeuProAlaLysProGluAsn 40
 Db 71 TGGATGCTCCCTCCAGCTGCAAAATTCAGCTGGAGCTCTGCAGGTAAAGCTGAGAAC 130
 QY 41 ILSSerCysValIleTyrTyrAlaGlyAsnLeuThrCysThrTrpSerProGlyLysGlu 60
 Db 131 ATTTCTGTGCTCACTACATAGAAAATTTAACTGCACTTGAGTCCAGAGCAAGAAAGAA 190
 QY 61 ThrSerTyrThrGlnTyrThrValLysArgThrTyrAlaPheGlyGlyLysPheAspAsn 80
 Db 191 ACCAGTTATACCAAGTACAGATTAAGAGAACTTACGCTTTGGAGAAAACATGATTAAT 250
 QY 81 CysThrThrAsnSerThrSerGluAsnArgAlaSerCysSerPhePheLeuProArg 100
 Db 251 TGTACAAACCAATAGTTCTACAACTGAAATCGTGCTTCGTTCTTTTCCCTCCAAAG 310
 QY 101 ILethrIleProAspIleTyrThrIleGluValGluAlaGluAsnGlyAspGlyValIle 120
 Db 311 ATTAACATCCCAAGTAAATTAATTAACATTAAGAGTGAAGTGAATAATGAGATGATTAAT 370
 QY 121 LysSerHisMetThrTyrTrpArgLeuGluAsnIleAlaLysThrGluProProLysIle 140
 Db 371 AAATCTCATATGACATACGAGATTAAGAGAACATTAAGCAAACTGAACCACTTAAGATT 430
 QY 141 PheArgValLysProValLeuGlyIleLysArgMetIleGlnIleGluTrpIleLysPro 160
 Db 431 TTCGGTGAACAACAGTTTGGGCATCAACGAATGATTAATTAATTAATTAATTAATTAAT 490
 QY 161 GluLeuAlaProValSerSerAspLeuLysTyrThrLeuArgPheArgThrValAsnSer 180
 Db 491 GAGTTGGCCGCTTTTCATCATGATTAATAATACACTTGATTCAGAGCAAGCAACAGT 550
 QY 181 ThrSerTrpMetGluValAsnPheAlaLysAsnArgLysAspLysAsnGlnTrpTrpAsn 200
 Db 551 ACCAGCTGGAGGAGCAACTTCGCTAAAGACCGTAAGATTAATAAACCAGGATCAAC 610
 QY 201 LeuThrGlyLeuGlnProPheThrGluTyrValIleAlaLeuArgCysAlaValLysGlu 220

Db 611 CTCACGGGGCTGACAGCTTTTACAGAAATATGATAGCTGCTGATGTCGGTCAAGAG 670
 QY 221 SerLysPheMetTrpSerAspTrpSerGlnGlyLysMetGlyMetThrGluGluLysPro 240
 Db 671 TCAAAAGTTCTGGAGTGAAGCTGAGGCAAGAAAAATGGGATATACATGAGAAACATCTCA 730
 QY 241 CysGlyLysLeuGluLeuTrpArgValLeuLysProAlaGluAlaAspGlyArgArgProVal 260
 Db 731 TGTGGCTTGAACCTGTGAGAGTCTTGAAACCAAGCTGAGCCGATGGAAGAGCCAGTG 790
 QY 261 ArgLeuLeuTrpLysLysAlaArgGlyAlaProValLeuGluLysThrLeuGlyTyrAsn 280
 Db 791 CGTTGTTATGAGAAGGCAAGAGAGGCCCAAGTCCATGAGAAAACCTTGCTTACAAAC 850
 QY 281 IletTrpTyrTrpProGluSerAsnThrAsnLeuThrGluThrMetAsnThrTrpAsn 300
 Db 851 ATATGCTACTATCCAGAAAGCAACTAACTTCACAGAAACATGAACACTTAACAG 910
 QY 301 GlnLeuGluLeuHisLeuGlyLysLeuSerPheTrpValSerMetIleSerTyrAsnSer 320
 Db 911 CAGCTTGAACCTGATCTGGAGAGCCAGAGCTTTGGGTCTATGATTTCTTATTAATCT 970
 QY 321 LeuGlyLysSerProValAlaThrLeuArgIleProAlaIleGlnGlyLysSerPheGln 340
 Db 971 CTTGGGAAGCTTCCAGTGGCCACCTGAGAGATTCCAGATTAACAAGAAAATCATTTGAG 1030
 QY 341 CysIleGluValMetGlnAlaCysValAlaGluAspGlnLeuValValLysTrpGlnSer 360
 Db 1031 TGCATTTAGGTATGACAGGCTGCGTCTGAGAGCAAGCTATGATGATGAAGTGGCAAAAC 1090
 QY 361 SerAlaLeuAspValAsnThrTrpMetIleGluTrpPheProAspValAspSerGluPro 380
 Db 1091 TCTGCTCTAGAGTGAACCTTGATGATTAATGATTTCCGATGTGATCAAGAGCC 1150
 QY 381 ThrThrLeuSerTrpGluSerValSerGlnAlaThrAsnTrpThrIleGlnGluAspLys 400
 Db 1151 ACCACCTTTCTCGGGAATCTGTCTCAGGCCAGCAAGATGACATCAGCAAGATTAATA 1210
 QY 401 LeuLysProPheMetProCysLeuThrAsnIleSerValIleTyrProMetLeuHisAspLysValGly 420
 Db 1211 TTAAAACTTTCTGTGGCTATTAACATCTCTGTGATTCATATGTGCATGAACAAAGTTGGC 1270
 QY 421 GluProTyrSerIleGlnAlaTyrAlaLysGluGlyValProSerGluGlyProGluTrp 440
 Db 1271 GAGCCATATTCATTCAGGCTTATGCCAAAGAGCGTTCCATCAGAGGCTCTGAGACC 1330
 QY 441 LysValGluAsnIleGlyValLysThrValThrIleThrTrpLysGluIleProLysSer 460
 Db 1331 AAGGTGAGAAACATTTGGCGTGAAGACGTCAGATCAATGAAAGAGATTCCTCAAGAGT 1390
 QY 461 GluArgLysGlyIleIleCysAsnTyrThrIlePheTyrGlnAlaGluGlyLysGly 480
 Db 1391 GAGAGAAAGGATATATCTGCAACATCAACATCTTTTACCAAGCTGAAAGTGAAGAAAGGA 1450
 QY 481 PheSerLysThrValAsnSerSerIleLeuGlnTyrGlyLysLeuLysSerLysArgLys 500
 Db 1451 TTCTCCAAACAGTCAATTCAGCATCTTGCAATAGGCTGAGAGTCCCTGAAGCAAG 1510
 QY 501 ThrSerTyrIleValGlnValMetAlaSerThrSerAlaGlyLysThrAsnGlyThrSer 520
 Db 1511 ACCTCTTACATTTGTTCAAGTATGAGCAGACACAGAGCTGGGGAAACCAACGGAGCAAC 1570
 QY 521 IleAsnPheLysThrLeuSerPheSerValPheGluIleIleLeuIleThrSerLeuIle 540
 Db 1571 ATTAATTTCAACACATTTGATTCATGATGCTTTTGAGATTAATCTCATTAATCTTCTGATT 1630
 QY 541 GlyGlyLysLeuLeuIleLeuIleIleLeuThrValAlaTyrGlyLysLysPheProAsn 560
 Db 1631 GGTGAGGCTTCTTATTTCTATCTTATCTGACAGTGGCATAGGCTCAAAAACCAAC 1690
 QY 561 LysLeuThrHisLeuLysCysTrpProThrValProAsnProAlaGluSerSerIleAlaThr 580

CC	infection. They are also useful for inducing cytotoxicity and for		
CC	treating leukemias. Antagonist of zycyortit polypeptides are useful for		
CC	treating autoimmune diseases (e.g. rheumatoid arthritis and multiple		
CC	sclerosis), inflammatory diseases (e.g. Crohn's disease), cancer,		
CC	pancreatitis, and inflammatory bowel disease. Zycyortit was mapped to		
CC	chromosome 5, specifically to the 5q11 chromosomal region. ABA93767 to		
CC	ABA93843 and ABB05730 to ABB05745 represent sequences used in the		
CC	exemplification of the present invention		
XX			
XX	Sequence 2903 BP, 862 A; 620 C; 664 G; 757 T; 0 U; 0 Other;		
US-10-006-265-17 (1-662) x ABA93808 (1-2903)			
Alignment Scores:			
Pred. No.:	0	Length:	2903
Score:	3528.00	Matches:	662
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	6	Gaps:	0
QY	1	MethylauserProGlnProSerCysValAsnLeuGlyMetMetTrpThrPalaIen	20
DB	497	ATGAAGCTCTCTCCCAACCTTCATGTGTAACTCGGGGATATGTGACCTGGGACATG	556
QY	21	TrpMetLeuProSerLeuCysAlaPheSerLeuAlaLeuProAlaLeuProGluAn	40
DB	557	TGGATGCTCCCTTCACTCTGCAGAAATTACGCTGCAGCTCTCCAGCTTACGCTGAAC	616
QY	41	ILeserCysValTyrTyrTyrArgLysAsnLeuTrpCysThrTrpSerProGlyLysGlu	60
DB	617	ATTTCCTGTGTCTACTACTATATGAAAAATTTAACCTGCATCTGAGTCCAGAAAGAA	676
QY	61	ThiSerTyrThrGlnTyrThrValLysArgThrTyrAlaPheGlyGlyLysHisAspAn	80
DB	677	ACCACTTATACCCAGTACACAGTTAAGAACCTTACGCTTTGGAGAAAAACATGATAT	736
QY	81	CysThrThraenseSerThrSerGluAsnArgAlaSerCysSerPhePheLeuProArg	100
DB	737	TGTACAAACCAATAGTTCTACAAAGTAAATCGTCTGTCTCTTTTCTTCCACAGA	796
QY	101	ILethrILeProAspAerTyrThrILeGluValGluAlaGluAsnGlyAspGlyValILe	120
DB	797	ATAACGAATCCAGATTAATTTATACCTTACGAGGAAAGCTGAAAAATGAGATGGTTAAT	856
QY	121	LysSerHisMetThrTyrTrpArgLeuGluAsnILeAlaLysThrGluProProLysIle	140
DB	857	AAATCTCATAGACATCTACTGAGATTAGAGACATAGCGAANAACCTGMAACCACTTAAGAT	916
QY	141	PheArgValLysProValLeuGlyILeLysArgMetILeGlnILeGluTrpILeLysPro	160
DB	917	TTCCGTGTGAACACAGTTTGGGATCAACAGAAATTCAAATTGAATGATGAAGACCT	976
QY	161	GluLeuAlaProValSerSerAspLeuLysTyrThrLeuArgPheArgThrValAsnSer	180
DB	977	GAGTTGGGCGCTGTTCATCTGATTAAAAATACACACTTCGATTCAGACACTCAACAT	1033
QY	181	ThiSerTrpMetGluValAsnPheAlaLysAsnArgLysAspLysAsnGlnThrTyrAsn	200
DB	1037	ACCAAGCTGAGATGAGATCACTTGCTTAAGAACCTTAAGATTAATAACCAACGTAACAC	1093
QY	201	LeuThrGlyLeuGlnProPheThrGluTyrValILeAlaLeuArgCysAlaValLysGlu	220
DB	1097	CTCACGGGGCGTCAAGCCCTTTTACGAATATGTCAATAGCTCTGCGATGTGCGGCTCAAGGAG	1155
QY	221	SerLysPheTrpSerAspTrpSerGlnGluLysMetGlyMetThrGluGluGluAlaPro	240
DB	1157	TCAAAAGTTCTGAGAGACTGAGAGCCAGAAAAAATGCGAAATGACCTGAGAGAAACACTCCA	1213
QY	241	CysGlyLeuGluGluLeuTrpArgValLeuLysProAlaGluAlaAspGlyArgArgProVal	260
DB	1217	TGTGGCTGGAACCTGTGAGAGTCTCTTAAACCAAGCTGAGGCGGATGAGAAAGGCCAATG	1276

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QY 261 ArgLeuLeuTrpIlyslsAlaArgGlyAlaProValIleuGluIlyThrIleuGlyTyrrAsn 280
Db 1277 CGGTTGTTATGGAAGAAGCAGAGAGAGCCCGAGTCTTAGAGAAAACACTTGGCTACAAC 1336
QY 281 ILTTrpTyrrProGluSerAsnThrAsnLeuThrGluIlyThrMetAsnThrThrAsnGln 300
Db 1337 ATATGGACTATACAGAAACCAACACTAACCTCACAGAAAACAACTACTTAACAG 1396
QY 301 GlnLeuGluLeuHisIleuGlyGlyIleuSerPheTrpValSerMetIleSerTyrrAsnSer 320
Db 1397 CAGCTTGAATGCATCTGGAGAGCGAGAGCTTTGGGTGCTATGATTTCTTAATTC 1456
QY 321 LeuGlyIlySerProValAlaThrLeuArgIleProAlaIleGlnIlyIlySerPheGln 340
Db 1457 CTGGGGAAGTCTCAGAGGCGCACCTGAGGATTCAGCTTACAGAAAATCATTTAG 1516
QY 341 CysIleGlnValMetGlnAlaCysValAlaGluAspGlnLeuValIlyIlyTrpGlnSer 360
Db 1517 TGCATTGAGGTACAGAGGCTCGGTTGCTGAGAGACCAAGTACAGTGGCAAGC 1576
QY 361 SerAlaLeuAspValAsnThrTrpMetIleGluTrpPheProAspValAspSerGluPro 380
Db 1577 TCTGCTCTACAGCTGAACCACTTGGATGATGATGTTCCGATGAGCTCAGAGCCC 1636
QY 381 ThrThrIleuSerTrpGluSerValSerGlnAlaThrAsnTrpThrIleGlnIlyAspIys 400
Db 1637 ACCACCTTCTCGGAGATCTGTCTCAGAGCCAGACGATCGACGAAGTAA 1696
QY 401 LeuIlyProPheTrpCysTyrrAsnIleSerValTyrrProMetLeuHisAspIysValGly 420
Db 1697 TTAACACCTTCTGAGCTATTAACATCTGTGTATTCAAATGTGACAAAGTTGGC 1756
QY 421 GluProIlySerIleGlnAlaTyrrAlaIlyGluIlyValProSerGluGlyProGluThr 440
Db 1757 GAGCCATATTCATCCAGGCTTATGCCAAGAAAGGCTTCATCAGAGAGTCTGAGACC 1816
QY 441 IlyValGluAsnIleGlyValIlyThrValThrIleThrIlyIlyGluIleProIlySer 460
Db 1817 AAGGTGAGAAACATGGCGTGAAGACGATCACATCAGTGAAGAGATTCACCAAGAGT 1876
QY 461 GluArgIlyGlyIleIleCysAsnTyrrThrIlePheTyrrGlnIleGluGlyIlyIlyGly 480
Db 1877 GAGAGAAAGGTATCATCTCACTCACTACACATCTTTAACCAACCTGAAGGTGAGAAAAGA 1936
QY 481 PheSerIlyThrValAsnSerSerIleLeuGlnTyrrGlyIleuGluSerIleIlyAspGly 500
Db 1937 TTCTCCAGACATCATTTCCAGCATTTTCAGATACGCGCTGAGAGTCCCGAAGCAAG 1996
QY 501 ThrSerTyrrIleValGlnValMetValAsnThrSerAlaGlyIlyThrAsnGlyThrSer 520
Db 1997 ACCTCTTACATTTGTTCAGTCTATGGCCAGACACAGTCTGGGGAACCAACGGGAGCAGC 2056
QY 521 IlaAsnPheIlyThrIleuSerPheSerValPheGlnIleIleuLeuIleThrSerIleIle 540
Db 2057 ATTAATTTCAAGACATTTGATTCAGTGTGTTGAGATTAATCTCAATACCTTCTCGATT 2116
QY 541 GlyGlyIlyLeuLeuIleLeuIleIleLeuThrValAlaTyrrGlyIleuIlyIlyProAsn 560
Db 2117 GGTGGAGGCTTCTTATTCATTCATTCACAGTGCAGATAGTCTCAAAAAACCAAC 2176
QY 561 IlyLeuLeuThrHisIleuCysTrpProThrValProAsnProAlaGluSerSerIleAlaThr 580
Db 2177 AAATTGCTCATCTGTGTGGCCACCGTTCCCAACCTCTGTAAGAGTAGTATAGCCACA 2236
QY 581 TrpHisGlyAspAspPheIlyAspIlyIlyLeuAsnLeuIlyGluSerAspAspSerValAsn 600
Db 2237 TGGCATGGAATATTTCAAGAGTAAGCTAAACCTGAAGAGCTGATGCTGTGAAC 2296
QY 601 ThrGluAspArgIleLeuIlyIlyProCysSerThrProSerAspIlyLeuValIleAspIys 620
Db 2297 ACGAGAGACAGCATCTTAAACATCTTCCACCCCGATACAAAGTTGGTGGATTGACAG 2356
QY 621 LeuValValAsnPheGlyAsnValLeuGlnGluIlePheThrAspGluAlaArgThrGly 640

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Db 2357 TTGGTGGTAACTTTGGGAAATTTTCACAGATGAAACCGGCT 2416
QY 641 GlnIlaAsnAsnLeuGlyIlyGlyIlyAsnGlyThrArgIleLeuSerSerCysProThr 660
Db 2417 CAGAAAACAAATTTAGAGGGGAAAGAAATGGGACTAGAAATCTGTCTGCGCACT 2476
QY 661 SerIle 662
Db 2477 TCAATA 2482

RESULT 3
ADD68146
ID ADD68146 standard; cDNA; 2903 BP.
XX
AC ADD68146;
XX
DE 15-JAN-2004 (first entry)
XX
DE Human zcytor17 cDNA SEQ ID NO:4.
XX
KW ss; gene; human; zcytor17; antiinflammatory; dermatological;
KW immunosuppressive; antimicrobial; vaccine; inflammatory disease;
KW inflammatory bowel disease; ulcerative colitis; Crohn's disease;
KW atopic dermatitis; eczema; psoriasis; endotoxaemia; septicemia;
KW toxic shock syndrome; infectious disease.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 497..2485
FT /tag= a
FT /product= "zcytor17"
XX
PN MO2003060090-A2.
XX
PD 24-JUL-2003.
XX
PF 21-JAN-2003; 2003WC-US001984.
XX
PR 18-JAN-2002; 2002US-0350325P.
PR 25-APR-2002; 2002US-0375323P.
PR 19-DEC-2002; 2002US-0435315P.
XX
PA (ZYMO ) ZYMOGENETICS INC.
XX
PI Sprenger CA, Kuiper JL, Dasovich MM, Grant FU, Hammond AK;
PI Novak DE, Gross JA, Dillon SR;
XX
DR MPI; 2003-618179/58.
DR P-PSDB; ADD68147.
XX
PT New zcytor17 ligand polypeptides, useful for treating inflammatory
PT diseases, such as inflammatory bowel disease, ulcerative colitis, Crohn's
PT disease, atopic dermatitis, eczema, psoriasis, endotoxaemia, septicemia.
XX
PS Example 3; SEQ ID NO 4; 372pp; English.
XX
CC The invention relates to a novel isolated zcytor17 ligand polypeptide. A
CC polypeptide of the invention has antiinflammatory, dermatological,
CC immunosuppressive, and antimicrobial activity, and may have a use in a
CC vaccine. The polypeptide is useful for treating inflammatory diseases,
CC such as inflammatory bowel disease, ulcerative colitis, Crohn's disease,
CC atopic dermatitis, eczema, psoriasis, endotoxaemia, septicemia, toxic
CC shock syndrome or infectious diseases. The present sequence is used in
CC the exemplification of the invention.
XX
SQ Sequence 2903 BP; 862 A; 620 C; 664 G; 757 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 0 Length: 2903
Score: 3528.00 Matches: 662
Percent Similarity: 100.00% Conservative: 0

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Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 10 Gaps: 0
 US-10-006-265-17 (1-662) x ADD68146 (1-2903)

QY 1 MetLysLeuSerProGlnProSerCysValAenLeuGlyMetMetTrpThrAlaLeu 20
 Db ATGAAGCTCTCTCCCAAGCTTCAATGTGTTAACTGGGATGATGTGAAGCTGGGCACTG 556

QY 21 TrpMetLeuProSerLeuCysLysPheSerLeuAlaLeuProAlaLysProGln 40
 Db TGGATGCTCCCTCACTCTGGAAAATTCAAGCTGGAGCTGCTCCAGCTTAAGCTGAGAAC 616

QY 41 LLeSerCysValTyrTyrTyrArgLysAenLeuThrCysThrTrpSerProGlyLysGlu 60
 Db ATTTCCTGTGCTACTACTATAGGAAAAATTACCTCACTTGAAGTCCAGGAAAGAA 676

QY 61 ThrSerTyrThrGlnTyrThrValLysArgThrTyrAlaPheGlyGluLysHisAspAsn 80
 Db ACCAGTTATACCACTACACAGTTAAGAGAACTTACGCTTTGGAGAAAACATGATAT 736

QY 81 CysThrThrAsnSerSerThrSerGluAsnArgAlaSerCysSerPhePheLeuProArg 100
 Db TGTACAACCAATAGTTCTACAAGTGAATGCTGCTGCTCTTTTCTCTCAAGA 796

QY 101 LLeThrLLeProAspAsnTyrThrLLeGluValGluAlaGluAsnGlyAspGlyValIle 120
 Db ATAAAGATCCCAAGATTAATATACATTGAGGTGAAGCTGAATGAGATGTGTAT 856

QY 121 LysSerHisMetThrTyrTrpArgLeuGluAsnIleAlaLysThrGluProProLysIle 140
 Db AAATCTCTATGACACTACTGAGATTAGAACATAGGAAACTGAACACCTTAAGATT 916

QY 141 PheArgValLysProValLeuGlyLLeLysArgMetLLeGlnLLeGluTrpLLeLysPro 160
 Db TTCGGTGGAAACAGTTTGGGCAATCAAGAAATGATTCAATTGATGATAAGCT 976

QY 161 GluLeuAlaProValSerSerAspLeuLysTyrThrLeuArgPheArgThrValAsnSer 180
 Db GAGTGGGGCTGTTCTTCATCTGATTTAAATACACACTTCATCAGACAGTCAACGT 1036

QY 181 ThrSerTrpMetGluValAsnPheAlaLysAsnArgLysAspLysAsnGlnThrTrpAsn 200
 Db ACCAGCTGGATGAAAGTCAACTGCTAAGAACCTGAAGATTAAGAAACGTAAC 1096

QY 201 LeuThrGlyLeuGlnProPheThrGlnTyrValIleAlaLeuArgCysAlaValLysGlu 220
 Db CTCACGGGGCTGCAGCCTTTTACAGAAATGTGCATAGCTGCGCATGTGCGGTCAAGAG 1156

QY 221 SerLysPheTrpSerAspTrpSerGlnGluLysMetGlyMetThrGluGluAlaPro 240
 Db TCAAAGTCTGAGAGTGAAGCCAAAGAAAAATGGAAATGATGAGAGAAAGAGCTCCA 1216

QY 241 CysGlyLeuGluLeuTrpArgValLeuLysProAlaGluAlaAspGlyArgArgProAla 260
 Db TGTGGCTGGAACTGTGAGAGTCTCTGAACCAAGTGAAGCGAGTGAAGAAAGCGCACTG 1276

QY 261 ArgLeuLeuTrpLysAlaArgGlyAlaProValLeuGluLysThrLeuGlyTyrAsn 280
 Db CGGTTGTTATGGAAGAAAGCAAGAGAGCCCAAGTCCATAGAGAAAACCTTGGCTACAC 1336

QY 281 LLeTrpTyrTyrProGluSerAsnThrAsnLeuThrGluThrMetAsnThrThrAsnGln 300
 Db ATATAGTACTACTCAAGAAAGCAACACTAACCTCAGAGAAACAATGAAACACTACTAACAG 1396

QY 301 GlnLeuGluLeuHisLeuGlyGlyLysSerPheTrpValSerMetLLeSerTyrAsnSer 320
 Db CAGCTTGAACAGCACTGGAGCGAGCTTTGGGTGTCTATGATTTCTTAATATCT 1456

QY 321 LeuGlyLysSerProValAlaThrLeuArgLLeProAlaLLeGlnGluLysSerPheGln 340
 Db CTGGGAAGTCTCCAGTGGCCACCTGAGATTCAGCTATTCAAGAAAATCATTTTCAG 1516

QY 341 CysLLeGluValMetGlnAlaCysValAlaGluAspGlnLeuValValLysTrpGlnSer 360
 Db TGCATGTGGTCAATGACAGCGCTGCTGTCTAGAGAACAGCTAGTGTGAAGTGGAAAGC 1576

QY 361 SerAlaLeuAspValAsnThrTrpMetLLeGluTrpPheProAspValAspSerGluPro 380
 Db TCTGCTACAGCGTAACACTTGGATGATTAATGAGTTTCCGATGTGCACTCAGAGGCC 1636

QY 381 ThrThrLeuSerTrpGluSerValSerGlnAlaThrAsnTrpThrLLeGlnGlnAspLys 400
 Db ACCACCTTTCTCTGGAAATCTGTGTCTCAGGCGCACGAAGTGAAGATCCACAGATTA 1696

QY 401 LeuLysProPheTrpCysTyrAsnLLeSerValTyrProMetLeuHisAspLysValGly 420
 Db TTAACACCTTCTGTGTATTAACATCTGTGTATTAACATGTTGATGACAGACAAAGTTGGC 1756

QY 421 GluProTyrSerLLeGlnAlaTyrAlaLysGluGlyValProSerGluGlyProGluThr 440
 Db GAGCATATTCATCCAGCTTATGCCAAGAGCGCTTCATCAGAAAGTCTGAGAGC 1816

QY 441 LysValGluAsnLLeGlyValLysThrValThrLLeThrTrpLysGluLLeProLysSer 460
 Db AAGGTGAGAACTTGGCGTGAAGACGCTCAGATCAGATGAGAAAGATTCCCAAGAGT 1876

QY 461 GluArgLysGlyLLeLLeCysAsnTyrThrLLePheTyrGlnAlaGluGlyLysGly 480
 Db GAGAGAAAGGTATCATCTGCATCAACCACTCTTTAACCAGGTGAAGGTGAGAAAGGA 1936

QY 481 PheSerLysThrValAsnSerSerLLeGlnTyrGlyLeuGlnSerLLeLysArgLys 500
 Db TTCTCCAGACAGTCATTCAGCATCTTGCAGATCCGCTGGAGTCCCTGAACGAAG 1996

QY 501 ThrSerTyrLLeValGlnValMetLLeSerThrSerAlaGlyGlyThrAsnGlyThrSer 520
 Db ACCTTACATTTGTTCAAGTCAATGCGCAGCACCACTGCGGGAGAACCAAGGAGCAGC 2056

QY 521 LLeAsnPheLysThrLeuSerPheSerValPheGluLLeLLeLLeLLeLLeLLeLLeLLe 540
 Db ATAAATTTCAAGACATTTGTCTAGTGTCTTGAATTAATCTCATTAATCTCTGATT 2116

QY 541 GlyLysGlyLeuLeuLLeLLeLLeLLeLLeLLeLLeLLeLLeLLeLLeLLeLLeLLeLLe 560
 Db GGTGAGGCTCTTATTCTTATCTTATCTGACAGTGGCATGTGTCMAAAAAACCCAAC 2176

QY 561 LysLeuThrHisLeuCysTrpProThrValProAsnProAlaGlnSerSerLLeAlaThr 580
 Db AAATTGACTCATGTGTGGCCCAACCGTCCCAACCTGCTGAAGATATGACACA 2236

QY 581 TrpHisGlyAspAspPheLysAspLysLeuAsnLeuLysGlnSerAspAspSerValAsn 600
 Db TGGCATGAGATGATTTCAAGATGATCAACTGAAGAGTCTGATGATCTGTGTAAC 2296

QY 601 ThrGluAspArgLLeLLeLysProCysSerThrProSerAspLysLeuValLLeAspLys 620
 Db ACAAGACAGATCTTAACACATGTTCCACCCCACTGACACAGTTGGTGAATGACAG 2356

QY 621 LeuValValAsnPheGlyAsnValLeuGlnGluLLePheThrAspGluAlaArgThrGly 640
 Db TTGGTGGGAACCTTGGGAATGTTCTGCAAGAAATTTTCAAGATGAAAGCAGAACGGGT 2416

QY 641 GlnGluAsnAsnLeuGlyGlyGluLysAsnGlyThrArgLLeLeuSerSerCysProThr 660
 Db CAGGAAAAACAATTAAGAGGAGGAAAGAAATGGGACTGAATTTGTCTTCTGCCCCA 2476

QY 661 SerIle 662
 Db TCAATA 2482

RESULT 4
 ADL26569
 ID ADL26569 standard; cDNA; 2903 BP.
 XX

AC ADL26569;
 XX
 XX 20-MAY-2004 (first entry)
 XX
 DE Human cytokine receptor zcytor17 DNA seqid 4.
 XX
 KW antiinflammatory; antitumor; dermatological; antiallergic; antipsoriatic;
 KW antibacterial; immunosuppressive; cell proliferation inhibitor;
 KW immune response inhibitor; inflammatory response inhibitor;
 KW multimeric cytokine receptor; heterodimeric cytokine receptor; cancer;
 KW cytokine-binding domain; class I cytokine receptor; haematopoietic cell;
 KW zcytor171g-induced proliferation; zcytor171g-induced differentiation;
 KW haematopoietic progenitor cell; zcytor171g-induced inflammation;
 KW inflammatory disease; inflammatory bowel disease; ulcerative colitis;
 KW Crohn's disease; atopic dermatitis; eczema; psoriasis; endotoxaemia;
 KW septicæmia; toxic shock syndrome; zcytor17; human; gene; ss.
 XX
 OS Homo sapiens.
 XX
 PN US2003215838-A1.
 XX
 PD 20-NOV-2003.
 XX
 PF 21-JAN-2003; 2003US-00351157.
 XX
 PR 18-JAN-2002; 2002US-0350325P.
 PR 14-JUN-2002; 2002US-0389108P.
 PR 19-DEC-2002; 2002US-0435361P.
 XX
 PA (SPRE/) SPRECHER C A.
 PA (GAOZ/) GAO Z.
 PA (KUIJ/) KUIJPER J L.
 PA (DASO/) DASOVICH M M.
 PA (GRAN/) GRANT F J.
 PA (PRES/) PRESNELL S R.
 PA (WHIT/) WHITMORE T E.
 PA (HAMM/) HAMMOND A K.
 PA (NOVA/) NOVAK J E.
 PA (GROS/) GROSS J A.
 PA (DILL/) DILLON S R.
 XX
 PI Sprecher CA, Gao Z, Kuijper JL, Dasovich MM, Grant FJ,
 PI Presnell SR, Whitmore TE, Hammond AK, Novak JE, Gross JA, Dillon SR;
 DR P-PSDB; ADL26570.
 XX
 PT Novel multimeric or heterodimeric cytokine receptors useful for treating
 PT chronic inflammatory disease such as inflammatory bowel disease,
 PT ulcerative colitis, acute inflammatory disease such as endotoxaemia,
 PT septicæmia.
 XX
 PS Example 3; SEQ ID NO 4; 205pp; English.
 XX
 CC The invention describes an isolated multimeric or heterodimeric cytokine
 CC receptor (I) having at least one polypeptide having 90 percent sequence
 CC identity with a 732 (S1) or 649 (S2) amino acid sequence given in
 CC specification, and where (I) binds a ligand comprising a 164 (S3) amino
 CC acid sequence, given in specification, or at least one polypeptide
 CC comprising residue 20-227 of (S1). (I) is useful for killing cancer cells
 CC and producing an antibody to (I) and a cytokine-binding domain of a class
 CC I cytokine receptor. A composition (C1) comprising (I) and a cytokine-
 CC binding domain of a class I cytokine receptor and a vehicle is useful
 CC for: reducing haematopoietic cells and haematopoietic progenitor cells in
 CC a mammal; inhibiting zcytor171g-induced proliferation or differentiation
 CC of haematopoietic cells and haematopoietic progenitor cells; reducing
 CC zcytor171g-induced inflammation; treating a mammal afflicted with an
 CC inflammatory disease in which zcytor171g plays a role. The disease is a
 CC chronic inflammatory disease such as inflammatory bowel disease,
 CC ulcerative colitis, Crohn's disease, atopic dermatitis, eczema and
 CC psoriasis. The disease is acute inflammatory disease such as
 CC endotoxaemia, septicæmia, toxic shock syndrome and infectious disease.
 CC An immune response inhibiting composition is useful for inhibiting an

CC immune response in a mammal exposed to an antigen or pathogen. An
 CC inflammatory response inhibiting composition is useful for suppressing an
 CC inflammatory response in a mammal with inflammation. An antibody that
 CC specifically binds to (I) is useful for detecting the presence of a
 CC multimeric or heterodimeric cytokine receptor in a biological sample.
 CC This sequence encodes a human zcytor17 cytokine receptor.
 CC
 XX

Sequence 2903 BP; 862 A; 620 C; 664 G; 757 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.:	0	Length:	2903
Score:	3528.00	Matches:	662
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	11	Gaps:	0

US-10-006-265-17 (1-662) x ADL26569 (1-2903)

QY	1	MctLySLeUsErProGlnProSeRcYsValAenLeuGlyMeCMeTTrpThrTpaAlaen	20
DB	497	ATGAAGCTCTCTCCAGCCTTCATGTGTTAACTGGGATGATGTGACCTGGGACCTG	556
QY	21	TTrpMeLLeuProSeRLeuCYsLySPheSeRLeuAlaAlaLeuProAlaLySProGluAn	40
DB	557	TGATGCTCCCTTCACTCTGCAAAATTCAGCTGGAGCTCTCCAGCTTAAGCTTGAGAC	616
QY	41	ILeSeRcYsValLyTrTyTrTyRArgLySAenLeuThrCYsThTrSeRProGlyLySGlu	60
DB	617	ATTTCTGTGCTACTACTATAGAAAATTTAACTTGACCTTGAGTTCAGAAAGAA	676
QY	61	ThrSeRTrTyThGlnTyRThrValLySArgThrTyRAlaPheGlyGlyLyShISApaSn	80
DB	677	ACCAGTTATACCAAGTACAGTAAAGACCTTAAGCACTTGGAGAAAACATGATAAT	736
QY	81	CySThrThAsnSeRSeRThSeRgluAenAArgAlaSeCYsSeRPhetheuProArg	100
DB	737	TGTACAAACCAATAGTCTACAAAGTGAATCGTCTGCTCTTTTCCCTTCACAA	796
QY	101	ILeThrILeProAspaSnTyRThrILeGluValAGluAlaGluAsnGlyLySPGlyValILe	120
DB	797	ATPACGATCCCAATATATTAACATTGAGTGGAGACTGAAAATGAGATGTGTAAT	856
QY	121	LySeSerIAsMeCThrTyRTrpArgLeuGluAenILeAlaLySThrGluProProLySILe	140
DB	857	AAATCATATATACATACATGAGATTAGAGAACATATGCAAACTCAACCATAGATT	916
QY	141	PheArgValLySProValLeuGlyLyLeysArgMetILeGlnILeGluTrpILeLySPro	160
DB	917	TTCGGTGTAAACCAAGTTTGGGCAATCAAAATGATTCAAAATGAAATGATAAAGCCT	976
QY	161	GluLeuAlaProValSerSeRAspLeuLySTyRThrLeuArgPheArgThrValAenSer	180
DB	977	GAGTTGGCCCTGTTTCATCTGATTAATTAATACACTTCGATTCCAGACAGTCAACAT	1036
QY	181	ThrSeRTrpMeGluValAenPheAlaLySAenArgLyASpLySAenGlnThrTyraSn	200
DB	1037	ACAGCTGATGAGATGCAACTTCGTTAGAAACCGTAAGATTAATAAACCAACGTAACAAC	1096
QY	201	LeuThrGlyLeuGlnProPheThrGluTyRValILeAlaLeuArgCYsAlaValLySGlu	220
DB	1097	CTCACCGGGCTCAGAGCTTTTACAGAAATGTGATATGCTCTCGAATGTCGGTCAAGGAG	1156
QY	221	SeLySPheTrSeRAspTrpSerGlnGlyLySMetGlyMeThGluGluGluAlaPro	240
DB	1157	TCAAACTTCTGAGTGACCTGAGCCCAAGAAAATGGGATATCGAGGAAGAAGCTCCA	1216
QY	241	CySGlyLeuGluLeuTrpArgValLyLeuLySProAlaGluAlaAspGlyArgArgProVal	260
DB	1217	TGTGGCTGGAACGTGAGAGATCTCGAATCAACAGCTGAGCGGATGGAAGAGCCAGTG	1276
QY	261	ArgLeuLeuTrpLySAlyAlaArgGlyAlaProValLeuGluLySThrLeuGlyTyraSn	280

Db	1277	CGGTTGTTATGGAGAGGCAAGAGAGCCCAAGTCTTAGAGAAAAACCTGGCTAAC	1336
Qy	281	ILETPYRYTPProGluSerAsnThrAsnLeuThrGluThrMetAsnThrThrsAsnGln	300
Db	1337	ATATGGTACTATCCAGAAAGCAACCTAACTCAGAGAAACAATGAACACTACTAACG	1396
Qy	301	GlnLeuGluLeuHisLeuGlyGlyGluSerPheThrValSerMetIleSerThrsAsnSer	320
Db	1397	CAGCTTGAACATGCATCTGGAGAGCGAGAGCTTTGGGTGTCTATGATTTCTTAATCT	1456
Qy	321	LeuGlyLysSerProValAlaThrLeuThrGlyIleProAlaIleGlnGlnLysSerPheGln	340
Db	1457	CTTGGGAAGTCTCCAGTGGCCCACTCGAGGAATTCAGGCTATTCAGAAACATCTTACG	1516
Qy	341	CysIleGlyValaMetGlnAlaCysValaIaGluAspGlnLeuValValIleTPGInsSer	360
Db	1517	TGCATTAGAGTCATCAGGCGCTGCCTTCTGTAAGACCAAGTACTGTGTAAAGTGGCAAGC	1578
Qy	361	SerAlaLeuAspValaAsnThrTrpMetIleGluTrpPheProAspValaAspSerGluPro	380
Db	1577	TCTGCTTAGAGTGAACACTGGATGATGATTGAATGGTTTCCGAGATGTGAATCAGAGCC	1636
Qy	381	ThrThrLeuSerTPTrpGluSerValSerGlnAlaThrAsnTPThrIleGlnGlnAspLys	400
Db	1637	ACCACCCCTTCTCTGGGAATCTGTGCTCAGGCGCAAGAACTGGACCATCAGCAAGATAA	1696
Qy	401	LeuLysProPheTPCysThrAsnIleSerValTYrProMetLeuHisAspLysValaGly	420
Db	1697	TTAAACCTTTCTGTGTCTATACACTCTGTGTATCCAAAGTTTCATAGCAAAATTTGAC	1756
Qy	421	GluProTYrSerIleGlnAlaTYrAlaLysGluGlyValProSerGluGlyProGluThr	440
Db	1757	GAGCATATTCATCATCAGGCTTAATGCCAAAGAGCGTTTCATCAGAAAGTCTTGAGACC	1816
Qy	441	LysValaGluAsnIleGlyValaLysThrValThrIleThrTPLysGluIleProLysSer	460
Db	1817	AAGGTGGGAACATTTGGCGTGAAGCGGTGACGATCAATGGAAGAAATGCCCAAGAGT	1876
Qy	461	GluLysrGlyAspGlyIleIleCysAsnTYrThrIlePheTYrGlnAlaGluGlyGlyGly	480
Db	1877	GAGAGAAAGGGATATCATCTGCACATCAACCATTTTTCACAACTGAAAGGTGGAAGAA	1936
Qy	481	PheSerLysThrValaAsnSerSerIleLeuGlnTYrGlyLeuGluSerLeuLysrGlys	500
Db	1937	TTCTCCAAAGACAGTCAATTCACAGCATCTTGCAAGTACGGCGTGGATCCCTTAACGAAG	1996
Qy	501	ThrseryTYrIleValGlnValMetAlaSerThrsrAlaGlyTYrAsnGlyThrsSer	520
Db	1997	ACCTCTTACATTTGTTCAAGTATGCGCCAGCAACAGTGTGGGGGGAACCAAGGGGACAGC	2056
Qy	521	IleAsnPheLysThrLeuSerPheSerValPheGluIleIleLeuIleThrsSerLeuIle	540
Db	2057	ATTAATTTCCAAAGACCTGTCTCATCTTCAGTCTTTGGATTATTCCTATTAATCTCTGTAT	2116
Qy	541	GlyGlyGlyLeuLeuIleLeuIleIleLeuThrValaIaTYrGlyLeuLysLysProAsn	560
Db	2117	GGTGGAGGCGCTTCTTATTTCTCATTAATCTGCAAGTGGGCAATGTGCTCAAAAACCCAC	2176
Qy	561	LysLeuThrHisLysLeuCYrTPProThrValProAsnProAlaGluSerSerIleAlaThr	580
Db	2177	AAATTTGACTCATCTGTGTGGCCCACTGTTCCCAACCTGTGTAAGATGATATGACCA	2236
Qy	581	TrpHisGlyAspAspPheLysAspLysLeuAsnLeuLysGlyLysAspAspSerValAsn	600
Db	2237	TGGCATGGAGATGATTTCAAGGATTAAGCTAAACCTGAAGAGAGTCAAGACTCTGTGAAC	2296
Qy	601	ThrGluAspATyGlyLeuLysProCYrSerThrProSerAspLysLysValaIleAspLys	620
Db	2297	ACAGAGACAGAGATTTTAAACCAAGTTCACACCCCACTGACCAAGTTGTGATATGACAA	2356
Qy	621	LeuValValaAsnPheGlyAsnValaIleuGlnGluIlePheThrAspGlnAlaTYrThrGly	640
Db	2357	TTGGGTGGGAACCTTTGGGAATGTTCTGCAAGAAATTTTCAAGATGAAGCCAGAACGGGT	2416

Qy	661	GInGUaSaAnLeuGlyGluLySaAnGlyThraGlyLeLeuSeSeCyBProThr	660
Db	2417	CAGGAAAAACAATTATGAGGGGAAAAAGAAATGGAGCTGAAATTCGTCTTCTGCCCACT	2476
Qy	661	SeRile 662	
Db	2477	TCaATa 2482	
RESULT 5			
ID	ABA93803	standard; cDNA; 2529 BP.	
XX	ABA93803;		
DT	01-MAY-2002	(first entry)	
DE	Human zcytor17 cDNA sequence SEQ ID NO:45.		
KM	Zcytor17; chromosome 5; 5q11; cytokine receptor; immunomodulatory;		
KM	antiinflammatory; antiviral; antirheumatic; antiarthritic; cytostatic;		
KW	muscular; lymphoid; immune; inflammatory; splenic; blood; bone;		
KW	infection; immunosuppression; cytotoxicity; leukopenia; Crohn's disease;		
KM	autoimmune disease; rheumatoid arthritis; multiple sclerosis; cancer;		
KW	inflammatory disease; pancreatitis; inflammatory bowel disease; se.		
XX			
OS	Homo sapiens.		
PN	WO200200721-A2.		
XX			
PD	03-JAN-2002.		
XX			
PF	26-JUN-2001; 2001WO-US020484.		
XX			
PR	26-JUN-2000; 2000US-0214282P.		
XX	29-JUN-2000; 2000US-0214955P.		
PR	08-FEB-2001; 2001US-0267963P.		
XX			
PA	(ZYMO) ZYMOGENETICS INC.		
XX			
PI	Speicher CA, Presnell SR, Gao Z, Whitmore TE, Kuijper JL;		
PI	Maurer MF;		
XX			
DR	WPI; 2002-090519/12.		
XX	P-ESDB; ABB05738.		
PT	Isolated polynucleotide encoding a cytokine receptor zcytor17 which is		
PT	useful for treating and diagnosing lymphoid, immune, inflammatory,		
PT	splenic, blood or bone disorders.		
XX			
PS	Claim 2; Page 190-194; 235pp; English.		
XX			
CC	The present invention describes a cytokine receptor designated zcytor17.		
CC	Zcytor17 has immunomodulatory, antiinflammatory, antiviral, cytostatic,		
CC	antirheumatic, antiarthritic and muscular activities. The zcytor17		
CC	proteins are useful for treating and diagnosing lymphoid, immune,		
CC	inflammatory, splenic, blood or bone disorders. Agonists or anti-		
CC	zcytor17 antibodies are useful in stimulating cell-mediated immunity and		
CC	for stimulating lymphocyte proliferation, such as in the treatment of		
CC	infections involving immunosuppression, including certain viral		
CC	infections. They are also useful for inducing cytotoxicity and for		
CC	treating leupemias. Antagonist of zcytor17 polypeptides are useful for		
CC	treating autoimmune diseases (e.g. rheumatoid arthritis and multiple		
CC	sclerosis), inflammatory diseases (e.g. Crohn's disease), cancer,		
CC	pancreatitis, and inflammatory bowel disease. Zcytor17 was mapped to		
CC	chromosome 5, specifically to the 5q11 chromosomal region. ABA93767 to		
CC	ABA93843 and ABB05730 to ABB05745 represent sequences used in the		
CC	exemplification of the present invention		
XX			
SEQ	Sequence 2529 BP; 764 A; 530 C; 576 G; 659 T; 0 U; 0 Other;		
Alignment Scores:	0	Length:	2529
Pred. No.:	0		

Score: 3518.00 Matches: 660
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 99.72% Indels: 0
DB: 6 Gaps: 0
US-10-006-265-17 (1-662) x ABA93803 (1-2529)

QY 3 LeuSerProGlnProSerCysValaLeuLeuGlyMetMetTrpThrTrpAlaLeuTrpMet 22
DB 129 CTCTCTCCAGAGCTTCATGTGTTAACCTGGGAGTGTGAGACCTGGGACCTGGAGT 188
QY 23 LeuProSerLeuCysLysPheSerLeuAlaAlaLeuProAlaLysProGluLeuIleSer 42
DB 189 CTCCCTCATCTCGCAAAATTCAAGCTGGGACGCTCGCAAGCTTAAGCTGGAACATTTCC 248
QY 43 CysValaTyrTyrTyrArgLysAsnLeuThrCysThrTrpSerProGlyLysGluThrSer 62
DB 249 TGTGTCTACTACTATAGGAAAAATTTAACTGCACCTGGAGTCCAGGAAAGAACACAGT 308
QY 63 TyrThrGlnTyrThrValaLysArgThrTyrAlaPheGlyGluLysHisAspAsnCysThr 82
DB 309 TATATCCAGTACAGATTAGAGAACTTACGCTTTGGAGAAAAACATGATATGTACA 368
QY 83 ThrAsnSerSerThrSerGluAsnArgAlaSerCysSerPhePheLeuProArgIleThr 102
DB 369 ACCAATAGCTTCAAGTGAATAATCGTGTGCTCTTTTCCCTTCCAAAGATTAAG 428
QY 103 IleProAspAsnTyrThrIleGluValGluAlaGluAsnGlyAspGlyValIleLysSer 122
DB 429 ATCCCATATATATATACATTTGAGGTGAGAGCTGAAATGAGATGGGTATTAATCT 488
QY 123 HisMetThrTyrTrpArgLeuGluAsnIleAlaLysThrGluProProLysIlePheArg 142
DB 489 CATATGACATACAGAGATTAAGAACATAGCGAAAACTGAACCACTTAAGATTTTCGT 548
QY 143 ValLysProValLeuGlyIleLysArgMetIleGlnIleGluTrpIleLysProGluLeu 162
DB 549 GTGAACACGATTTTGGGCATCAACGAAATGATTCAAATTTGAATGAAGCCGTAGTTG 608
QY 163 AlaProValSerSerAspLeuLysTyrThrLeuArgPheArgThrValaAsnSerThrSer 182
DB 609 GGCCTGTTCATCTGATTTTAAATACACACTTCGATTCAGGACAGCAACAGTACAGC 668
QY 183 TrpMetGluValaAsnPheAlaLysAsnArgLysAspLysAsnGlnThrTyrAsnLeuThr 202
DB 669 TGAATGAAATCAACTTCGCTTAAGAACCGTAAGATTAACCAACAGTACCAACTCAG 728
QY 203 GlyLeuGlnProPheThrGluTyrValaIleAlaLeuArgCysAlaValLysGluSerLys 222
DB 729 GGGCTGAGCCTTTTACGAATATGTCTAGTCTGCGATGTCGGGTCAAGAGTCAAG 788
QY 223 PheTrpSerAspTrpSerGlnGluLysMetGlyMetThrGluGluAlaProCysGly 242
DB 789 TTTCTGGAGTACTGAGCCCAAGAAAAATGGAATGACTGAGAGAGAGAGCTCATGTGCG 848
QY 243 LeuGlnLeuTrpArgValaLeuLysProAlaGluAlaAspGlyArgAspProValArgLeu 262
DB 849 CTGAAGCTGTGGAGAGTCTGAAACCGCTGAGGCGGATGAGAGAGGCCAGTGGCTTG 908
QY 263 LeuTrpLysLysAlaArgGlyAlaProValLeuGluLysThrLeuGlyTyrAsnIleTrp 282
DB 909 TTATGGAAGAGGAGAGAGAGGCCCGCTCTAGAGAAAAACATTGGCTTCAACATATGG 968
QY 283 TyrTyrProGluSerAsnThrAsnLeuThrGluThrMetAsnThrThrAsnGlnGlnLeu 302
DB 969 TACTATCAGAAAGCAACACTTAACCTCAAGAAAAATGAACACTAATAACAGCAGCTT 1028
QY 303 GluLeuHisLeuGlyGlyGluSerPheTrpValSerMetIleSerTyrAsnSerLeuGly 322
DB 1029 GAATCTGATCTGGAGGCGGAGAGCTTTTGGGTGTCTATVAGATTTCTATVAAATTTCTTGGG 1088
QY 323 LysSerProValaAlaThrLeuArgIleProAlaIleGlnGluLysSerPheGlnCysIle 342

DB 1089 AAGTCTCCAGGTGACCAACCTGAGATTCAGCTATTTCAAGAAAAATCAATTCAGTGCAAT 1148
QY 343 GluValMetGlnAlaCysValaAlaGluAspGlnLeuValaValLysTrpGlnSerSerAla 362
DB 1149 GAGGTATGACAGGCGCTGCTGTGCTGAGACCGAGTGTGTAAAGTGGCAAGCTCTGTGT 1208
QY 363 LeuAspValaAsnThrTrpMetIleGluTrpPheProAspValaAspSerGluProThrThr 382
DB 1209 CTAGACGTACAACATTGATGATTAATGCTTTCCGAGATGTGACTCAGAGCCCAACACC 1268
QY 383 LeuSerTrpGluSerValSerGlnAlaThrAsnTrpThrIleGlnGlnAspLysLeuLys 402
DB 1269 CTTTCTGGGAATCTGTGCTCAGGCCACGAATGAGCATGACATCAAGATTAATTAATA 1328
QY 403 ProPheTrpCysTyrAsnIleSerValTyrProMetLeuHisAspLysValaGlyGluPro 422
DB 1329 CTTTCTGTGTATTAACATCTCTGTATCCAAATGTGCATGACAAAGTTGGCCAGCCA 1388
QY 423 TyrSerIleGlnAlaTyrAlaLysGluGlyValProSerGluGlyProGluThrLysVal 442
DB 1389 TATTCATTCAGGCTTATGCCAAAGAGCGCTTCATCAGAAAGTCTGAGACCAAGGTG 1448
QY 443 GluAsnIleGlyValLysThrValaThrIleThrTrpLysGluIleProLysSerGluArg 462
DB 1449 GAGAACATTTGGCGTGAAGAGCGTCAAGATCAATGAGAAAGAAATTTCCCAAGAGTGA 1508
QY 463 LysGlyIleIleCysAsnTyrThrIlePheTyrGlnAlaGluGlyGlyLysGlyPheSer 482
DB 1509 AAGGGTATATATGTGACATCACACATCTTTTACCAAGCTGAAGGTGAAAGAAATTTCTC 1568
QY 483 LysThrValaAsnSerSerIleLeuGlnTyrGlyLeuGluSerLeuLysArgLysThrSer 502
DB 1569 AAGACAGTAAATTTCCAGCATCTTGACATGAGCGCTGAGATCCCTGAACGAAGACCTT 1628
QY 503 TyrIleValaGlnValMetAlaSerThrSerAlaGlyGlyTyrAsnGlyThrSerIleAsn 522
DB 1629 TACATTTGTCAGGTACATGCGCAGCACAGTCTGGGGGCAACCAAGCGCACAGTAAAT 1688
QY 523 PheLysThrLeuSerPheSerValaPheGluIleIleLeuIleThrSerLeuIleGlyGly 542
DB 1689 TTCAAACATTTGATTCATCTGATCTTTGATTAATCTCTATTAATCTCTGATGGTGA 1748
QY 543 GlyLeuLeuIleLeuIleIleLeuThrValaAlaTyrGlyLeuLysLeuProAsnLysLeu 562
DB 1749 GGCCTTTTATTTCTATTAATCTGACAGTGGCATGTGCTCAAAAAACCAACAATTTG 1808
QY 563 ThrHisLeuCysTrpProThrValaProAsnProAlaGluSerSerIleAlaThrTrpHis 582
DB 1809 ACTCATCTGTGTGGGCCACCGTCCCAACCTGCTGAAGATGATATACCAATGCGCAT 1868
QY 583 GlyAspAspPheLysAspLysLeuAsnLeuLysGluSerAspAspSerValaAsnThrGlu 602
DB 1869 GAGATGATTTCAAGATTAAGATTAACCTGAAGAGAGTCTGATGACTCTGTGAACACAGAA 1928
QY 603 AspArgIleLeuLysProCysSerThrProSerAspLysLeuValaIleAspLysLeuVal 622
DB 1929 GACAGATCTTTAAACCACTTCCACCCCACTGACAAATTTGTGATTAACAAGTTGGTG 1988
QY 623 ValAsnPheGlyAsnValLeuGlnGluIlePheThrAspGluAlaArgThrGlyGlnGlu 642
DB 1989 GTGAATTTGGGAATTTCTGCAAGAAATTTTCAAGATGAAGACCAAGCGGTCAGAA 2048
QY 643 AsnAsnLeuGlyGlyGluLysAsnGlyThrArgIleLeuSerSerCysProThrSerIle 662
DB 2049 AACCAATTTAGAGGGGAAAAAGAAATGGACTGAATTTGTGTCTTCCGCCCACTTCAATA 2108

RESULT 6
ADL26671
ID ADL26671 standard; cDNA; 2529 BP.
XX
AC
XX ADL26671;

DT 20-MAY-2004 (first entry)

XX Human cytokine receptor zcytor17 DNA seqid 108.

XX antiinflammatory; antitumor; dermatological; antiallergic; antipsoriatic;

DE antibacterial; immunosuppressive; cell proliferation inhibitor;

XX immune response inhibitor; inflammatory response inhibitor;

KW multimeric cytokine receptor; heterodimeric cytokine receptor; cancer;

KW cytokine-binding domain; class I cytokine receptor; hematopoietic cell;

KW zcytor171g-induced proliferation; zcytor171g-induced differentiation;

KW hematopoietic progenitor cell; zcytor171g-induced inflammation;

KW inflammatory disease; inflammatory bowel disease; ulcerative colitis;

KW Crohn's disease; atopic dermatitis; eczema; psoriasis; endotoxaemia;

KW septicemia; toxic shock syndrome; zcytor17; human; gene; ss.

OS Homo sapiens.

XX US2003215838-A1.

XX 20-NOV-2003.

PD 21-JAN-2003; 2003US-00351157.

XX 18-JAN-2002; 2002US-0350325P.

PR 14-JUN-2002; 2002US-0389108P.

PR 19-DEC-2002; 2002US-0435361P.

XX (SPRE/) SPRECHER C A.

PA (GAOZ/) GAO Z.

PA (KUIJ/) KUIJER J L.

PA (DASO/) DASOVICH M M.

PA (GRAN/) GRANT F J.

PA (PRES/) PRESNELL S R.

PA (WHIT/) WHITMORE T E.

PA (HAMM/) HAMMOND A K.

PA (NOVA/) NOVAK J E.

PA (GROS/) GROSS J A.

PA (DILL/) DILLON S R.

XX Sprecher CA, Gao Z, Kuijper JL, Dasovich MM, Grant FJ,

P1 Presnell SR, Whitmore TE, Hammond AK, Novak JE, Grosse JA, Dillon SR;

XX MPI: 2003-876545/81.

DR P-PSDB: ADL26672.

PT Novel multimeric or heterodimeric cytokine receptors useful for treating

PT chronic inflammatory disease such as inflammatory bowel disease,

PT ulcerative colitis, acute inflammatory disease such as endotoxaemia,

PT septicemia.

XX

PS Disclosure; SEQ ID NO 108, 205pp; English.

XX

CC The invention describes an isolated multimeric or heterodimeric cytokine

CC receptor (I) having at least one polypeptide having 90 percent sequence

CC identity with a 732 (SI) or 649 (S2) amino acid sequence given in

CC specification, and where (I) binds a ligand comprising a 164 (S3) amino

CC acid sequence, given in specification, or at least one polypeptide

CC comprising residue 20-227 of (SI). (I) is useful for killing cancer cells

CC and producing an antibody to (I) and a cytokine-binding domain of a class

CC I cytokine receptor. A composition (CI) comprising (I) and a cytokine-

CC binding domain of a class I cytokine receptor and a vehicle is useful

CC for: reducing hematopoietic cells and hematopoietic progenitor cells in

CC a mammal; inhibiting zcytor171g-induced proliferation or differentiation

CC of hematopoietic cells and hematopoietic progenitor cells; reducing

CC zcytor171g-induced inflammation; treating a mammal afflicted with an

CC inflammatory disease in which zcytor171g plays a role. The disease is a

CC chronic inflammatory disease such as inflammatory bowel disease,

CC ulcerative colitis, Crohn's disease, atopic dermatitis, eczema and

CC psoriasis. The disease is acute inflammatory disease such as

CC endotoxaemia, septicemia, toxic shock syndrome and infectious disease.

CC An immune response inhibiting composition is useful for inhibiting an

CC immune response in a mammal exposed to an antigen or pathogen. An

CC inflammatory response inhibiting composition is useful for suppressing an

CC inflammatory response in a mammal with inflammation. An antibody that

CC specifically binds to (I) is useful for detecting the presence of a

CC multimeric or heterodimeric cytokine receptor in a biological sample.

CC This sequence encodes a human zcytor17 cytokine receptor that can be used

CC in a comparison with other zcytor17 receptors.

XX

SQ Sequence 2529 BP; 764 A; 530 C; 576 G; 659 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.:	Length:	Matches:	Mismatches:	Indels:	Gaps:
Score: 3518.00	2529	660	0	0	0
Percent Similarity: 100.00%					
Best Local Similarity: 100.00%					
Query Match: 99.72%					
DB: 11					

US-10-006-265-17 (1-662) x ADL26671 (1-2529)

QY 3 LeuSerProGlnProSerCysValAsnLeuGlyMetThrTrpAlaLeuTrpMet 22

DB 129 CTCTCTCCCGACCTTCATGTTTAACTGGGAGATGATGAGACCTGGACCTGTGATG 188

QY 23 LeuProSerLeuCylysPheSerLeuAlaLeuProAlaLysProGluAsnIleSer 42

DB 189 CTCCCTCCTCCTCGAATTGACGCTGGCAGCTCTGCGAGCTTAAGCTGAGAACATTTCC 248

QY 43 CysValIleTyrTyrPheGlyAsnLeuThrCysThrTrpSerProGlyLysGluThrSer 62

DB 249 TGTGCTACTACTATGAGAAAATTTAACTGCACTTGGAGTCCAGAGAAAGAAACCGT 308

QY 63 TyrThrGlnTyrTrpValLysArgThrTyrAlaPheGlyGlyLysAspAsnCysThr 82

DB 309 TATACCCAGTACACGTTTAAAGAACTTACGCTTTGGAGAAAACATGATTAATTGACA 368

QY 83 ThrAsnSerSerThrSerGluAsnArgAlaSerCysSerPhePheLeuProArgIleThr 102

DB 369 ACCAATGTTTACAAGGAAATCGTGCTTGGCTTTTCTTCCCAAGATAACG 428

QY 103 IleProAspAsnTyrThrIleGluValGluAlaGluAsnGlyLysArgValIleLysSer 122

DB 429 ATCCAGATTAATTTATACATTGAGGTGAGCTGAAATGAGATGATGATTAATTTCT 488

QY 123 HisMetThrTyrTrpArgLeuGluAsnIleAlaLysThrGluProPheValIlePheArg 142

DB 489 CATATGACATATCTGAGATTGAGAACATACGAAACCTGAAACCATTAATTTCCGT 548

QY 143 ValIysProValIleGlyIleLysArgMetIleGlnIleGluTyrIleLysProGluLeu 162

DB 549 GTGAACCAAGTTTGGCGCATCAACGAATGATTAATGATTAAGCTGAGTTG 608

QY 163 AlaProValSerSerAspLeuLysTyrThrLeuArgPheArgThrValAsnSerThrSer 182

DB 609 GCGGCTGTTTATCTGATTTAAATTAACACTTGCATTCAGGACAGTCAAGTACAGC 668

QY 183 TrpMetGluValAsnPheAlaLysAsnArgLysAspLysAsnGlnTyrAsnLeuThr 202

DB 669 TGGATGGAAGTCACTTCGTAACACGTTAAGGATTAAGAAACCAACGTTAACTCAAG 728

QY 203 GlyLeuGlnProPheThrGlnTyrValIleAlaLeuArgCysAlaValLysGlySerLys 222

DB 729 GGGGTGACGCTTTTACGAAATATGTCATAGCTTGGAGTGGCGTCAAGGATCAAG 788

QY 223 PheTyrSerAspTrpSerGlnLysMetGlyMetThrGluGluGluAlaProCysGly 242

DB 789 TTCTGGAGTGTCTGAGACCAAGAAATGGGATGACTGAGGAAGAACTCCATGTGGC 848

QY 243 LeuGluLeuTrpArgValIleLysProAlaGluAlaAspGlyArgProValArgLeu 262

DB 849 CTGGAACCTGTGAGAGATCTGAAACCGCTGAGGAGGAGGAGGAGGAGGAGGAGG 908

QY 263 LeuTrpLysLysAlaArgGlyAlaProValLeuGluLysThrLeuGlyTyrAsnIleTrp 282

DB 909 TTATGGAAGAAAGCAAGAGAGGCCCACTGATGAGAAACACTTGGCTTCAACATATGG 968


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QY 283 TyrTyrProGluSerAsnThrAsnLeuThrGluThrMetAsnThrThrAsnGlnGlnLeu 302
Db 969 TACTATCCAGAAAGCAACTAACCTCAGAGAAACATGACCTACTAACCGACGACTT 1028
QY 303 GluLeuHisLeuGlyGlyGluSerPheTrpValSerMetIleSerTyrAsnSerLeuGly 322
Db 1029 GAACGTCATCGGAGGCGGAGAGCTTTGGGTGTATGATTTCTTAATAATTCCTTGGG 1088
QY 323 LysSerProValAlaThrLeuArgIleProAlaIleGlnGluSerPheGlnCysIle 342
Db 1089 AAGTCTCCAGGTGGCCACCCTGAGAGATTCAGTATTCAGAAAAATCATTTGAGTCAT 1148
QY 343 GluValMetGlnIaCysValaIaGluAspGlnLeuValaValIleTyrProGlnSerSerAla 362
Db 1149 GAGGTATGAGGCGCTCCGTTGCTGAGGACCACTAGTGTGAAGTGGCAAACTCTGCT 1208
QY 363 LeuAspValAsnThrTyrMetIleGluTrpPheProAspValAspSerGluProThrThr 382
Db 1209 CTAGACGCGAACACTTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1268
QY 383 LeuSerTrpGluSerValSerGlnAlaThrAsnTrpThrIleGlnGlnAspValLeuVal 402
Db 1269 CTTTCCGGAATCTGTCTCAGCCAGACGACGACGATCCAGCAAGATTAATTAATAA 1328
QY 403 ProPheTrpCysTyrAsnIleSerValTyrProMetLeuHisAspValaIaGlyGluPro 422
Db 1329 CTTTCCGGAATCTGTCTCAGCCAGACGACGATCCAGCAAGATTAATTAATAA 1388
QY 423 TyrSerIleGlnAlaTyrAlaValysGluGlyValProSerGluGlyProGluThrVal 442
Db 1389 TATTCATCAGAGCTTATGCGCAAGAGCGCTTCATCAAGAGTCCCTGAGACCAAGTG 1448
QY 443 GluAsnIleGlyValIleTyrThrValThrIleThrTrpLeuGlnIleProLysSerGluArg 462
Db 1449 GAGAACATTTGGCGTGAAGAGCGTACGATCACATGAAAGATTTCCCAAGATGAGAGA 1508
QY 463 LysGlyIleIleCysAsnTyrThrIlePheTyrGlnAlaGluGlyLysGlyPheSer 482
Db 1509 AAGGTAATCATCTGCAACTACACCATCTTTTACCAAGCTGAAGTGAAGAAAGATTCTCC 1568
QY 483 LysThrValAsnSerSerIleLeuGlnTyrGlyLeuGluSerLeuValGlyThrSer 502
Db 1569 AAGACAGTCAATTCAGCATCTTGAGTACGAGTACGAGTACGAGTACGAGTACGAGT 1628
QY 503 TyrIleValGlnAlaMetAlaSerThrSerAlaGlyGlyThrAsnGlyThrSerIleAsn 522
Db 1629 TACATTTGTCAGGTCATGCGCAGACCAAGTCTGGGGGAAACCAAGGACGACATTAAT 1688
QY 523 PheLysThrLeuSerPheSerValaPheGlnIleIleLeuIleThrSerLeuIleGlyGly 542
Db 1689 TTCAGACATGTCATTCATTCATGCTTTGAGATTATCTCTTAATCTTCTGATTGGTGA 1748
QY 543 GlyLeuLeuIleLeuIleIleLeuThrValaIaTyrGlyLeuLysLysProAsnValLeu 562
Db 1749 GGCCTTCTTATCTCATCTTATCTGACAGTGGCATATGTCCTCAAAAAACCAAAATTTG 1808
QY 563 ThrHisLeuGlyTrpProThrValaProAsnProAlaGluSerSerIleAlaThrTrpHis 582
Db 1809 ACTCATCTGTGTGGCCCGCCAGCTTCCCAACCTGCTGAAAGTGAATAGCCACATGGCAT 1868
QY 583 GlyAspAspPheLysAspLysLeuAsnLeuLysGluSerAspAspSerValaAsnThrGlu 602
Db 1869 GAGATGATTTCAAGAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAA 1928
QY 603 AspArgIleLeuLysProCysSerThrProSerAspLysLeuValaIleAspValLeuVal 622
Db 1929 GACAGGATCTTAAACCATGATTCACCCCGAGTGAAGATTTGATGATGATGATGATGAT 1988
QY 623 ValAsnPheGlyAsnValaIleGlnGlnIlePheThrAspGluAlaAsnThrGlyGlnGlu 642
Db 1989 GTGAATCTTGGAGATTTGTGCAAGAAATTTTTCACAGATGAAGCCAGAAAGGCTGAGAA 2048

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QY 643 AsnAsnLeuGlyGlyGluLysAsnGlyThrArgIleLeuSerSerCysProThrSerIle 662
Db 2049 AACCAATTTGAGGGGAGAAAGATGGAGCTAGCAATTTCTGCTGCGCCACTTCAATA 2108

RESULT 7
ABQ83363
ID ABQ83363 standard; cDNA; 4315 BP.
XX
AC ABQ83363;
XX
DT 20-JUN-2003 (first entry)
XX
DE Human NR10.3 splicing variant encoding cDNA SEQ ID NO:1.
XX
KW NR10; splicing variant; haematopoietic receptor; immunomodulator;
KW haematopoietic; haematopoietic factor; immunological disease;
KW haematopoietic disease; haematopoietic cell regulation; gene; ss.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 7..2052
FT /tag= a
FT /product= "NR10.3"
XX
PN W0200277230-A1.
XX
PD 03-OCT-2002.
XX
PE 22-MAR-2002; 2002W0-JP002769.
XX
PR 26-MAR-2001; 2001JP-00087298.
XX
PA (CHUS ) CHUGAI SEIYAKU KK.
XX
PI Maeda M, Yaguchi N, Hasegawa M;
XX
DR MPI; 2003-018925/01.
XX
DR P-PSDB; ABP54363.
XX
PT NR10 splicing variants of hematopoietic receptor proteins and encoded
PT genes, applicable in searching hematopoietic factors and developing
PT remedies for immunological and hematopoietic diseases.
XX
PS Example 2; Fig 1-2; 250bp; Japanese.
XX
CC The present invention describes haematopoietic receptor NR10 splicing
CC variants (1). (I) have immunomodulator and haemostatic activities. The
CC proteins and encoded genes are applicable in searching for novel
CC haematopoietic factors, and developing remedies for immunological and
CC haematopoietic diseases. The haematopoietic receptor genes participate
CC in vivo immunomodulation and haematopoietic cell regulation, and in the
CC search for haematopoietic factors capable of functionally binding to the
CC receptors. The present sequence encodes the human NR10.3 protein from the
CC present invention
XX
SQ Sequence 4315 BP; 1187 A; 1008 C; 1061 G; 1059 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 0 Length: 4315
Score: 3518.00 Matches: 660
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 99.72% Indels: 0
DB: 8 Gaps: 0

US-10-006-265-17 (1-662) x ABQ83363 (1-4315)
QY 3 LeuSerProGlnProSerCysValaAsnLeuGlyMetTrpThrTrpAlaLeuTrpMet 22
Db 70 CTCTCTCCCGAGCTTCACTGTGTTAACTGGGAGATGATGACCTGGGACCTGTGATG 129
QY 23 LeuProSerLeuCysLysPheSerLeuAlaIleLeuProAlaLysProGluAsnIleSer 42

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Db 130 CTCCTCACTCTGAAATTCAGCTGGACGCTCTGCCAGCTAACCTGAGAACCTTTCC 189
 Qy 43 CysValTyrTyrTyrArgLysAsnLeuThrCysThrTrpSerProGlyLysGluThrSer 62
 Db 190 TGTGTCTACTACTATAGAAAAATTTAACTGTCATCTGGAGTCCAGAAAGGAAACCACT 249
 Qy 63 TyrThrGlnTyrThrValLysArgThrTyrAlaPheGlyGluLysHisAspAsnCythr 82
 Db 250 TATACCAGTACACAGTTAAGAACTTACGCTTTTGAGAAAAACATGATTAATGTACA 309
 Qy 83 ThrAsnSerSerThrSerGluAsnArgLysSerCysSerPhePheLeuProGlnLeuThr 102
 Db 310 ACCAATAGTTCTCAAGTGAATAATCTGCTCTGCTCTTTTCTCTTCCCAAGAAATAAG 369
 Qy 103 IleProAspAsnTyrThrIleGluValGluAlaGluAsnGlyAspGlyValIleLysSer 122
 Db 370 ATCCAGATTAATTAATACATTGAGGTGGAAGCTGAAATGAGATGCTAATTAATCT 429
 Qy 123 HisMetThrTyrTrpArgLeuGluAsnIleAlaLysThrGluProProLysIlePheArg 142
 Db 430 CATATGACATACTGAGATTAGAGAACATAGCGAAACCTGAACCACTTAAGATTTTCCGT 489
 Qy 143 ValLysProValIleGluGlyIleLysArgMetIleGlnIleGluTrpIleLysProGluLeu 162
 Db 490 GTGAACCAAGTTTGGCATCAACCAATGATTCAATTAATGATTAAGCTTGAAGTTG 549
 Qy 163 AlaProValSerSerAspLeuLysTyrThrLeuArgPheArgThrValAsnSerThrSer 182
 Db 550 GCGCTGTTCATCTGATTTAAATTAACACTTCGATTCAGGACAGTCAACAGTCCAGC 609
 Qy 183 TrpMetGluValAsnPheAlaLysAsnArgLysAspLysAsnGlnThrTyrAsnLeuThr 202
 Db 610 TGGAGGAAAGTCAACTTGCTAAGAACCTGAAGATTAACCAACCACTGAACCTCAGC 669
 Qy 203 GlyLeuGlnProPheThrGluTyrValIleAlaLeuArgCysAlaValIleGluSerLys 222
 Db 670 GGGCTGCAGCTTTTACAGAAATATCTCATAGCTCTGCATGTGCGGTCAAGAGTCAAG 729
 Qy 223 PheTrpSerAspTrpSerGlnGlyLysMetGlyMetThrGluGluGluAlaProCysGly 242
 Db 730 TTCTGAGTGACTGAGCCAGAAATAATGGGAATGATGAGAGAAAGGCTCATGTGTC 789
 Qy 243 LeuGluLeuTrpArgValIleLysProAlaGluAlaAspGlyArgArgProValArgLeu 262
 Db 790 CTGGAACGTGGAGAGTCTCTGAACACAGTGAAGGAGTGAAGAAAGCCACATGGGTG 849
 Qy 263 LeuTrpLysLysAlaArgGlyValAlaProValLeuGluLysThrLeuGlyTyrAsnIleTrp 282
 Db 850 TTATGGAAGAAAGGCAAGAGAACCCCACTCTAGAGAAACACTTGCTCAACAATATAG 909
 Qy 283 TyrTyrProGluSerAsnThrAsnLeuThrArgIleMetAsnThrThrAsnGlnLeu 302
 Db 910 TACTATCCAGAAAGCAACACTCACTCAAGAAACATAGAACACTAACAGCAGCTT 969
 Qy 303 GluLeuHisLeuGlyGlyGluSerPheTrpValSerMetIleSerTyrAsnSerLeuGly 322
 Db 970 GAACGTCACTCTGGAGGAGAGCTTTGGGTGTCTATGATTTCTTAATATCTCTTGGG 1029
 Qy 323 LysSerProValAlaThrLeuArgIleProAlaIleGlnGluLysSerPheGlnCysIle 342
 Db 1030 AAGTCTCAAGTGGCCACCTCGAGATTCAGCTATTCAGAAATAATCTTTCAGTGCATT 1089
 Qy 343 GluValMetGlnAlaCysValAlaGluAspGlnLeuValIleLysTrpGlnSerSerAla 362
 Db 1090 GAGGTCAATGCAAGGCTGCGTGTCTAGAGCAAGCTAGTGAATGGCAAAAGCTCTGCT 1149
 Qy 363 LeuAspValAsnThrTrpMetIleGluTrpPheProAspValAspSerGluProThrThr 382
 Db 1150 CTAGACGTGAACACTTGATGATTAATGATTTCCGAGTGTGACTCAGAGCCCAAC 1209
 Qy 383 LeuSerTrpGluSerValSerGlnAlaThrAsnTrpTrpIleGlnGluAspLysLeuLys 402

Db 1210 CTTTCTGGAATCTGTGTCTCAGGCCAGAACTGACATCCAGACATTAATTAATA 1269
 Qy 403 ProPheTrpCysTyrAsnIleSerValTyrProMetLeuHisAspLysValGlyGluPro 422
 Db 1270 CTTTCTGTGCTATTAACATCTGTGTATCAATGTGTGACAAAGTTGGCGAGCCA 1329
 Qy 423 TyrSerIleGlnAlaTyrAlaLysGluGlyValIleProSerGluGlyProGluThrLysVal 442
 Db 1330 TATTCATCCAGGCTTATGCAAGAGAGGCTTCAATCAGAAAGTCTGAGACCAAGGTG 1389
 Qy 443 GluAsnIleGlyValLysThrValThrIleThrTrpLysGluIleProLysSerGluArg 462
 Db 1390 GAGAACATTTGCGTGAAGACGCTCAGCATCACTAGAAAGATTTCCCAAGATGAGAGA 1449
 Qy 463 LysGlyIleIleCysAsnTyrThrIlePheTyrGlnAlaGluGlyGlyLysPheSer 482
 Db 1450 AAGGTATCATCTGCATACACCATCTTTTACCAAGCTGAAGGTGAAAAAGATTCCTCC 1509
 Qy 483 LysThrValAsnSerSerIleLeuGluTyrGlyLeuGluSerLeuLysArgLysThrSer 502
 Db 1510 AAGACATCAATTCAGCATCTTGACGTACGAGCTGAGTCCCTGAACGAAACCTCT 1569
 Qy 503 TyrIleValGlnValMetAlaSerThrSerAlaGlyLysThrAsnGlyThrSerIleAsn 522
 Db 1570 TACATTTGTCAGTCAATGCGCACGACCAAGCTGCGGGAACCAACGGGACCATTAAT 1629
 Qy 523 PheLysThrLeuSerPheSerValPheGluIleIleLeuIleThrSerLeuIleGlyGly 542
 Db 1630 TTCAAGCATTTGATTCAGTCTTGAGATTAATCCCATACATCTCTCATATTGTGGA 1689
 Qy 543 GlyLeuLeuIleLeuIleIleLeuThrValAlaTyrGlyLeuLysLysProAsnLysLeu 562
 Db 1690 GGCCTTCTTATTCATTAATCTTCAACGTGGCAATGTCTCAAAAAACCAAAATTG 1749
 Qy 563 ThrHisLeuCyTrpProThrValProAsnProAlaGluSerSerIleAlaThrTrpHis 582
 Db 1750 ACTCATCTGTGTGGCCACCGTTCCCAACCTGCTGAATAAGTACATGAGCAT 1809
 Qy 583 GlyAspAspPheLysAspLysLeuAsnLeuLysGluSerAspAspSerValAsnThrGlu 602
 Db 1810 GGAGATGATTTCAAGATTAACCTTAACCTGAAGAGTGTATGACTGTGTAACACAGAA 1869
 Qy 603 AspArgIleLeuLysProCysSerThrProSerAspLysLeuValIleAspLysLeuVal 622
 Db 1870 GACGAGATCTTAACCACTGTTCAACCCCACTGAACAGATTGGATGACAAAGTTG 1929
 Qy 623 ValAsnPheGlyAsnValLeuGlnGluIlePheThrAspGluAlaArgThrGlyGlnGlu 642
 Db 1930 GTGAACCTTTGGGAATGTTCTCAAGAAATTTTCAAGATGAAGCAAGACGGGTACGAA 1989
 Qy 643 AsnAsnLeuGlyGlyGlyLysAsnGlyThrArgIleLeuSerSerCysProThrSerIle 662
 Db 1990 AACAAATTAGAGAGGGAAGAAATGAGACTGAATTTCTGTCTCTGCCCAATTCATA 2049
 RESULT 8
 AAC92337
 ID AAC92337 standard; cdna; 2969 BP.
 AC AAC92337;
 DT 26-MAR-2001 (first entry)
 DE Human haemopoietic receptor protein NR10.1 encoding cdna SEQ ID NO.1.
 KW Human; haemopoietic receptor; NR10.1; NR10.2; NR10.3; NR10;
 KW immunoregulation; haematopoietic cell regulation; transmembrane;
 KW immune disorder; haematopoietic disorder; autoimmune disease; allergy;
 KW metal allergy; pollen allergy; ss.
 OS Homo sapiens.
 XX
 XX
 OS
 XX
 XX
 PN MO200075314-A1.

PD 14-DEC-2000.
 XX 01-JUN-2000; 2000MO-JP003556.
 XX 02-JUN-1999; 99JP-00155797.
 PR 30-JUL-1999; 99JP-00217797.
 XX
 PA (CHUGAI) CHUGAI RES INST MOLECULAR MEDICINE INC.
 XX
 PI Maeda M, Yaguchi N;
 XX WPI; 2001-061720/07.
 DR P-PSDB; AAB51242.
 XX
 PT Hematopoietin receptor protein NR10 for screening potential ligands for
 PT treatment of immune and hematopoietic disorders such as autoimmune
 PT diseases and allergies.
 XX
 PS Claim 1; Fig 3-5; 127pp; Japanese.
 XX
 CC The present sequence encodes a human haemopoietin receptor protein
 CC (NR10), specifically designated NR10.1. NR10 occurs as a transmembrane
 CC protein and a soluble protein. NR10 is a haemopoietin receptor molecule
 CC which participates in immunoregulation and haematopoietic cell regulation
 CC in vivo, and is useful in searching for haematopoietic factors capable of
 CC binding to the receptor. NR10 can be used for the identification of
 CC substances for the treatment and prevention of immune and haematopoietic
 CC disorders including autoimmune diseases and allergies such as metal and
 CC pollen allergy
 XX
 SQ Sequence 2969 BP; 939 A; 618 C; 662 G; 750 T; 0 U; 0 Other;
 Alignment Scores:
 Pred. No.: 0 Length: 2969
 Score: 3512.00 Matches: 661
 Percent Similarity: 99.85% Conservative: 1
 Best Local Similarity: 99.70% Mismatches: 0
 Query Match: 99.55% Indels: 1
 DB: Gaps: 0
 US-10-006-265-17 (1-662) x AAC92337 (1-2969)
 QY 1 MetLysLeuSerProGlnProSerCysValAsnLeuGlyMetThrTrpThrPalaleu 20
 DB 523 ATGAAGCTCTCTCCACGCTTCATGTGTAACTGGGAGATGATGGACCTGGCACTG 582
 QY 21 TrpMetLeuProSerLeuCysLysPheSerLeuAlaLeuProAlaLysProGluAsn 40
 DB 583 TGGATGCTCCCTCAGCTCTGCAAAATTCAGCTGGCAGCTCTGCCAGCTAAAGCTGAGAAC 642
 QY 41 IleSerCysValTyrTyrTyrArgLysAsnLeuThrCysThrTrpSerProGlyLysGlu 60
 DB 643 ATTTCCGTGTCTACTACTATAGGAAAAATTTAAACCTGCACCTTGGAGCTCAGAGAAAGGA 702
 QY 61 ThrSerTyrThrGlnTyrThrValLysArgThrTyrAlaPheGlyGlyLysPheAsn 80
 DB 703 ACCAGTTATACCCAGTACAGATTAGAGAACTTACGCTTCGAGAAAAACATGATTAAT 762
 QY 81 CysThrThrAsnSerSerThrSerGluAsnArgAlaSerCysSerPhePheLeuProArg 100
 DB 763 TGTACAAACCAATAGTTCTACAGTGAAGAAATCGTGTCTCTTTTCTTCCCAAGA 822
 QY 101 IleThrIleProAspAsnTyrThrIleGluValGluValGluValAsnGlyAspGlyValIle 120
 DB 823 ATAACAGATCCCAAGTATATTAATTAACATTGAGTGAAGCTGAAAATGAGATGAGTAAAT 882
 QY 121 LysSerHisMetThrTyrTrpArgLysGluAsnIleAlaLysThrGluProProLysIle 140
 DB 883 AAATTCATATGACATCTGAGATTAGAAACATAGCGAAAACTGAACCACTTAAGATT 942
 QY 141 PheArgValLysProValIleGluGlyIleLysArgMetIleGlnIleGluTProLysPro 160
 DB 943 TTCGTGTGAACCAAGTTTGGGCATCAACGAATGATTCAAATGATGATTAAGCCT 1002

QY 161 GluLeuAlaProValSerSerAspLeuLysTyrThrLeuArgPheArgThrValAsnSer 180
 DB 1003 GAGTTGGCGCCTGTTTTCATCTGATTTAAATACACCTTCGATTGAGCACTCAACACT 1062
 QY 181 ThrSerTrpMetGluValAsnPheAlaLysAsnArgLysAspLysAsnGlnThrTyrAsn 200
 DB 1063 ACCAGCTGATGAGTCAACTTCGCTGAGAACCCGTAAAGATTAACCAACCGTAAAC 1122
 QY 201 LeuThrGlyLeuGlnProPheThrGlnTyrValIleAlaLeuArgCysAlaValLysGlu 220
 DB 1123 CTCACGGGCTGCGCCTTTTACAGATATGTCTATGCTCTCGATGTCCGCTCAAGAG 1182
 QY 221 SerLysPheTrpSerAspTrpSerGlnGlyLysMetThrGluGluGluAlaPro 240
 DB 1183 TCAAAGTTCTGAGTGACCTGAGGCAAGAAAAATGGAAATGATCGAGAGAAAGCTTCA 1242
 QY 241 CysGlyLeuGluLeuTrpArgValLeuLysProAlaGluAlaAspGlyArgArgProVal 260
 DB 1243 TGTGGCTGGAACTGTGGAGAGTCTGTAAACAGCTGAGCGGATGGAAGGCGCAGTG 1302
 QY 261 ArgLeuLeuTrpLysLysAlaArgGlyAlaProValIleGluLysThrLeuGlyTyrAsn 280
 DB 1303 CGGTGTATGGAAGAGGCAAGAGGCCCAAGTCTTGAAGAAAACATTGGCTTCAAC 1362
 QY 281 IleTrpTyrTyrProGluSerAsnThrAsnLeuThrGluThrMetAsnThrThrAsnGln 300
 DB 1363 ATATGTACTATCCAGAAAGCAACACTAACCTCAGAAACAAATGAACTACTAACCAAG 1422
 QY 301 GlnLeuGluLeuHisLeuGlyGlyGlySerPheTrpValSerMetIleSerTyrAsnSer 320
 DB 1423 CAGCTTGAACTGCATCTGGAGAGCGAGACTTTGGGTGTATGATATTTCTATTAATTTCT 1482
 QY 321 LeuGlyLysSerProValAlaThrLeuArgIleProAlaIleGlnGlyLysSerPheGln 340
 DB 1483 CTTGGGAATCTCCAGTGGCCACCTGAGGATTCACAGCTATTCAGAAAAACATTTCAG 1542
 QY 341 CysIleGluValMetGlnAlaCysValAlaGluAspGlnLeuValLysTrpGlnSer 360
 DB 1543 TGCATTGAGTCATGTCAGGCTGCGTGTGAGAGACACACTAGTGGTGAAGTGGCAAGC 1602
 QY 361 SerAlaLeuAspValAsnThrTrpMetIleGluTTrpPheProAspValAspSerGluPro 380
 DB 1603 TCTGCTCTAGAGGTGAACCTTGATGATGTATGATGTTTCCGAGTGTGAACCTCAGAGCCC 1662
 QY 381 ThrThrLeuSerTrpGluSerValSerGlnAlaThrAsnTrpThrIleGlnGlnAspLys 400
 DB 1663 ACCACCTTTCTGGGAATCTGTCTCAGGCCACGAACTGAGCAATCCAGCAAGTTAA 1722
 QY 401 LeuLysProPheTrpCysTyrAsnIleSerValTyrPrometLeuHisAspLysValGly 420
 DB 1723 TTAAACCTTTCTGGGTGATTAACATCTGTGATTCACATGTGATGATGACAAAGTTGAC 1782
 QY 421 GluProTyrSerIleGlnAlaTyrAlaLysGluGlyValProSerGluGlyProGluThr 440
 DB 1783 GAGCCATATTCATCCAGGCTTATGCAAGAGAGGGTTCATCCAGAAAGCTCTGAGACC 1842
 QY 441 LysValGluAsnIleGlyValLysThrValThrIleThrTrpLysGluIleProLysSer 460
 DB 1843 AAGGTGGAACAATTGGCGTGAAGACGTCAAGATCACATGAAAGAGATTCCCAAGAGT 1902
 QY 461 GluArgLysGlyIleIleCysAsnTyrThrIlePheTyrGlnAlaGluGlyLysGly 480
 DB 1903 GAGAGAAAGGATATCATCTGCAACTACACATCTTTACCAAGCTGAAGTGAAGAAAGGA 1962
 QY 481 PheSerLysThrValAsnSerSerIleLeuGlnTyrGlyLeuGluSerLeuLysArgLys 500
 DB 1963 TTCTCCAGACAGTCAATTCAGCACTTTCGAGTACGGCTGTGAAGTCCCTGAAACGAAAG 2022
 QY 501 ThrSerTyrIleValGlnValMetAlaSerThrSerAlaGlyGlyTyrAsnGlyThrSer 520
 DB 2023 ACCTCTTAATTTGTTTCAGTCTATGGCCACACCAAGTGTGGGGGAACCAACGGAGCCAGC 2082

QY 521 IleasnPhelyThrLeuSerPheSerValPheGluIleIleLeuIleThrSerLeuIle 540
 Db 2083 ATAAATTTCAAGACATTGTCTATGCTGCTTGGAGATTATCTCAATAATCTTCTGATT 2142
 QY 541 G1yG1yLeuLeuIleLeuIleIleLeuThrValAlaTYRGLYLeuLYsLeuLYsProasn 560
 Db 2143 GGTGAGGCGCTTCTATCTCTCATTCCTGACAGTGGCATATGCTCTCAAAAACCCCAAC 2202
 QY 561 LysLeuThrIleLeuCYeTrpProThrValProasnProAlaGluSerSerIleAlaThr 580
 Db 2203 AAATGACTCATCTGTGTGGCCCAACCGTCCCAACCTGCTGAAAGTAATAGTACCCACA 2262
 QY 581 TrpHisGLYAspAspPheLYsAspLYsLeuLeuLYsGLYLeuSerAspAspSerValasn 600
 Db 2263 TGGCATGAGATGATTTCAAGATTAAGCTTAACCTGAAAGAGCTCTGATGATCTTGTGAC 2322
 QY 601 ThrGluAspArgIleLeuLYsProCYsSerThrProSerAspLYsLeuValIleAspLYs 620
 Db 2323 ACAGAAACAGAGATCTTAAACCATGTTCCACCCCAAGTGAACAAAGTTGGTGTGACAAAG 2382
 QY 621 LeuValValasnPheGLYAsnValleuGluIleIlePheThrAspGluAlaArgThrGLY 640
 Db 2383 TTGGTGTGAACCTTGGGAATGTTCTGCAGAAATTTTCACAGATGAAGCCAGAAACGGGT 2442
 QY 641 GlnGlu-AsnAsnLeuGLYGLYGLYLeuLYsAsnGLYThrArgIleLeuSerSerCYsProTh 660
 Db 2443 CAGGAAACAACTTATAGAGGGGAAAGAAATGGAGCTGAAATTCCTGCTTCTGCTGCCAAC 2502
 QY 660 rSerIle 662
 Db 2503 TTCAATA 2509
 RESULT 9
 ID ABA93767 standard; cDNA; 2386 BP.
 XX ABA93767;
 XX 01-MAY-2002 (first entry)
 XX Human zcytor17 cDNA sequence SEQ ID NO:1.
 XX Zcytor17: chromosome 5; 5q11; cytokine receptor; immunomodulatory;
 KW antiinflammatory; antiviral; antirheumatic; antiarthritis; cytostatic;
 KW muscular; lymphoid; immune; inflammatory; splenic; blood; bone; disease;
 KW infection; immunosuppression; cytotoxicity; leukopenia; Crohn's disease;
 KW autoimmune disease; rheumatoid arthritis; multiple sclerosis; cancer;
 KW inflammatory disease; pancreatitis; inflammatory bowel disease; ss.
 XX Homo sapiens.
 OS
 XX WO200200721-A2.
 PN 03-JAN-2002.
 PD 26-JUN-2001; 2001WO-US020484.
 PF 26-JUN-2000; 2000US-0214282P.
 PR 26-JUN-2000; 2000US-0214282P.
 PR 29-JUN-2000; 2000US-0214955P.
 PR 08-FEB-2001; 2001US-0267963P.
 XX (ZYMO) ZYMOGENETICS INC.
 PA
 XX Sprechter CA, Presnell SR, Gao Z, Whitmore TE, Kuijper JL,
 PI Maurer MF;
 XX MPI: 2002-090519/12.
 DR P-PSDB: ABB05730.
 XX Isolated polynucleotide encoding a cytokine receptor zcytor17 which is
 PT useful for treating and diagnosing lymphoid, immune, inflammatory,
 PT splenic, blood or bone disorders.
 XX

PS Claim 2; Page 161-166; 235pp; English.
 XX The present invention describes a cytokine receptor designated zcytor17.
 CC Zcytor17 has immunomodulatory, antiinflammatory, antiviral, cytostatic,
 CC antirheumatic, antiarthritis and muscular activities. The zcytor17
 CC proteins are useful for treating and diagnosing lymphoid, immune,
 CC inflammatory, splenic, blood or bone disorders. Agonists or anti-
 CC zcytor17 antibodies are useful in stimulating cell-mediated immunity
 CC for stimulating lymphocyte proliferation, such as in the treatment of
 CC infections involving immunosuppression, including certain viral
 CC infections. They are also useful for inducing cytotoxicity and for
 CC treating leukopenias. Antagonist of zcytor17 polypeptides are useful for
 CC treating autoimmune diseases (e.g. rheumatoid arthritis and multiple
 CC sclerosis), inflammatory diseases (e.g. Crohn's disease), cancer,
 CC pancreatitis, and inflammatory bowel disease. Zcytor17 was mapped to
 CC chromosome 5, specifically to the 5q11 chromosomal region. ABA93767 to
 CC ABA93843 and ABB05730 to ABB05745 represent sequences used in the
 CC exemplification of the present invention
 XX
 SQ Sequence 2386 BP; 711 A; 525 C; 575 G; 575 T; 0 U; 0 Other;
 Alignment Scores:
 Pred. No.: 2,75e-314 Length: 2386
 Score: 3465.50 Matches: 651
 Percent Similarity: 99.24% Conservative: 1
 Best Local Similarity: 99.09% Mismatches: 2
 Query Match: 98.23% Indels: 3
 Gaps: 1
 US-10-006-265-17 (1-662) x ABA93767 (1-2386)
 QY 3 LeuSerProGlnProSerCYsValAsnLeuGLYMetMetTrpThrAlaLeuTrpMet 22
 Db 138 CTCTCTCCCAAGCCCTTCAATGTTAACTGGGAGTGAATGGAGCTGTGAGATG 197
 QY 23 LeuProSerLeuCYsLYsPheSerLeuAlaAlaLeuProAlaLYsProGluAsnIleSer 42
 Db 198 CTCCCTCAGCTCTGCAAAATTCAGCTGAGCTGTGCAAGTCAAGCTGAGAACATTTCC 257
 QY 43 CYsValTYRTYRYARGLYsAsnLeuThrCYsThrTrpSerProGLYLeuGLYThrSer 62
 Db 258 TGTGTCTACTACTCTATGAGAAATTTTAACTGCACTTGAGATCCAGAAAGAAACCAAGT 317
 QY 63 TYRThrGlnTYRThrValLYsArgThrTYRAlaPheIleGLYLeuLYsAspAsnCYeThr 82
 Db 318 TATACCCAGTACACAGTAAAGAACTTACGCTTTGGAGAAACAACTGATTAATGTACA 377
 QY 83 ThrAsnSerSerThrSerGluAsnArgAlaSerCYsSerPhePheLeuProArgIleThr 102
 Db 378 ACCAATAGTCTTCAAGTGAAGAAATCGTCTTCTGCTCTTTTCTTCCAGAAATTAAG 437
 QY 103 IleProAspAsnTYRThrIleGluValGluAlaGluAsnGLYAspGLYValIleLYsSer 122
 Db 438 ATCCAGATATATATATACATTTAGAGGTGAAGCTGAAATGAGATGTGTATTAATATCT 497
 QY 123 HisMetThrTYRTPAgleuGluAsnIleAlaLYsThrGluProPoleLYsIlePheArg 142
 Db 498 CATATGACATATCTGAGATTAAGAAACATGACGAAACCTAATGATTTTCGT 557
 QY 143 ValLYsProValleuGLYIleLYsArgMetIleGlnIleGluTrpIleLYsProGluLeu 162
 Db 558 GTGAAACCAAGTTTGGCATCAACGAAATGATTCAAATTAATGAGATTAAGACCTGAGTTG 617
 QY 163 AlaProValSerSerAspLeuLYsTYRThrLeuArgPheArgThrValAsnSerThrSer 182
 Db 618 GCGCCTGTTTCATCTGATTTTAAATACACACTTCGATTCAGACAGTCAAGTACAGC 677
 QY 183 TrpMetGluValasnPheAlaLYsAsnArgLYsAspLYsAsnGlnTYRAsnLeuThr 202
 Db 678 TGGATGGAATCAACTTCGCTTAAGAACCGTAAAGATTAACCAACCAAGTCAACCTCAGC 737
 QY 203 G1YleuGlnProPheThrGluTYRValIleAlaLeuArgCYsValAlaLYsGLYSerLYs 222

Db 738 GGGCTCAGCGCTTTTACAGAAATATGTCATAGCTCTGCGATGTCGGTCAAGAGTCAAA 797
 Qy 223 PheTSPeAspTSPeSerGlnGluYSMeTgLYMeThrGluGluGluAAlProCysGly 242
 Db 798 TTCTGAGTACCTGAGACCCAGAAATAATGGAAATGACTGAGAAAGAGCTCATGTGGC 857
 Qy 243 LeuGluLeuTrpArgValLeuYSProAlaGluAAlaSPglYArgrProValArgrLeu 262
 Db 858 CTGGAACGTGGAGAGTCTCGAAACAGGCTGAGCGGATGAGAAGAGCGCAGTGG 917
 Qy 263 LeuTrpLeuValAAlaArgValAProValLeuGluLeuYThrLeuGluYThrAAlaLeu 282
 Db 918 TTAGGAAAGAGGCAAGAGAGCCAGCTCTAGAGAAACACTGGCTACCAATATGG 977
 Qy 283 TyrTyrProGluSerAsnThrAsnLeuThrGluThrMetAsnThrThrAsnGlnGluLeu 302
 Db 978 TACTATCCAGAAAGCAACACTAATCTCAGAAACAAATGAACCTACTAATCCAGCAGCTT 1037
 Qy 303 GluLeuHisLeuGlyGlyGluSerPheTrpValSerMetIleSerTyrAsnSerLeuGly 322
 Db 1038 GAACCTCATCTGGAGGCGAGAGCTTTGGGTGTCTATGATTTCTATATATCTCTTGGG 1097
 Qy 323 LysSerProValAAlaThrLeuArgrIleProAlaIleGlnGluYSerPheGlnCysIle 342
 Db 1098 AAGTCTCCAGTGGCCACCCCTGAGAGATTCCAGCTATTCAAGAAATAATCATTTCACTGTCATT 1157
 Qy 343 GluValMetGlnAAlaCysValAAlaGluAspGluLeuValValYstrTrpGlnSerSerAla 362
 Db 1158 GAGGTATGCAAGGCTGCGTGTCTGAGACCACTAGTGTGAATGGCAAACTCTGCT 1217
 Qy 363 LeuAspValAsnThrTrpMetIleGluTrpPheProAspValAspSerGluProThrThr 382
 Db 1218 CTGAGCTGAAACACTTGATGATTTGAAATGATTTCCGATGTGAGCTCAGAGCCCAACACC 1277
 Qy 383 LeuSerTrpGluSerValSerGlnAAlaThrAsnTrpThrIleGlnGlnAspYsLeuYs 402
 Db 1278 CTTTCTGGAACCTGTGTCTGAGGCCACGAATGACGATTCACGAGAAATTAATTAATAA 1337
 Qy 403 ProPheTrpCysTyrAsnIleSerValTyrProMetLeuHisAspYsValGlyGluPro 422
 Db 1338 CTTTCTGAGTCTATTAACATCTGTGTATCCAAATGTTGCATACAAAGTGGCGAGCCA 1397
 Qy 423 TyrSerIleGlnAAlaTyrAlaYSglYValProSerGluGlyProGluThrYsVal 442
 Db 1398 TATTCCATCCAGGCTTATGCCAAAGAGGCGTTCATCAAGAGTCTCGAGCAAGAGTGS 1457
 Qy 443 GluAsnIleGlyValYsThrValThrIleThrTrpYsGluIleProYsSerGluArgr 462
 Db 1458 GAAACAATTGGCGCTGAAGAGGTCCAGATCACAAGAAAGATTCCTCAAGATGAGAGA 1517
 Qy 463 LysGlyIleIleCysAsnTyrThrIlePheTyrGlnAAlaGluGlyGlyYsGlyPheSer 482
 Db 1518 AAGGATATCATCTGCAACTACACCATCTTTTACCAAGCTGAAGGTGAAAGATTTCTCC 1577
 Qy 483 LysThrValAsnSerSerIleLeuGlnTyrGlyLeuGluSerLeuYsArgrYsThrSer 502
 Db 1578 AAGACAGTCAATTCCAGCATCTTGAGTAGGCGCTGGAAGTCCCTGAACCAAGACCTCT 1637
 Qy 503 TyrIleValGlnValMetAlaSerThrSerAlaGlyGlyYsThrAsnGlyYsThrSerIleAsn 522
 Db 1638 TACATGTTCAAGTTCAGGTGCGCACACCAAGTCTGGGGGAAACCAAGGACACACATAAA 1697
 Qy 523 PheLysThrLeuSerPheSerValPheGluIleIleLeuIleThrSerLeuIleGlyGly 542
 Db 1698 TTCAAGCATTTGATTCATGATGCTTTGAGATTATCTCTATTAATCTCTCGATTGGTGA 1757
 Qy 543 GlyLeuLeuIleLeuIleIleLeuThrValAlaTyrGlyLeuYsYsProAsnYsLeu 562
 Db 1758 GGCCTTCTTATCTCATTTATCTCGACAGTGGCATATGTTCTCAAAAAACCAACCAATTG 1817
 Qy 563 ThrHisLeuYsTrpProThrValProAsnProAlaGluSerSerIleAlaThrTrpHis 582
 Db 1818 ACTCATCTGTGTGGCCACCGTTCCAAACCTGTGAAAGTAGTATAGCCACATGGCAT 1877

Qy 583 GLYAspAspPheLYAspLYsLeuAsnLeuLYsGluSerAspAspSerValAsnThrGlu 602
 Db 1878 GGAAGATGATTTCAAGGATTAAGCTTAACCTGAAGAGTCTGATGACTCTGTGAACACAGA 1937
 Qy 603 AspArgIleLeuLYsProCysSerThrProSerAspLYsLeuValIleAspLYsLeuVal 622
 Db 1938 GACAGGATCTTAAACCAATGTTCCACCCCACTGTGCAACTGTGTGATTAACAAGTTGGTG 1997
 Qy 623 ValAsnPheGlyAsnValLeuGlnGluIlePheThrAspGluAlaArgrThrGlyGlnGlu 642
 Db 1998 GTGAACTTTGGAAATGTTCTGCAAGAAATTTTCAAGATGAAGCCCAAGCGGTCAGGA 2057
 Qy 643 AsnAsnLeuGlyGlyGluLYsAsnGlyThrArgIleLeuSerSerCysPro 659
 Db 2058 AACAAATTGAGAGGGGAAAGAAATGGG-----TATGTACCTGCCCC 2099
 RESULT 10
 ADL26673
 ID ADL26673 standard; cDNA, 2402 BP.
 XX
 AC ADL26673;
 XX
 DT 20-MAY-2004 (first entry)
 XX
 DE Human cytokine receptor zcytor17 DNA seqid 110.
 XX
 KW antiinflammatory; antiulcer; dermatological; antiallergic; antipsoriatic;
 KW antibacterial; immunosuppressive; cell proliferation inhibitor;
 KW immune response inhibitor; inflammatory response inhibitor;
 KW multimeric cytokine receptor; heterodimeric cytokine receptor; cancer;
 KW cytokine-binding domain; class I cytokine receptor; hematopoietic cell;
 KW zcytor17lig-induced proliferation; zcytor17lig-induced differentiation;
 KW hematopoietic progenitor cell; zcytor17lig-induced inflammation;
 KW inflammatory disease; inflammatory bowel disease; ulcerative colitis;
 KW Crohn's disease; atopic dermatitis; eczema; psoriasis; endotoxaemia;
 KW septicemia; toxic shock syndrome; zcytor17; human; gene; ss.
 XX
 OS Homo sapiens.
 XX
 PN US2003215838-A1.
 XX
 PD 20-NOV-2003.
 XX
 XX 21-JAN-2003; 2003US-00351157.
 PR 18-JAN-2002; 2002US-0350325P.
 PR 14-JUN-2002; 2002US-0389108P.
 PR 19-DEC-2002; 2002US-0435361P.
 XX
 PA (SPRE/) SPRECHER C A.
 PA (GAOZ/) GAO Z.
 PA (KUI/) KUIJPER J L.
 PA (DASO/) DASOVICH M M.
 PA (GRAN/) GRANT F J.
 PA (PRES/) PRESNELL S R.
 PA (WHIT/) WHITMORE T E.
 PA (HAMM/) HAMMOND A K.
 PA (NOVA/) NOVAK J E.
 PA (GROS/) GROSS J A.
 PA (DILL/) DILLON S R.
 XX
 PI Sprecher CA, Gao Z, Kuijper JL, Dasovich MM, Grant FJ;
 PI Presnell SR, Whitmore TE, Hammond AK, Novak JE, Gross JA, Dillon SR;
 XX
 XX MPI; 2003-876545/81.
 DR P-PSDB; ADL26674.
 XX
 XX Novel multimeric or heterodimeric cytokine receptors useful for treating
 PT chronic inflammatory disease such as inflammatory bowel disease,
 PT ulcerative colitis, acute inflammatory disease such as endotoxaemia,
 PT septicemia.
 XX

PS Disclousure; SEQ ID NO 110; 205pp; English.

XX The invention describes an isolated multimeric or heterodimeric cytokine receptor (I) having at least one polypeptide having 90 percent sequence identity with a 732 (S1) or 649 (S2) amino acid sequence given in specification, and where (I) binds a ligand comprising a 164 (S3) amino acid sequence, given in specification, or at least one polypeptide comprising residue 20-227 of (S1). (I) is useful for killing cancer cells and producing an antibody to (I) and a cytokine-binding domain of a class I cytokine receptor. A composition (CI) comprising (I) and a cytokine-binding domain of a class I cytokine receptor and a vehicle is useful for: reducing haematopoietic cells and hematopoietic progenitor cells in a mammal; inhibiting zcytor17lig-induced proliferation or differentiation of hematopoietic cells and hematopoietic progenitor cells, reducing zcytor17lig-induced inflammation; creating a mammal afflicted with an inflammatory disease in which zcytor17lig plays a role. The disease is a chronic inflammatory disease such as inflammatory bowel disease, ulcerative colitis, Crohn's disease, atopic dermatitis, eczema and psoriasis. The disease is acute inflammatory disease such as endotoxaemia, septicemia, toxic shock syndrome and infectious disease. An immune response inhibiting composition is useful for inhibiting an immune response in a mammal exposed to an antigen or pathogen. An inflammatory response inhibiting composition is useful for suppressing an inflammatory response in a mammal with inflammation. An antibody that specifically binds to (I) is useful for detecting the presence of a multimeric or heterodimeric cytokine receptor in a biological sample. This sequence encodes a human zcytor17 cytokine receptor that can be used in a comparison with other zcytor17 receptors.

CC Sequence 2402 BP; 713 A; 532 C; 580 G; 577 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.: 2,786-314 Length: 2402
Score: 3465.50 Matches: 651
Percent Similarity: 99.24% Conservative: 1
Best Local Similarity: 99.09% Mismatches: 2
Query Match: 98.23% Indels: 3
DB: 11 Gaps: 1

US-10-006-265-17 (1-662) x ADL26673 (1-2402)

OY 3 LeuSerProGluInProSerCyValAlaAsnLeuGlyMetMetTrpThrTriAlaLeuTrpMet 22
DB 138 CTCTCTCCCGACCTTCAATGTTTAACTGGGGAATGATGGACCTGGGCACTGGATG 197
OY 23 LeuProSerLeuCyAlaPheSerLeuAlaAlaLeuProAlaIleProGluAsnIleSer 42
DB 198 CTCCTCACTCTGCAAAATTGAGCTGGCAGCTGCCAGCTAAAGCTGAGAACATTTCC 257
OY 43 CyValAlaIleTrpTrpAlaGlyAsnLeuThrCyValTrpSerProGluValGluThrSer 62
DB 258 TGTGCTCTACTAATAGAAAATTTAACTGACCTTGGAGTCCGGAAGGAAACCACT 317
OY 63 TyrTrpGlnTyrThrValIleAspThrThrTyrAlaPheGlyGluValHisAspAsnCyThr 82
DB 318 TATACCCGATACACGTTAAGAACTTAACGCTTTGGAGAAAACATGATTAATGTACA 377
OY 83 ThrAsnSerSerThrSerGluAsnArgIleSerCySerPhePheLeuProArgIleThr 102
DB 378 ACCAATAGCTTCAACAAGTGAATGCTGCTCTCTTTTCTTCCCAAGATAACG 437
OY 103 IleProAspAsnTyrThrIleGluValAlaGluAsnGlyAspGlyValIleValSer 122
DB 438 ATCCAGATTAATTAATACATTAAGGTGAAGCTGAAATGAGAGGTGATTAATTAATCT 497
OY 123 HisMetThrTyrTrpArgLeuGluAsnIleAlaIleValThrGluProProIleValIlePheArg 142
DB 498 CATATGACATCTGAGATTAAGAAACATAGCGAAACCTGAACCACTTAAGATTTTCCGT 557
OY 143 ValIleProValIleGlyIleValArgMetIleGlnIleGluTrpIleValProGluLeu 162
DB 558 GTGAACCAAGTTTGGGATCAACGAATGATTAATTAATGAATGAATGAAGCTGAGTTG 617

OY 163 AlaProValSerSerAspLeuValSerTyrThrLeuArgPheArgThrValAsnSerThrSer 182
DB 618 GCGCTGTTTAACTGATTTAAATACACACTTGATTCAGACACATCAACATGACACG 677
OY 183 TrpMetGluValAsnPheAlaIleAsnArgIleValAspIleValAsnGlnThrTyrAsnLeuThr 202
DB 678 TGAATGAAAGTCAACTTGGTAAAGACCGTAAAGTAAACCAACGTAACCTCACTCAG 737
OY 203 GlyLeuGlnProPheThrGlnTyrValIleAlaLeuArgCyValAlaValGluSerIle 222
DB 738 GGGCTGCGCTTTTAACTGAATATGATCACTGCGATTTGGGCTCAAGAGTCAAG 797
OY 223 PheTrpSerAspTrpSerGlnGluValMetTrpGluGluGluAlaProCyGly 242
DB 798 TTCTGAGTGACTGAGGCCAAGAAAATGGGAATGACTGAGAGAACTCCATGTGCG 857
OY 243 LeuGluLeuTrpArgValIleValProAlaGluAlaAspGlyArgArgProValArgLeu 262
DB 858 CTGGAAGTGTGAGAGTCTGAAACCAAGCTGAGCGGATGAGAAAGCCAGTGGGTTG 917
OY 263 LeuTrpValValAlaArgGlyValProValLeuGluValThrLeuGlyTyrAsnIleTrp 282
DB 918 TTATGGAAGAAAGGCAAGAGGAGCCCACTCTAGAGAAACACTTGCTACAAATATGG 977
OY 283 TyrTrpProGluSerAsnThrAsnLeuThrGluThrMetAsnThrTrpAsnGlnLeu 302
DB 978 TACTATCCAGAAACCAACACTTAACCTCAACAAACATTAACACTTAACCAAGCTT 1037
OY 303 GluLeuHisLeuGlyGlyGluSerPheTrpValSerMetIleSerTyrAsnSerLeuGly 322
DB 1038 GAAGTCACTGAGAGGAGGAGGAGCTTTGGGTGCTATGATTTCTTATTAATCTCTGGG 1097
OY 323 LysSerProValAlaThrLeuArgIleProAlaIleGlnGluValSerPheGlnCysIle 342
DB 1098 AAGTCTCAGAGGCGCACCTGAGGATTCAGCTATTCAAGAAAATCAATTCAGTGCAT 1157
OY 343 GluValMetGlnAlaCyValAlaGluAspGlnLeuValValIleValTrpGlnSerSerAla 362
DB 1158 GAGGTCATGAGGCTGGTGTGTGAGAGACCAAGTGAAGTGAAGTGAAGTCTGTGCT 1217
OY 363 LeuAspValAsnThrTrpMetIleGluTrpPheProAspValAspSerGluProThrThr 382
DB 1218 CTAGACGTGAACACTTGATGATTAATGATGTTCCGATGTGACTCAGAGCCACCAACC 1277
OY 383 LeuSerTrpGluSerValSerGlnAlaIleThrAsnTrpThrIleGlnIleAspIleVal 402
DB 1278 CTTTCTGAGGAATCTGATGTCAGGCCAGAACTGACGATCCAGAAATTAATTAATA 1337
OY 403 ProPheTrpCyThrAsnIleSerValTyrProMetLeuHisAspIleValGluPro 422
DB 1338 CTTTCTGAGTCTATTAATCTGTGTATCCAAATGTGATGCAAAAGTTGGGAGCCA 1397
OY 423 TyrSerIleGlnAlaTyrAlaIleValGluGlyValProSerGluGlyProGluThrVal 442
DB 1398 TATTCATCCAGAGCTTATGCAAAAGAGGCTTCATCAAGAGCTCTGAGACCAAGTG 1457
OY 443 GluAsnIleGlyValIleValThrValThrIleThrTrpIleGluIleProValSerGluArg 462
DB 1458 GAGAACATTTGGCGTGAAGAGGTGATGATGAGAAAGATTCCTCAAGAGTGAAGA 1517
OY 463 LysGlyIleIleCysAsnTyrThrIlePheTyrGlnAlaGluGlyValGlyValPheSer 482
DB 1518 AAGGTATCACTGCAACTACACCATTTTAACTGAACCTGAAGGTGAAGAGATTCCTC 1577
OY 483 LysThrValAsnSerSerIleLeuGlnTyrGlyLeuGluSerLeuValArgValThrSer 502
DB 1578 AAGACATCAATTCACATCTTGCACTAGCGCTGAGAGTCCCTGAACCAAGACCTCT 1637
OY 503 TyrIleValGlnValMetAlaSerThrSerAlaGlyGlyThrAsnGlyThrSerIleAsn 522
DB 1638 TACATTTGTCAGGTCAATGAGCAGACCAAGTGGGGAACCAACGAGCAAGCATTAAT 1697
OY 523 PheIleThrLeuSerPheSerValPheGluIleIleLeuIleThrSerLeuIleGlyGly 542

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Db      | 1698 TTCAGACATTCATTCAGTCCTTGACATTATCTGATTAACCTTGATGGTGGGA 1757
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Qy      | 543 G|YleuLeu|leu|leu|leu|leu|Th|Val|Ala|Tyr|G|Yleu|Ys|Ys|Pro|Asn|Ys|Leu 562
        | 1758 GGCCTTCCTTATTCATTCATTCATTCGACAGTGGCATGTGTCTCAAAAACCAAAATTTG 1817
        | |||
Qy      | 563 Th|H|s|leu|Cy|s|T|P|P|O|T|H|Val|Pro|Asn|Pro|Ala|G|U|s|e|S|e|r|I|e|A|T|H|T|P|H|s 582
        | 1818 ACTCATCTGTGTGGCCCAACCGTTCCCAACCTGCTGAAGCTGTATAGCCACATGGCAT 1877
        | |||
Qy      | 583 G|Y|Asp|Asp|Phe|Ys|Asp|Ys|Leu|Asn|Leu|Ys|G|U|s|e|S|e|r|Asp|Asp|S|e|r|Val|Asn|T|H|Y|U 602
        | 1878 GGAGATGATTTCAAGAGATTAAGCTTAACCTGAGAGAGCTGATGACTCTGTGAACACAGAA 1937
        | |||
Qy      | 603 Asp|Arg|I|e|u|Ys|Pro|Cy|S|e|S|e|T|H|Pro|S|e|r|Asp|Ys|Leu|Val|I|e|Asp|Ys|Leu|Val 622
        | 1938 GACAGGATCTTAAACCATTCATTCACCCCGACGACAAAGTTGATTCACAAAGTTGGTG 1997
        | |||
Qy      | 623 Val|Asn|Phe|G|Y|Asn|Val|Leu|G|I|N|G|I|N|L|e|P|H|e|Th|Asp|G|U|A|A|A|T|G|T|H|Y|G|I|N|G|U 642
        | 1998 GTGAACTTGGGATGTTCTGCAGAAATTTTCAAGATTAAGCCAGAACGGGTCAAGAA 2057
        | |||
Qy      | 643 Asn|Asn|Leu|G|Y|G|Y|G|U|Ys|Asn|G|Y|Th|Arg|I|e|u|S|e|S|e|T|Cy|S|P|ro 659
        | 2058 AACAAATTAGAGAGGAGAAAGAAATGGG-----TATGTGACCTGTGCCCC 2099
        | |||

```

RESULT 11

AAD38772 standard; cDNA; 2480 BP.

AAD38772;

23-SEP-2002 (first entry)

Human haematopoietin receptor 1 (HPRI) cDNA.

Human haematopoietin receptor; receptor; HPRI; HPR2; cell proliferation;
 myelodysplastic syndrome; leukemia; carcinoma; hematologic disorder;
 cancer; myeloid cell vasocclusive crisis; myelofibrosis; myeloid metaplasia;
 osteoclast disorder; peridontitis; acute polynuropathy; Bell's palsy;
 anorexia nervosa; chronic fatigue syndrome; Creutzfeldt-Jacob disease;
 demyelinating neuropathy; Guillain-Barre syndrome; Gulf war syndrome;
 vertebral disc disease; myasthenia gravis; chronic neuronal degeneration;
 stroke; fatigue; tumor; sarcoma; osteoporosis; obesity; infertility;
 ischaemic disease; gene; ss.

Homo sapiens.

Location/Qualifiers

/product= "Human HPRI protein"

/transl_except= (pos:1680..1682, aa:Asn)

/note= "This region is specifically claimed as SEQ ID NO: 5 in claim 6 of the specification"

sig_peptide

mat_peptide

variation

variation

variation

variation

variation

variation

variation

variation

FT variation replace(1660, G)
 FT /*tag= i
 FT variation replace(1680, G)
 FT /*tag= j
 FT variation replace(2166, G)
 FT /*tag= k

MO200229060-A2.

11-APR-2002.

05-OCT-2001; 2001WO-US031634.

06-OCT-2000; 2000US-0238706P.

13-OCT-2000; 2000US-0240476P.

20-FEB-2001; 2001US-0270282P.

(IMMV) IMMUNEX CORP.

Cosman DJ, Mosley BA, Bird TA, Dubose RF, Wiley SR,
 WPI, 2002-330172/36.

P-PSDB; AAE24024.

Human and murine hematopoietin receptor polypeptides HPRI and HPR2,
 useful for treating cell proliferation, metabolic, and reproductive
 hormone related conditions.

Claim 6; Page 83-84; 136pp; English.

The present invention relates to human and murine haematopoietin receptor
 polypeptides HPRI and HPR2. Sequences of the invention are useful for
 treating cell proliferation conditions e.g., pancytopenia, leukopenia,
 anaemia, thrombocytopaenia, neurodegenerative disorders and osteoporosis
 resulting from a lack of bone-forming cells. They are also useful for
 treating cell proliferation conditions such as leukaemia and tumour
 metastasis, osteoporosis resulting from an excess of bone-resorbing
 cells. HPR sequences are also useful for treating medical conditions and
 diseases such as cell proliferation, metabolic and reproductive hormone
 related conditions. They are useful for treating various haematologic and
 oncologic disorders e.g., Epstein-Barr virus-positive nasopharyngeal
 carcinoma, myelogenous leukaemia, colon, stomach, prostate, renal cell,
 cervical and ovarian cancers, lung cancer (SCLC and NSCLC), including
 cancer-associated cachexia, fatigue, solid tumours (e.g., osteosarcoma,
 sarcoma), carcinoma (e.g., adenocarcinoma (for example, breast cancer),
 squamous cell carcinoma), hematologic disorders, anaemias (e.g., anaemia
 of chronic disease, aplastic anaemia, Fanconi's aplastic anaemia), myelo-
 dysplastic syndromes (including refractory anaemia, refractory anaemia
 with ringed sideroblasts or with excess blasts), idiopathic thrombocyto-
 penic purpura (ITP), sickle cell vasocclusive crisis, myelofibrosis/
 myeloid metaplasia, osteoclast disorders that lead to bone loss such as
 osteoporosis including post-menopausal osteoporosis, peridontitis
 resulting in tooth loosening or loss, prosthesis loosening after joint
 replacement, neurodegenerative conditions (e.g., acute polynuropathy,
 Bell's palsy, anorexia nervosa, chronic fatigue syndrome, transmissible
 dementia including Creutzfeldt-Jacob disease, demyelinating neuropathy,
 Guillain-Barre syndrome, vertebral disc disease, stroke including
 myasthenia gravis, chronic neuronal degeneration, Gulf war syndrome,
 cerebral ischaemic diseases. HPRI and HPR2 polypeptides are also useful
 for treating various other disorders such as osteoporosis, obesity,
 deficient mammary development and infertility. The present sequence is
 human HPRI cDNA

SQ Sequence 2480 BP; 722 A; 558 C; 600 G; 600 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.: 2.91e-314 Length: 2480

Score: 3465.50 Matches: 651

Percent Similarity: 99.09% Conservativity: 2

Best Local Similarity: 98.79% Mismatches: 3

Query Match: 98.23% Indels: 3

DB: 6 Gaps: 1

US-10-006-265-17 (1-662) x AAD38772 (1-2480)

QY 1 MetIylleuSerProGlnProSerCyValAsnLeuGlyMetMetTrpThrTrpAlaIleu 20
 Db 132 ATGAAGCTCTCCCTCCAGCTTCATGTGTAACTGGGGATGATGTGGCCCTGGACCTG 191
 QY 21 TrpMetLeuProSerLeuCyAllyPheSerLeuAlaIleuProAlaLysProGluAsn 40
 Db 192 TGGATGCTCCCTTCCTGCAATTCACCTGGACGCTTCGCAAGCTTAAGCTTAAGAAC 251
 QY 41 IleserCyValTyrTyrTyrAlaGlyAsnLeuThrCySerThrTrpSerProGlyLysGlu 60
 Db 252 ATTCTCTGTGTCTACTACTATAGAAAATTAACTGCATCTGAGCTTGAAGTCCAGAAAGGA 311
 QY 61 ThrSerTyrThrGlnTyrThrValLysArgTyrTyrAlaPheGlyGlyLysHisAspAsn 80
 Db 312 ACCAGTTATACCCAGATTAACAAGTAAAGAACTTTCGCTTTGGAGAAAACATATATAT 371
 QY 81 CysThrThrAsnSerSerThrSerGluAsnArgAlaSerCySerPhePheLeuProArg 100
 Db 372 TGTACACCAATAGTCTTACAAAGTAAATCGTCTGTGCTCTTTTCTTCTTCAAGA 431
 QY 101 ILeThrIleProAspAsnTyrThrIleGluValGluAlaGluAsnGlyAspGlyValIle 120
 Db 432 ATTAAGATCCCAAGATTAATTAACATTTGAGGTGGAAGCTGAAATGGAGATGTCTAATT 491
 QY 121 LysSerHisMetThrTyrTyrArgLeuGluAsnIleAlaLysThrGluProProLysIle 140
 Db 492 AAATCTCATATGACACTACTGAGATTAGAAACATAGCGAAACCTGAACCACTAAGATT 551
 QY 141 PheArgValLysProValLeuGlyIleLysArgMetIleGlnIleGluTrpIleLysPro 160
 Db 552 TTCCTGTGAACCAAGTTTGGGCTCAAAACCAATGATTCATTAATGGAATTAAGCTT 611
 QY 161 GluLeuAlaProValSerSerAspLeuLysTyrThrLeuArgPheArgThrValAsnSer 180
 Db 612 GAGTTGGGGCGCTTTCATCTGATTTAAATAACAACCTTCATTCAGGACGTCAACAGT 671
 QY 181 ThrSerTrpMetGluValAsnPheAlaLysAsnArgLysAspLysAsnGlnThrTyrAsn 200
 Db 672 ACCAGCTGAGTGAAGTCAACTTCGCTAAGAAACCTTAAGATTAACCAACCAACGTAAC 731
 QY 201 LeuThrGlyLeuGlnProPheThrGluTyrValIleAlaLeuArgCysAlaValLysGlu 220
 Db 732 CTCACGGGGCTGCACCTTTTACAAATATGTCATAGCTTCGCGATGGCGGTCAAGAG 791
 QY 221 SerLysPheTrpSerAspTrpSerGlnGluLysMetGlyMetThrGluGluAlaPro 240
 Db 792 TCANAAGTCTGAGAGTGAAGTGAAGCCAAAGAAAATGGGAATGACTGAGAGAAAGCTCA 851
 QY 241 CysGlyLeuGluLeuTrpArgValLeuLysProAlaGluAlaAspGlyArgArgProVal 260
 Db 852 TGTGGCTCGGAACCTGTGAGAGTCTTGAACCAAGCTGAGCGAGGAGAAAGGCGACGTG 911
 QY 261 ArgLeuLeuTrpLysValAlaArgLysAlaProValLeuGluLysThrLeuGlyTyrAsn 280
 Db 912 CGGTGTATAGAAAGCAAGAGAGAGCCCAAGTCCTAAGAAAAACCTTGGCTACAC 971
 QY 281 IleTrpTyrTyrProGluSerAsnThrAsnLeuThrGluThrMetAspThrThrAsnGln 300
 Db 972 ATATGTACTATCCAGAAAGCAACTTAACCTCAAGAAACATGAACTACTACACAG 1031
 QY 301 GlnLeuGluLeuHisLeuGlyGlyLysSerPheTrpValSerMetIleSerTyrAsnSer 320
 Db 1032 CAGCTTGAACCTGACTGTGGAGGCGAGAGCTTTTGGGTGTATATTTCTTATATCT 1091
 QY 321 LeuGlyLysSerProValAlaThrLeuArgIleProAlaIleGlnGluLysSerPheGln 340
 Db 1092 CTGGGAAGTCTCCAGTGGCCACCTGAGAGATTCAGCTATTCAGAAATAATCATTTAG 1151
 QY 341 CysIleGluValMetGlnAlaCysValAlaGluAspGlnLeuValValLysTrpGlnSer 360
 Db 1152 TGCATTGAGGTCAATGCAAGCGCTTGTCTGAGGACCAAGCTAGTGTGTAAGTGGCAAGC 1211

QY 361 SerAlaLeuAspValAsnThrTrpMetIleGluTrpPheProAspValAspSerGluPro 380
 Db 1212 CTGTCTTAGACGTGAACATTTGATGATTAATGTTTCCGAGTGGACTCAGAGCC 1271
 QY 381 ThrThrLeuSerTrpGluSerValSerGlnAlaThrAsnTrpThrIleGlnGluAspLys 400
 Db 1272 ACCAACCTTCTCTGGAACTGTGTCTCAGGCCCAAGACTGGACATCCACAGATTA 1331
 QY 401 LeuLysProPheTrpCySerTyrAsnIleSerValTyrProMetLeuHisAspLysValGly 420
 Db 1332 TTTAAACCTTCTGTGTCTATAATCATCTGTGATACCAATGTTGATGACAAAGTTGGC 1391
 QY 421 GluProTyrSerIleGlnAlaTyrAlaLysGluLysValProSerGluGlyProGluThr 440
 Db 1392 GAGCCATTTCTATCCAGGCTTATAGCCAAAGAGCGCTTCATCAAGAGGTCTGAGACC 1451
 QY 441 LysValGluAsnIleGlyValLysThrValThrIleThrTrpLysGluIleProLysSer 460
 Db 1452 AAGGTGAGAACATTTGGCGTGAAGACGGTCAAGTCAATCATGAAAGAGATTTCCAGAGT 1511
 QY 461 GluArgLysGlyIleIleCysAsnTyrThrIlePheTyrGlnAlaGluGlyLysGly 480
 Db 1512 GAGAGAAAGGTATCATCTGCACATCAACCATCTTTTACCAAGCTGAAGGTGAAAAAGA 1571
 QY 481 PheSerLysThrValAsnSerSerIleLeuGlnTyrGlyLeuGluSerLeuLysArgLys 500
 Db 1572 TTCCTCAAGACAGTCATTTCCAGATCTTGAAGTGGCGCTGAGTCCCTGAAGGAAAG 1631
 QY 501 ThrSerTyrIleValGlnValMetAlaSerThrSerAlaGlyLysThrAsnGlyThrSer 520
 Db 1632 ACCCTTACATTTGTCAGTATATGCGCACGACCGCTGGGGGAACCGAGCGAAC 1691
 QY 521 IleAsnPheLysThrLeuSerPheSerValPheGluIleIleLeuIleThrSerLeuIle 540
 Db 1692 ATTAATTTCAAGACATTTGTCATTCAGTGTCTTTAGATTAATCTCATATCTTCTGATT 1751
 QY 541 GlyGlyGlyLeuLeuIleIleIleLeuThrValAlaTyrGlyLysLysLysProAsn 560
 Db 1752 GGTGAGGCTTCTTATTTCTTATTAATCTGCACTGGCATATGTGTTCAAAAAACCCAAC 1811
 QY 561 LysLeuThrHisLeuCySerTrpProThrValProAsnProAlaGluSerSerIleAlaThr 580
 Db 1812 AAATTAATCTATCTGTGTGGCCCAACCGTTCCCAACCTGCTGAAGATGATGACCACA 1871
 QY 581 TrpHisGlyAspAspPheLysAspLysLeuAsnLeuLysGluSerAspAspSerValAsn 600
 Db 1872 TGGCATGGAATGATTTCAAGATTAAGTAACTGAAGAGTGTGATGACTGTGTGAAC 1931
 QY 601 ThrGluAspArgIleLeuLysProCySerThrProSerAspLysLeuValIleAspLys 620
 Db 1932 ACAGAAAGACAGATCTTAAACCATGTTCCACCCCGAGTGCACAAAGTTGGTATGACAMG 1991
 QY 621 LeuValValAsnPheGlyAsnValLeuGlnIlePheThrAspGluAlaArgThrGly 640
 Db 1992 TTGGTGTGAATTTGGGAATGTTTCTGCAGAAATTTTTCACAGATGAAACCAAGCGGT 2051
 QY 641 GlnGluAsnAsnLeuGlyGlyLysAsnGlyThrArgIleLeuSerSerCyPro 659
 Db 2052 CAGAAAACATTTAGAGGGGGAAGAAATGG-----TATGTGACTGTGCCC 2099

RESULT 12
 ACF36434
 ID ACF36434 standard; cDNA; 2481 BP.
 AC ACF36434;
 XX 18-DEC-2003 (first entry)
 DT Human type-1 cytokine receptor, GLM-R encoding cDNA.
 DE Human type-1 cytokine receptor; gene therapy; gene mapping; human;
 XX GLM-R; type-1 cytokine receptor; gene therapy; gene mapping; human;
 KW transgenic; gene; ss.


```
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XX
FH Key Location/Qualifiers
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FT /note= "type-1 cytokine receptor"
FT sig_peptide 63..119
FT /*tag= b
FT mat_peptide 120..2258
FT /*tag= c
FT
XX MO2003072740-A2.
XX
XX 04-SEP-2003.
XX
XX 24-FEB-2003; 2003WO-US005616.
XX
XX 25-FEB-2002; 2002US-0359806P.
XX
XX (GETH ) GENENTECH INC.
XX
XX De Sauvage FJ, Ghilardi NP, Goddard A, Godowski PJ, Grimaldi CJ,
XX Gurney AL, Wood WI;
XX
XX WPI; 2003-712721/67.
XX
XX P-PSDB; ABR82790.
XX
XX New isolated nucleic acid molecule encoding a GLM-R polypeptide, useful
XX for treating disorders characterized by the over or under abundance of
XX monocytes or macrophages.
XX
XX Claim 3; Fig 1; 156pp; English.
XX
XX The invention relates to an isolated nucleic acid molecule encoding a
XX type-1 cytokine receptor GLM-R polypeptide. The nucleic acid molecules,
XX polypeptides, antibodies, agonists or antagonist, and compositions are
XX useful for treating disorders characterized by the over or under
XX abundance of monocytes or macrophages. The nucleic acid molecules are
XX useful as hybridization probes, in chromosome and in gene mapping, and in
XX generating antisense RNA or DNA. The present sequence represents a cDNA
XX encoding a human GLM-R polypeptide
XX
XX
XX Sequence 2481 BP; 729 A; 553 C; 603 G; 596 T; 0 U; 0 Other;
XX
XX
XX Alignment Scores:
XX Pred. No.: 2,91e-314 Length: 2481
XX Score: 3465.50 Matches: 651
XX Percent Similarity: 99.24% Conservative: 1
XX Best Local Similarity: 99.09% Mismatches: 2
XX Query Match: 98.23% Indels: 3
XX DB: 10 Gaps: 1
XX
XX
XX US-10-006-265-17 (1-662) x ACF36434 (1-2481)
XX
XX 3 LeuSerProGlnProSerCysValAsnLeuGlyMetLeuTrpThrTPAlaLeuTrpMet 22
XX |||
XX 30 CTCTCTCCAGAGCTTCATGTGTTAACTGGAGATGATGAGACTGGGCACTGTGATG 89
XX |||
XX 23 LeuProSerLeuCysAluysPheSerLeuAlaLeuProAlaLysProGluAsnIleSer 42
XX |||
XX 90 CTCCTTCACCTCTGCAAAATTCAAGCTGCGAGCTCTGCACTAAGCTTGAGAAATTTC 149
XX |||
XX 43 CysValIleTyrrTyrrAlaGlyAsnLeuThrCysThrTrpSerProGlyIleGluThrSer 62
XX |||
XX 150 TGGTGCTACTACTAATAGAAAATTTTAACTGCACCTTGAGTCAGGAAAGGAAACCACT 209
XX |||
XX 63 TyrThrGlnIleThrValIleAspArgThrTyrAlaPheGlyGlyIleLysHisAspAsnCysThr 82
XX |||
XX 210 TATATCCAGTACACAGTTTAAAGAACTTACGCTTTTGGAGAAAACATGATTAATGTACA 269
XX |||
XX 83 ThrAsnSerSerThrSerGluAsnArgAlaSerCysSerPhePheLeuProArgIleThr 102
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DB ATCCAGCAATTAATTAATCAATTAAGGTGAGAGCTGAAATGAGATGTATTAATCT 389
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QY HisMetThrTyrrTrpArgLeuGluAsnIleAlaLysThrGluProProLysIlePheArg 142
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DB CATATGACATACTGAGATTAAGAAACATGAGAAACCTGAACCTTAAGATTTCCGT 449
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QY 143 ValLysProValIleuGlyIleLysArgMetIleGlnIleGluTrpIleLysProGluLeu 162
|||
DB GTGAAACCAAGTTTGGGCATCAAAACGAATGAATGAATGAATGAATGAATGAATGA 509
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QY 163 AlaProValSerSerAspLeuLysTyrrThrLeuAspPheArgThrValAsnSerTrpSer 182
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DB GGCCCTGTTTCATCTGATTTTAAATACACATTCGATTCAGACATCAACAGTACAC 569
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QY 183 TrpMetGluValAsnPheAlaLysAsnArgLysAspLysAsnGlnIleThrTyrrAsnLeuThr 202
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DB TGGATGGAAGTCAACTTCCTTAAGAACCTTAAGATTAAGAAACCAACCTTAACCTCA 629
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QY 263 LeuTrpLysLysAlaArgGlyAlaProValIleuGluLysThrLeuGlyTyrrAsnIleTrp 282
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DB 870 TACTATCCAGAAAGCAACCTAACTCACAGAAACATATACATTAACCAAGCAGCTT 929
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QY 303 GluLeuHisLeuGlyGlyLysSerPheTrpValSerMetIleSerTyrrAsnSerLeuGly 322
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QY 403 ProPheTrpCysTyrrAsnIleSerValTyrrProMetLeuHisAspLysValGlyGluPro 422
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DB 1230 CTTTCTGTGTGCTATTAACATCTGTGTATCCAAATGTGCAAGCAAAATTTGGCGAG 1289
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 Db 1410 AAGGGAGATCATCTGCACCTACCCATCTTTTACCAGCTGGAAGGAGGAGAAAGATTCC 1469
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 Db 1470 AAGACAGCAATTCAGACATCTTGCAATGAGGCTGGAGTCCCTGAAAGAAAGCTCT 1529
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 Qy 603 AsparGlyIleLeuLysProCysSerThrProSerAspLysLeuValIleAspLysLeuVal 622
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 Qy 623 ValAsnPheGlyAsnValLeuGlnIlePheThrAspGlyAlaArgThrGlyGlnGlu 642
 Db 1890 GTGAACCTTGGGAATGTTCTGCAGAAATTTTCACAGATGAAGCCAGAACGGGTGAGAA 1949
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 Db 1950 AACCAATTGAGGAGGAGAAAGATGG-----TATGTGACCTGCCCC 1991
 RESULT 13
 ID AB083365 standard; cDNA; 2952 BP.
 AC AB083365;
 DT 20-JAN-2003 (first entry)
 XX Human NR10.4 splicing variant encoding cDNA SEQ ID NO:5.
 DE NR10, splicing variant; haematopoietin receptor; immunomodulator;
 KW haematopoietic factor; immunologic disease;
 KW haematopoietic disease; haematopoietic cell regulation; gene; ss.
 OS Homo sapiens.
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 XX Key Location/Qualifiers
 XX FT CDS 7..2301
 XX FT /+tag= a
 XX FT /product= "NR10.4"
 XX MO30277230-A1.
 XX
 XX PD 03-OCT-2002.
 XX PF 22-MAR-2002; 2002MO-JP002769.
 XX PR 26-MAR-2001; 2001JP-00087298.
 XX PA (CHUS) CHUGAI SEIVAKU KK.
 XX

PI Maeda M, Yaguchi N, Hasegawa M;
 XX
 XX WPI; 2003-018925/01.
 DR P-PSDB; ABP54365.
 XX
 PT NR10 applying variants of hematopoietin receptor proteins and encoded
 PT genes, applicable in searching hematopoietic factors and developing
 PT remedies for immunological and hematopoietic diseases.
 XX
 PS Claim 1; Fig 7-9; 250pp; Japanese.
 CC The present invention describes haematopoietic receptor NR10 applying
 CC variants (II). (I) have immunomodulator and haematopoietic activities. The
 CC proteins and encoded genes are applicable in searching for novel
 CC haematopoietic factors, and developing remedies for immunological and
 CC haematopoietic diseases. The haematopoietin receptor genes participate in
 CC in vivo immunomodulation and haematopoietic cell regulation, and in the
 CC search for haematopoietic factors capable of functionally binding to the
 CC receptors. The present sequence encodes the human NR10.4 protein from the
 CC present invention
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 SQ Sequence 2952 BP; 821 A; 688 C; 727 G; 716 T; 0 U; 0 Other;
 Alignment Scores:
 Pred. No.: 3,74e-314 Length: 2952
 Score: 3465.50 Matches: 651
 Percent Similarity: 99.24% Conservative: 1
 Best Local Similarity: 99.09% Mismatches: 2
 Query Match: 98.23% Indels: 3
 DB: 8 Gaps: 1
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 Db 70 CTCTCTCCCAAGCCTTCATGTTAATCTGGGAGATGATGAGACTGGGACTGTGATG 129
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 Db 190 TGTGTCTACTACTATAGGAAAAATTTAACTGCACTTGAGAGTCCAGAAAGAAACCAAGT 249
 Qy 63 TyrThrGlnTyrThrValLysArgThrTyrAlaPheGlyGlyLysValAspAsnCysThr 82
 Db 250 TATACCCAGTACACAGTTTAAGAGAACTTACGCTTTGGAGAAAAACATGATTAATTGACA 309
 Qy 83 ThrAsnSerSerThrSerGluAsnArgAlaSerCysSerPhePheLeuProArgIleThr 102
 Db 310 ACCAATAGTTCTACACATGAAATCGGCTTCGCTCTTTTCCCTTCCAAAGATTAACG 369
 Qy 103 IleProAsnTyrTyrIleGluValGluAlaGluAsnGlyAspGlyValIleLysSer 122
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 QY 263 LeuTTPLysLysAlaArgGlyAlaProValLeuGluLysThrLeuGlyTyrAsnIleTTP 282
 DB 850 TTATGGAAGAGGCAAGAGAGGCCCACTGCTCTGAGAAAACTTGCTGCTCAACATATGG 909
 QY 283 TTTTTPProGlnSerAsnThrAsnLeuThrGluThrMetAsnThrThrAsnGlnGlnLeu 302
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 QY 403 ProPheTTPCysTyrAsnIleSerValTyrProMetLeuHisAspLysValGlyGluPro 422
 DB 1270 CTTTCTGGGTATTAACATCTGTGTATCCAAATGTGCATCAAAAGTGGCAGACCA 1329
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 QY 443 GluAsnIleGlyValLysThrValThrIleThrTTPLysGluIleProLysSerGluArg 462
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 DB 1870 GACAGATCTTAAACATGTTCCACCCCACTGACAGATTGTGATGACAAAGTTGGTG 1929
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 RESULT 14
 ABO83364
 ID ABO83364 standard; cDNA; 5271 BP.
 AC ABO83364;
 DT 20-JAN-2003 (first entry)
 XX
 DE Human NR10.4 splicing variant encoding cDNA SEQ ID NO:3.
 XX
 KW NR10.4 splicing variant; haematopoietic receptor; immunomodulator;
 KW haemostatic; haematopoietic factor; immunological disease;
 KW haematopoietic disease; haematopoietic cell regulation; gene; ss.
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT CDS 7..2301
 FT /*tag= a
 FT /product= "NR10.4"
 XX
 PN WO20027230-A1.
 XX
 PD 03-OCT-2002.
 XX
 PF 22-MAR-2002; 2002WO-JP002769.
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 PR 26-MAR-2001; 2001JP-00087298.
 XX
 PA (CHUS) CHUGAI SEIYAKU KK.
 XX
 PI Maeda M, Yaguchi N, Hasegawa M;
 XX
 DR WPI; 2003-018925/01.
 DR F-PDB; ABP54364.
 XX
 PT NR10 splicing variants of hematopoietic receptor proteins and encoded
 PT genes, applicable in searching hematopoietic factors and developing
 PT remedies for immunological and hematopoietic diseases.
 XX
 PS Claim 1; Fig 4-5; 250pp; Japanese.
 XX
 PS The present invention describes haematopoietic receptor NR10 splicing
 CC variants (I). (I) have immunomodulator and haemostatic activities. The
 CC proteins and encoded genes are applicable in searching for novel
 CC haematopoietic factors, and developing remedies for immunological and
 CC haematopoietic diseases. The haematopoietic receptor genes participate in
 CC in vivo immunomodulation and haematopoietic cell regulation, and in the
 CC search for haematopoietic factors capable of functionally binding to the
 CC receptors. The present sequence encodes the human NR10.4 protein from the
 CC present invention
 XX
 SQ Sequence 5271 BP; 1312 A; 1302 C; 1318 G; 1339 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.: 8 616-314 Length: 5271
 Score: 3465.50 Matches: 651
 Percent Similarity: 99.24% Conservative: 1
 Best Local Similarity: 99.09% Mismatches: 2
 Query Match: 98.23% Indels: 3
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US-10-006-265-17 (1-662) x ABQ83364 (1-5271)

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 Db CTCTCTCCCGAGCCTTCACTGTGTAACTGGGGATGATGTGACCTGGGCACTGTGGATG 129
 QY 23 LeuProSerLeuCysLeuPheSerLeuAlaAlaLeuProAlaLeuProGluAsn11Ser 42
 Db CTCCCTCACTCTGMAATTCAGCTGGAGCTCTGGCAGCTMACTGAGAACTATTC 189
 QY 43 CysValTyrTyrTyrArgLeuAsnLeuThrCysThrTrpSerProGluValGluThrSer 62
 Db TGTGTCTACTACTATAGGAAATTTAACTGCACTTGGAGTCCAGAAAGAAACCACT 249
 QY 63 TyrThrGlnTyrThrValLeuArgThrTyrAlaPheGlyGluLeuHisAspAsnCysThr 82
 Db TATACCAAGTACACAGTTAAGAACTTAACCTTTGGAGAAACATGATATTGTACA 309
 QY 83 ThrAsnSerSerThrSerGluAsnArgAlaSerCysSerPhePheLeuProArg11eThr 102
 Db ACCATATGTTCTACAAAGTGAATCGTCTGCTCTTTTTCCTTCCAAAGAAATAACG 369
 QY 103 IleProAspAsnTyrThr11eGluValGluAlaGluAsnGlyAspGlyVal11eYser 122
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 QY 203 GlyLeuGlnProPheThrGluTyrVal11eAlaLeuArgCysAlaVal11eGluSerLeu 222
 Db GGGGCGCAGCCTTTTACAGAAATATGTCACTGCGCATGCGGTCAGGAGCAAG 729
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 Db TTCGAGATGATGAGCCAAAGAAATAGGAAATGAGTACGAGAAAGAGCTTCACTGAC 789
 QY 243 LeuGluLeuTrpArgValLeuLeuProAlaGluAlaAspGlyArgArgProValArgLeu 262
 Db CTGGAACGTGGAGAGTCTCTGAACCACTGAGCGGATGAGAAAGGCGACGTGGCTTG 849
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 Db TATTCATCCAGGCTTATGCAAGAAAGGCTTCATCAGAAAGTCTGAGAACCAAGGTG 1389
 QY 443 GluAsn11eGlyValLeuThrValThr11eThrTrpLeuGlu11eProLeuSerGluArg 462
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 Db AAGGTATCATCTGCATCACTCAATCTTTTACCAAGTGAAGTGAAGAAAGATTTCTCC 1509
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RESULT 15
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 ID ABQ83366 standard; cDNA; 3072 BP.
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AC	ABQ83366;
XX	20-JAN-2003 (first entry)
DT	
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DE	Human NR10.5 splicing variant encoding cDNA SEQ ID NO:7.
XX	
KW	NR10; splicing variant; haematopoietic receptor; immunomodulator;
KM	haemostatic; haematopoietic factor; immunological disease;
KX	haematopoietic disease; haematopoietic cell regulation; gene; ss.
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OS	Homo sapiens.
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PN	WO200277230-A1.
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PD	03-OCT-2002.
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PF	22-MAR-2002; 2002MO-JP002769.
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PR	26-MAR-2001; 2001JP-00087298.
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PA	(CHUS) CHUGAI SEIYAKU KK.
XX	
PI	Maeda M, Yaguchi N, Hasegawa M;
XX	
DR	WPI: 2003-018925/01.
DR	P-PSTDB; ABP54366.
XX	
PT	NR10 splicing variants of haematopoietic receptor proteins and encoded
PT	genes, applicable in searching haematopoietic factors and developing
PT	remedies for immunological and haematopoietic diseases.
XX	
PS	Claim 1; Fig 10-12; 250pp; Japanese.
XX	
CC	The present invention describes haematopoietic receptor NR10 splicing
CC	variants (I). (I) have immunomodulator and haemostatic activities. The
CC	proteins and encoded genes are applicable in searching for novel
CC	haematopoietic factors, and developing remedies for immunological, and
CC	haematopoietic diseases. The haematopoietic receptor genes participate in
CC	in vivo immunomodulation and haematopoietic cell regulation, and in the
CC	search for haematopoietic factors capable of functionally binding to the
CC	receptor. The present sequence encodes the human NR10.5 protein from the
CC	present invention
XX	
SQ	Sequence 3072 BP; 849 A; 721 C; 755 G; 747 T; 0 U; 0 Other;
XX	
Alignment Scores:	
Pred. No.:	2,57e-311
Score:	3435.50
Percent Similarity:	93.54%
Best Local Similarity:	93.40%
Query Match:	97.38%
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Dt	CTCTCTCTCCAGCCTTCATGTGTAACTGGGGATGATGTGAACCTGGGCACCTGTGATG 129
OY	23 LeuProSerLeuGlySerPheSerLeuAlaAlaLeuProAlaLysPProGluAAsnIleSer 42
Dt	CTCCCTCCCATCTGGCAAAATTCAGCCCGAGCTGCCAGCTTAAGCCTGAGAACAATTCC 189
OY	43 CySeValTyTyrTyraRglYsaAsnLeuThrCySThrTPSerProGlyLYeGIuThSer 62
Dt	TGTGTCTACTACTATATGAAAATTTAACTTGACCTTGATGGATCCAGAAAGAAACCACT 249
OY	63 TyrThrGlnTythrValValysArGThrTyralaPhelGylJuLyShIsASPasnCySThr 82

Db	250	TATACCACTACACAGTTTAAGAACTTACGCTTTTGAGAAAAACATGATATTGACCA	309
Oy	83	ThraanserSerThrserGiuaasnargAlaSerCysSerPhePheLeuProArgIleThr	102
Db	310	ACCAATAGTTCTCAACAGTAAACCGTGCTCGTCTTTTTCCTTCCAGAAATACG	369
Oy	103	IleProAspAntyIrrThrIleGlValaGluaIagIuaenGIyaspGIyValIleIysSer	122
Db	370	ATCCCAATATATTATACCATTTAGTGGTGAAGCTGAATAATGAGATGGTATTAATTAATCT	429
Oy	123	HisMetThrYrTrTPAArgLeuGluasnIleAlaIalserThrguPProPolysilePheArg	142
Db	430	CATATGACATACCTGAGATTATAGACAATAGCGAAAACCTGAACCACTTAAGATTTCGT	489
Oy	143	ValIysProValleuGIyIleIysArgMetIleGlnIleGIutrpIleIysProGluLeu	162
Db	490	GTGAACCAAGTTTGGGCACTCAACAGATGATTCAAATTGATGATTAAGATTAAGCTGAAGTTG	549
Oy	163	AlaProValSerSerSerAspLeuIysYrTrThleuArgPheArgThrValaasnSerThrSer	182
Db	550	GCGCGTTCATCATGTGATTTAAATACACTTCGATTCAGGACAGTCAACAGTACCAAGC	609
Oy	183	TryMetGIuaIaasnPheAlaIysAsnArgIlyasAspIlysaenGIuThrYrAsnLeuThr	202
Db	610	TGATATGAAAGCAACTTCGCTTAAGAACCGTATGATTAATAACCAAGTACCAACTCAGC	669
Oy	203	GIyLeuGIuInProPheThrGIuYrValIleAlaLeuArgCysAlaValIysGIuSerIys	222
Db	670	GGCGTCGACGCTTTTACAGAAATATGATCATGAGCTCTCGATGTGGGTCAAGAGATCAAG	729
Oy	223	PheTrSerAspTrpSerGIuIlyMetGIyMetThrGIuGIuIuaIaProCyeGIy	242
Db	730	TTCTGAGATGCTGAGACCCAAAGAAATATGGAGATGACTGAGAGAAAGCTCCATGTGGC	789
Oy	243	LeuGIuLeuTrpArgValleuIysProAlaGIuaIaaspGIyaArgaArgProValArgLeu	262
Db	790	CTGGAACCTGTGGAAGTCTGAAAACCAAGCTGAGCGGATGGAAGAACGCCAGTGGGTG	849
Oy	263	LeuTrpIlysuIaIaArgGIyaIaProValleuGIuIysThrLeuGIyYrAsnIleTrp	282
Db	850	TTATGGAAGAAAGGCAAGAGAGACCCCAAGCTCTAGAGAAAACACTTGGCTACACATATGG	909
Oy	283	TyrTrTrProGIuSerAsnThrAsnLeuThrGIuThrMetCAsnThrThraenGIuLeu	302
Db	910	TACTATCCAGAAACAACAACCTAACCTACAGAAACAATGAAACTTAACACAGACACTT	969
Oy	303	GIuLeuHISleuGIyGIyGIuSerPheTrpValSerMetIleSerYrAsnSerLeuGIy	322
Db	970	GAACTGCATCGGAGGCGAGAGAGCTTTGGGTGTCATGATTTCTTAAATTCCTTGGG	1029
Oy	323	LysSerProValaIaTrnLeuArgIleProAlalleGIuGIuIysSerPheGlnCysIle	342
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Oy	363	LeuAspValaAsnThrTrpMetIleGIuTrpPheProAspValaAspSerGIuProThrThr	382
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Oy	383	LeuSerTrpGIuSerValaSerGlnaIaThraAsnTrpThrIleGIuGlnIaAspIlyLeuIys	402
Db	1210	CTTTCCTGGGAAATCTGTGTCTCAGGCAACGAACTGAGCATCCAGCAAGATTAATTAATA	1269
Oy	403	ProPheTrpCysYrAsnIleSerValYrProMetLeuHISAspIlyValaGIyGIuPro	422
Db	1270	CGTTTCTGGTGCATTAACATCTCTGTGTATCCATATGTGCATGACAAAGTTGGGAGCA	1329
Oy	423	TyrSerIleGlnaIaYrAlaIyGIuGIyValaProSerGIuGIyProGIuThrIlyVal	442

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QY 443 G|U|A|S|I|E|G|Y|V|A|L|Y|E|T|H|V|A|L|T|H|I|E|T|H|T|P|L|Y|G|I|L|E|P|O|L|Y|S|E|R|G|U|A|G 462
Db 1390 GAGAACATTTGGCGTGAAGACGGTCACGATCACATGAAAGAGATTCCCAAGAGTGAGAGA 1449
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Db 1570 TACATTTGTCAGTCTATGCGCACGACGATGCTGGGGGAAACCAAGGACCGCATTAAT 1629
QY 523 P|H|E|L|Y|S|T|H|L|E|U|S|E|R|P|H|E|G|I|U|I|E|I|L|E|U|I|E|T|H|S|E|R|L|E|I|G|I|Y|L|Y 542
Db 1630 TTCAAGACATTTGCTCATTCAGTGTCTTGAAGATTATCTCATTACTTCTGTGATGTGA 1689
QY 543 G|I|L|E|U|L|E|I|L|E|U|I|E|I|L|E|U|T|H|V|A|L|A|T|Y|G|I|L|E|U|Y|L|Y|S|P|R|O|A|N|L|Y|S|E|U 562
Db 1690 GGCCTTCTTATTTCTCATTCCTGACAGTGGCATATGCTCAAAAACCAACAATTG 1749
QY 563 T|H|R|I|E|L|E|U|C|Y|E|T|P|P|T|H|V|A|L|P|R|O|A|N|P|R|O|A|G|I|U|S|E|R|I|E|A|T|H|T|P|H|S 582
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QY 588 -----A|S|P|L|Y|S|L|E|U|A|N|L|E|U|Y|S|G|I|U|S|E|R|A|S|P|S|E|R|V|A|L|S|E|R|G|I|U 602
Db 1930 ACTTCTGATTTTCTGTGATTAACCTAAACCTGAAGAGTCTGATGACTGTGTGAACACAGAA 1989
QY 603 A|S|P|A|R|G|I|L|E|U|L|Y|S|P|R|O|C|Y|S|E|R|T|H|P|R|O|S|E|R|A|S|P|L|Y|S|L|E|U|V|A|I|L|E|A|S|P|L|Y|S|L|E|U|V|A|I 622
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Db 2050 GTGAACCTTTGGGAATGTTCTGCAAGAAATTTTTCACAGATGAAGCCAGAACGGGTGAGGAA 2109
QY 643 A|S|N|A|N|L|E|U|G|I|Y|G|I|L|Y|A|S|N|G|I|Y|T|H|A|R|G|I|L|E|U|S|E|R|C|Y|A|P|P|R|O 659
Db 2110 AACAAATTAGAGGGGAAAGAAATGGG-----TATGTGACCTGCCCC 2151

Search completed: February 23, 2005, 09:55:29
Job time : 1052.78 secs

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GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Run on: February 23, 2005, 08:59:57 ; Search time 304.791 Seconds
(without alignments)
3553.966 Million cell updates/sec

Title: US-10-006-265-17

Perfect score: 3528
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Ygapop 10.0, Ygapext 0.5
Fgapop 6.0, Fgapext 7.0
Delop 6.0, Delext 7.0

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

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-LOOPEXT=0-UNITS=bits-START=1-END=1-MATRIX=Blomsum62-TRANS=human40.cdi
-LIST=45-DOCALLIGN=200-THR SCORE=pct-THR MAX=100-THR MIN=0-ALIGN=15
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-FGAPEXT=7-YGAPOP=10-YGAPEXT=0.5-DELOP=6-DELEXT=7

Database :

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	691	19.6	2995	4	US-09-700-820C-17
2	685	19.4	3085	4	US-09-023-655-1131
3	683	19.4	2754	2	US-08-825-558-5
4	683	19.4	3174	3	US-09-312-611-5
5	683	19.4	3085	3	US-08-795-473B-4
6	683	19.4	3085	3	US-09-439-856-4
7	678.5	19.2	2369	1	US-07-797-556-1
8	678.5	19.2	2369	1	US-08-308-881-1
9	678.5	19.2	2369	2	US-09-058-263-1
10	678.5	19.2	2369	2	US-09-059-099-1
11	678.5	19.2	2369	3	US-09-058-264-1
12	678.5	19.2	2369	4	US-09-455-962-1

13	678.5	19.2	2369	5	PCT-US95-06530-1
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16	616	17.5	3477	4	US-09-313-942-25
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21	490	13.9	2563	6	5422248-1
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23	465.5	13.2	3293	1	US-07-923-976-1
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44	247	7.0	2589	1	US-08-653-740-6
45	247	7.0	2589	2	US-09-073-554-6

ALIGNMENTS

RESULT 1

US-09-700-820C-17
; Sequence 17, Application US/09700820C
; Patent No. 6610485
; GENERAL INFORMATION:
; APPLICANT: Tsuchiya, Masayuki
; APPLICANT: Saito, Makiyoshi
; APPLICANT: Ohmoto, Toshihiko
; TITLE OF INVENTION: NOVEL METHOD FOR GENE CLONING
; FILE REFERENCE: 06501-07001
; CURRENT APPLICATION NUMBER: US/09/700,820C
; CURRENT FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: PCT/JP99/02341
; PRIOR FILING DATE: 1999-04-30
; PRIOR APPLICATION NUMBER: JP 10/138652
; PRIOR FILING DATE: 1998-05-20
; PRIOR APPLICATION NUMBER: JP 10/279876
; PRIOR FILING DATE: 1998-10-01
; NUMBER OF SEQ ID NOS: 39
; SEQ ID NO 17
; LENGTH: 2995
; TYPE: DNA
; ORGANISM: Mus musculus
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (29) .. (2839)
; US-09-700-820C-17

Alignment Scores:

Pred. No.: 6.23e-66
Score: 691.00
Percent Similarity: 46.83%
Best Local Similarity: 28.28%
Query Match: 19.59%
Length: 2995
Matches: 183
Conservative: 120
Mismatch: 286
Indels: 58
Gaps: 18

US-10-006-265-17 (1-662) x US-09-700-820C-17 (1-2995)

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 QY 55 TrpSerProGlyLysGluThrSerTyr---ThrGluTyrThrValLysArgThrTyrAla 73
 Db 524 TGGGACCCCGAAGGAGACTTACCTTGAACAACAACTACCTTGAAATCAGAGTGCGCA 583
 QY 74 PheGluGluLysIleAspAsnGlyThrThrAsnSerSerThrSerGluAsnAlaSer 93
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 Db 626 TGTATGTGACGTACACAGCCCACTTATATGTC-----AACATTGAAGCTGGGCGAA 679
 QY 113 AlaGluAsnGlyAspGlyValIleLysSerHisMetThrTyrTrpArgLeuGluAsnIle 132
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 QY 133 AlaLysThrGluProProLysIlePheArgValLysProValLeuGlyIleLysArgMet 152
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 Db 800 TTAAACTATCATGGGTCACTTCAAGGCTGGCGGCTTT---TTAGATCTAAAGTCTGAC 856
 QY 173 LeuArgPheArgThrValAsnSerThrSerTrpMetGluValAsnPheAlaLysAsnArg 192
 Db 857 ATCCAAATATAGGACCAAAAGATGCTCAACTTGATCAGAGTCCCTCT---GAAGATACA 913
 QY 193 LysAspLysAsnGlnThrTyrAsnLeuThrGlyLeuGlnProPheThrGluTyrValIle 212
 Db 914 AAGTCTCTCGAACTTCTCACTGACGACGACCTCAAGCCTTTACAGAAATGTGTTT 973
 QY 213 AlaLeuArgCysAlaValLysGluSer-----LysPheTrpSerAspTrpSerGlnGlu 230
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 QY 310 SerPheTrpValSerMetIleSerTyrAsnSerLeuGlyLysSerProValAlaThrLeu 329
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 QY 450 ValThrIleThrTrpLysGluIleProLysSerGluArgLysGlyIleCysAsnTyr 469
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 Db 1745 TCCATATCTTACAGAAACGCGTGGAAAGAGATGTGTTCATGTGATGATCTTCTCAC 1804
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 QY 510 SerThrSerAlaGlyGlyThrAsnGlyThrSerIleAsnPheLysThrLeuSerPheSer 529
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 QY 530 ValPheGluIleIleLeuIleThrSerLeuIleGlyGlyLeuLeuIleLeuIleIle 549
 Db 1925 CAAGAGAAATGAGACCAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1984
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 Db 1985 CTGGGCGTCTGTGCTCTTAAACAGACGCAATTAATAAAACATCTGGCTTAAT 2044
 QY 570 ValProAsnProAlaGluSerSerIleAlaThrTrp-----His 582
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 QY 599 -----ValAsnThrGluAspArgIleLeuLysProCysSerThrProSerAspLysLeu 616
 Db 2156 ACGTTGTGGAATGAAAGCAAAACAAGAAAGCCCTGT-----CGAGTACCTGAAG 2209
 QY 617 ValIleAspLysLeuValValAsnPheGluAsnValLeuGlnGluIlePheThrAspGlu 636
 Db 2210 TCCGTGAC-----CTGTTCAAGAAAGAG 2233
 QY 637 -----AlaArgThrGlyGlnGluAsnLeuGlyGlyLysAsnGlyThrArgIle 654
 Db 2234 AAAGTGAATGACGAAGGCGACAGTGCATCGGGGC----- 2272
 QY 655 LeuSerSerCysProThrSer 661
 Db 2273 ---TCTCATGATGTCCTTC 2290

RESULT 2
 US-09-023-655-1131
 ; Sequence 1131, Application US/09023655
 ; Patent No. 6607879
 ; GENERAL INFORMATION:
 ; APPLICANT: Cocks, Benjamin G.
 ; APPLICANT: Susan G. Stuart
 ; APPLICANT: Jeffrey J. Seilhamer
 ; TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF BLOOD CELL GENE
 ; ;
 ; NUMBER OF SEQUENCES: 1508
 ; CORRESPONDENCE ADDRESS:


```

QY 522 AsnHelysThrLeuSerPheSerValPheIleuIleLeuIleIleThnSerLeuIleGly 541
Db 2074 ACTTTACTACCCCAAGTTGTCTCAAGAGAAATTGAAGCATATGTCGCTGTTGC 2133
QY 542 GlyIleuLeuIleuIleuIleIleuThrValAlaTyrIleuIleuIleuIleuIleu 561
Db 2134 TTACCATCTCATTTAGCAACAACCTCTGGAGATGCTGTTCTTAAATAACGAGACCTA 2193
QY 562 LeuIleuIleuIleuIleuIleuIleuIleuIleuIleuIleuIleuIleuIleuIleu 581
Db 2194 ATTTAAAAACACATCTGGCTTAATGTTCCAAATCCTTCAAAAGATCATATTGGCCCAAGGG 2253
QY 582 -----HIGLYAspAspPheIleuAspIleuAspIleuGlu 594
Db 2254 TCACCTCACACTCCTCCAAAGCAACAATTTAAATTCAAAAGATCAAAAGT-----TAT 2304
QY 595 SerAspAspSer-----ValAsnThrGluAspArgIleLeuIleuPro 608
Db 2305 TCACATGGCATTTTCACATGATGATGAAGTGTGTGGAAATAGAAAGCAAAATGACMAAAAGCCT 2364
QY 609 CysSerThrProSerAspIleuValIleAspIleuValValAsnPheGlyAsnVal 628
Db 2365 -----TTTCCAGAAGATCTGAATAATCATGTGAC----- 2391
QY 629 LeuGlnGluIlePheThrAspGluAla-----ArgThrGlyGlnGluAsnAsnLeuGly 646
Db 2392 -----CGTTCCAAAAGAAAGAAAATTAATATCTAGAGAGACACAGCATGCTATTGGG 2442
QY 647 GlyIleuIleuIleuIleuIleuIleuIleuIleuIleuIleuIleuIleuIleuIleu 661
Db 2443 GGG-----TCTTCATGATGATGATCT 2463

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RESULT 3
 US-08-825-558-5
 Sequence 5, Application US/08825558
 Patent No. 5965724
 GENERAL INFORMATION:
 APPLICANT: SHARKEY, ANDREW
 APPLICANT: SMITH, STEPHEN K.
 APPLICANT: DELLOW, KIMBERLEY A.
 TITLE OF INVENTION: Gp 130 Lacking the Transmembrane Domain
 NUMBER OF SEQUENCES: 14
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: STERNER, KESSLER, GOLDSTEIN & FOX
 STREET: 1100 NEW YORK AVENUE
 CITY: WASHINGTON
 STATE: DC
 COUNTRY: USA
 ZIP: 20005
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent In Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/825,558
 FILING DATE: 19-MAR-1997
 CLASSIFICATION: 536
 ATTORNEY/AGENT INFORMATION:
 NAME: ESMOND, ROBERT W.
 REGISTRATION NUMBER: 32,893
 REFERENCE/DOCKET NUMBER: 0623.0530001
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (202)371-2600
 TELEFAX: (202)371-2540
 INFORMATION FOR SEQ ID NO: 5:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 2754 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: both
 TOPOLOGY: linear
 MOLECULE TYPE: cDNA

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;      FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  1..2754
;
US-08-825-558-5

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Alignment Scores:	
Pred. No.:	4, 2e-65
Score:	683.00
Percent Similarity:	46.26%
Best Local Similarity:	28.55%
Query Match:	19.36%
DB:	2
Length:	275
Matches:	116
Conservative:	116
Mismatches:	280
Indels:	72
Gaps:	20

US-10-006-265-17 (1-662) X US-08-825-558-5 (1-2754)

[illegible][illegible]

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Db      1159 CTGACAGTAATCTCACAATATGATCTATAGCAACCTTAAGAAATCTGT 1218
Qy      322 GLVYSSERPROVALAlaThrLeuArgIleProAlaIleGlnGluYSerPheGlnCys 341
Db      1219 GGCAAATAGATGACAGCTGTTTAACTATCCCTGCTGTGACCTTCAAGCTACACCT 1278
Qy      342 ILeGluValMeGlnAlaCysValAlaGluPheGlnLeuValValLeuTrpGlnSer 361
Db      1279 GTAATGATCTTAAAGCATTCCTCCAAAGATTAACATGCTTTGGGTGAATGACTCTCA 1338
Qy      362 AlaLeuAPValAsnThrTrpMetIleGluTrpPheProAPValAspSerGluProThr 381
Db      1339 AGGGAATCTGTAAAGAAATATATCTAGTGTGTGTGTATGATGAAGAACCCGTGT 1398
Qy      382 ThrLeuSerTrpGluSerValSerGlnAlaThrAsnTrpThrIleGlnGlnAspLeu 401
Db      1399 ATCAGAGCTGCACAAAGAAAGATGTACCCGTGATCCCACTTAATTAAAGAGGAATTA 1458
Qy      402 LysProPheTrpCysValTrpAsnIleSerValTyProMetLeuHisAspLysValGlu 421
Db      1459 GCAGAGACCAATGCTATTGATTAACAGTACTCCAGTATATGCTGATGAGACAGAAAGC 1518
Qy      422 ProTrpSerIleGlnAlaTyraLalysGluGlyValProSerGluGlyProGluThrLys 441
Db      1519 CCTGATCTCATTAAGCATACCTTAACAGCTCCACCTTCCAAAGAGACTATCTGTGG 1578
Qy      442 ValGluAsnIleGlyValLysThrValThrIleThrTrpLysGluIleProLysSerGlu 461
Db      1579 ACAAAAAGTAAGGAAAGAAAGCAAGCTGCTTAAGTGGAGCAACTCTGTTGATGTT 1638
Qy      462 ArgLysGlyIleIleCysAsnTrpThrIlePheTyrglnAlaGluGlyLysGlyPhe 481
Db      1639 CAGATGATTTATGAAATATATATATATTTATTAAGACCATATGTAAGAAATGAAACT 1698
Qy      482 SerLysThrValAsnSerSerIleLeuGlnTyrglyLeuGluSerLeuLysArgLysThr 501
Db      1699 GCTGGAATGTGGATTTCTCCACACAGAAATATACATTTGCTCTTGAAGTACAGACA 1758
Qy      502 SerTyrlleValGlnValMetAlaSerThrSerAlaGlyGlyThrAsnGlyThrSerIle 521
Db      1759 TTGTACATGTGACGATGCGACATACACAGATGAAGTGGAGAGATGTCACGAATTC 1818
Qy      522 AsnPheLysThrLeuSerPheSerValPheGluIleIleLeuIleThrSerLeuIleGly 541
Db      1819 ACTTTTACTACCCCAAGATTGCTCAGAGAGAAATTAAGCCATATGCTGCTGTTGC 1878
Qy      542 GlyGlyLeuLeuIleLeuIleIleLeuThrValAlaTyrglyLeuLysProAsnLys 561
Db      1879 TTACGATTCCTATGACAACTCTTGGAGTGGCTGTTCTGCTTAATTAAGGAGACCTA 1938
Qy      562 LeuThrHisLeuCysTrpProThrValProAsnProAlaGluSerSerIleAlaThrTrp 581
Db      1939 ATTAATAAACACATCTGCTTAATGTTCCAGATCCTTCAAGAGATCATATGCTCCAGTGG 1998
Qy      582 -----HisGlyAspAspPheLysAspLysLeuAsnLeuLysGlu 594
Db      1999 TCACCTACACTCTCTCAAGGACAACTTTTAATTCAAAGATCAATG-----TAT 2049
Qy      595 SerAspAspSer-----ValAsnThrGluAspArgIleLeuLysPro 608
Db      2050 TCAGATGCAATTTACATGATGTAAGTGTGTGGAAATAGAAAGCAATGACAAAAGCTT 2109
Qy      609 CysSerThrProSerAspLysLeuValIleAspLysLeuValValAsnPheGlyAsnVal 628
Db      2110 -----TTTCCAGAGATCTGAATCATTTGAC----- 2136
Qy      629 LeuGlnGluIlePheThrAspGluAla-----ArgThrGlyGlnGluAsnAsnLeuGly 646
Db      2137 -----CTGTCAAAAAGAAAAAATTAATTAAGTGAAGGACACAGCATGTGTTGGG 2187
Qy      647 GlyGluLysAsnGlyThrArgIleLeuSerSerCysProThrSer 661
Db      2188 GGG-----TCTTCATGATCATGTCACT 2208

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RESULT 4
US-09-312-611-5
; Sequence 5, Application US/09312611
; Patent No. 6380160
; GENERAL INFORMATION:
; APPLICANT: SHARKEY, ANDREW
; APPLICANT: SMITH, STEPHEN K.
; APPLICANT: DELLOW, KIMBERLEY A.
; TITLE OF INVENTION: Gp130 Lacking the Transmembrane Domain
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: STERN, KESSLER, GOLDSTEIN & FOX
; STREET: 1100 NEW YORK AVENUE
; CITY: WASHINGTON
; STATE: DC
; COUNTRY: USA
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/312,611
; FILING DATE: 17-MAY-1999
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: ESMOND, ROBERT W.
; REGISTRATION NUMBER: 32,893
; REFERENCE/DOCKET NUMBER: 0623, 0530002
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)371-2600
; TELEFAX: (202)371-2540
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2754 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..2754
; US-09-312-611-5

Alignment Scores:
Pred. No.: 4,2e-65 Length: 2754
Score: 683.00 Matches: 187
Percent Similarity: 46.26% Conservative: 116
Best Local Similarity: 28.55% Mismatches: 280
Query Match: 19.36% Indels: 72
DB: 3 Gaps: 20

US-10-006-265-17 (1-662) x US-09-312-611-5 (1-2754)
Qy      35 ProAlaLysProGluAsnIleSerCysValTyTrpTyraGlyAsnLeuThrCysThr 54
Db      376 CCAGAAAAACCTAAATAATTTGATGATGTCAGACGAGGAGAAATAATGAGGTGAG 435
Qy      55 TrpSerProGlyLysGluThrSerTy-----ThrGlnTyThrValLys-----Arg 70
Db      436 TGGGATGTGTGAAGGAAACACACTTGGAGCAAACTTCACTTAATAATCTGAATGGCA 495
Qy      71 ThrTyraLapheGlyGlu-----LysHisAsp-----AsnCysThrThrAsn 84
Db      496 ACAACAAGTTTGTGATTTGCAAGCAAAACGTGACACCCCACTCATGCACTGTGAT 555
Qy      85 SerSerThrSerGluAsnArgAlaSerCysSerPhePheLeuProArgIleThrIlePro 104
Db      556 TATTTCTACT-----GTGTAATTTTGC----- 576
Qy      105 AspAsnTyThrIleGluValGluAlaGluAsnGlyAspGlyValIleLysSer---His 123

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Db 577 ---ACATTGAACTGGGTAGAGAGAGAAATGCCCTTGGGAAGGTACATCAGATCAT 633
Qy MetThrTyrTrpArgLeuGluAsnIleAlaIleValThrGluProPheGlySer 143
Db 634 ATCAATTTGATCTCTGATATTAAGTG--AAGCCCAATCGCCACATTAATTATCAGTG 690
Qy 144 LysProValLeuGlyIleLysArgMetIleGlnIleGluTrpIleLysProGluLeuAla 163
Db 691 ATCAACTCAGAGAACTGCTAGATCTTAAATTTGACATGACCAACCAAGATTAAG 750
Qy 164 ProValSerSerAspLeuLysTyrThrLeuArgPheArgThrValAsnSerThrTrp 183
Db 751 AGGTGTAATAATA---CTAAATATTAACATTCATTAATGAGACCAAGATGCTCAACTGG 807
Qy 184 MetGluValAsnPheAlaLysAsnArgLysAspLysAsnGlnThrTyrAsnLeuThrGly 203
Db 808 AGCCAGATTCT---CCTGAAGACACAGCATCCACCCGATCTTCATTCCTGTCACAGAC 864
Qy 204 LeuGlnProPheThrGluTyrValIleAlaLeuArgCysAlaValLysGluSerLys--- 222
Db 865 CTAAACCTTTTACAGATATGTTAGGATTGGCTGATGAGAGAGATGGTAAAGGGA 924
Qy 223 PheTrpSerAspTrpSerGlnGluLysMetGlyMetThrGluGluGluAlaProCys--- 241
Db 925 TACTGGAGTGACTGGAGTGAGAGAGCAAGTGGATCATCTATGAGATAGACCATCTTAA 984
Qy 242 GlyLeuGluLeuThrArgValLeuLysProAlaGluAlaAspGlyArgArgProValArg 261
Db 985 GCACCAAGTTCTGGTATTAATAATGATCCATCCATATCTCAAGGCTACACAACTGATCAA 1044
Qy 262 LeuLeuTrpLysLysAlaArgGlyAlaProValLeuGluLysThrLeuGlyTyrAsnIle 281
Db 1045 CTGCTGGAGAGACATGGCTCTCTTTGAAGCCAAATGAGAAATCTTGATTAAGAGTG 1104
Qy 282 TrpTyrTrpProGluSerAsnThrAsnLeuThrGluThrMetCysThrTrpAsnGln 301
Db 1105 ACTCTCAGACAGATGGAATCACAATTAACAAATTAACACGTTAATGCCACA-----AAA 1158
Qy 302 LeuGluLeuIleAsnGlyLysGluSerPheTrpValSerMetIleSerTyrAsnSerLeu 321
Db 1159 CTACAGTAAATCTCACAAATGATCGCTATCTAGACACCTTAACAGTAAAGAAATCTTGTT 1218
Qy 322 GlyLysSerProValAlaThrLeuArgIleProAlaIleGlnIleLysSerPheGlnCys 341
Db 1219 GGCAAATCAGATGACGCTGTTTAACTATCCCTGCGTGAAGCTTCAAGTACTCAACCCCT 1278
Qy 342 IleGluValMetGlnAlaCysValAlaGluAspGlnLeuValLysTrpGlnSerSer 361
Db 1279 GTATGAGATCTTAAAGCATTCCTCCCAAGATPAACATGCTTTGGGTGAGATGAGTACTCCA 1338
Qy 362 AlaLeuAspValAsnThrTrpMetIleGluTrpPheProAspValAspSerGluProThr 381
Db 1339 AGGGAATCTGTAAAGAAATATATATCTGAGTGTGTGTTCAGATTAAGACACCCCTGT 1398
Qy 382 ThrLeuSerTrpLysSerValSerGlnAlaThrAsnTrpThrIleGlnIleAspLysLeu 401
Db 1399 ATCAGAGACTGGCAACAGAAATGATGACGTCGATCGCATTAATTAAGAGAACTTA 1458
Qy 402 LysProPheTrpCysTyrAsnIleSerValTyrProMetLeuIleAspLysValGlyGlu 421
Db 1459 GCAGAGAGCAAAATGCTATTGATTAACAGTATCTCCAGTATATGCTGATGACCAAGAGC 1518
Qy 422 ProTyrSerIleGlnAlaTyrAlaLysGluGlyValProSerGluGlyProGluThrLys 441
Db 1519 CCGTAATCCATTAAGGATATCTTAACAGACTCCACCTTCCAAAGAGACTTACTGCTGG 1578
Qy 442 ValGluAsnIleGlyValLysThrValThrIleThrTrpLysGluIleProLysSerGlu 461
Db 1579 ACAAAAAAAGTAGAGAAAAAGCAAGCTGCTTGAAGTGGAGCAACACTCTCTGTGATGTT 1638
Qy 462 ArgLysGlyIleIleCysAsnTyrThrIlePheTyrGlnAlaGluGlyLysGlyPhe 481

Db 1639 CAGAAATGATTTATCAGAAATTAATCTATATTTTATAGAACATCATTCGAAATGAAC 1698
Qy 482 SerLysThrValAsnSerSerIleLeuGlnTyrGlyLeuGluSerLeuLysArgLysThr 501
Db 1699 GCTGTCAGATGTGATGATCTTCCACACAGAAATATATCTTCTCTTGAATAGTACACAA 1758
Qy 502 SerTyrIleValGlnValMetAlaSerThrSerAlaGlyGlyThrAsnGlyThrSerIle 521
Db 1759 TTGTACATGCTGACGATGACCATATACAGATGAAGGTGGAGAGATGCTCAGAAATTC 1818
Qy 522 AsnPheLysThrLeuSerSerValPheGluIleIleLeuIleThrSerLeuIleGly 541
Db 1819 ACTTTTACTTACCCCAAGTTCTCTCAAGAGAAATTAAGAACCATGCTGCTGTTTGC 1878
Qy 542 GlyGlyLeuLeuIleLeuIleIleLeuThrValAlaTyrGlyLeuLysLysProAsnLys 561
Db 1879 TTAGCATCTCTTATGACAACTCTTCGGAGAGTGCCTTCTGCTTAATTAAGGAGACCTA 1938
Qy 562 LeuThrIleLeuCysTrpProThrValProAsnProAlaGluSerSerIleAlaThrTrp 581
Db 1939 ATTAAAAAACATCATGCGCTAATGTTCCAGATCTTCAAGAGATCATGCTCCAGTGG 1998
Qy 582 -----HisGlyAspAspPheLysAspLysLeuAsnLeuLysGlu 594
Db 1999 TCACCTCAGACTCTCCAGAGCACATTTTAATTCAAAAGATCAAAATG-----TAT 2049
Qy 595 SerAspAspSer-----ValAsnThrGluAspArgIleLeuLysPro 608
Db 2050 TCAGATGCGCAATTCATCTATGATGATGATGTTGTGGAAATGAAAGCAATAGCAAAAAGCT 2109
Qy 609 CysSerThrProSerAspLysLeuValIleAspLysLeuValValAsnPheGlyAsnVal 628
Db 2110 -----TTTCCAGAAAGATCTGAATCATTTGAC----- 2136
Qy 629 LeuGlnGluIlePheThrAspGluAla-----ArgThrGlyGlnGluAsnLeuGly 646
Db 2137 -----CTGTCAAAAAGAGAAATTAATTAAGTGAAGGACACAGCATGTGATTTGGG 2187
Qy 647 GlyGluLysAsnGlyThrArgIleLeuSerSerCysProThrSer 661
Db 2188 GGG-----TCTTCATGATGATCATCT 2208

RESULT 5
US-08-795-473B-4
; Sequence 4, Application US/08795473B
; Patent No. 6217858
; GENERAL INFORMATION:
; APPLICANT: Galun, Elithan
; APPLICANT: Nahot, Orit
; TITLE OF INVENTION: A Pharmaceutical Composition for Treating
; TITLE OF INVENTION: Hepatitis B Virus (HBV) Infection
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Davidson, Davidson and Kappel, LLC
; STREET: 1140 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: MS-DOS EDITOR
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/795,473B
; FILING DATE: 11-FEB-1997
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Davidson, Clifford M.
; REGISTRATION NUMBER: 32,728
; REFERENCE/DOCKET NUMBER: 963.1007

Db 2392 -----CTGTTCAAAAAGAAAAAATTATATCTGAAGACACAGACGTGATTGGGGG 2445
Qy 648 GtLysAsnGlyThrArgIleLeuSerCysProThrSer 661
Db 2446 -----TCTCATGATGATCATCT 2463
RESULT 6
US-09-439-856-4
Sequence 4, Application US/09439856
Patent No. 641009
GENERAL INFORMATION:
APPLICANT: Galun, Etchan
APPLICANT: Nahot, Orit
APPLICANT: Blum, Herbert E.
TITLE OF INVENTION: A Pharmaceutical Composition for Treating
TITLE OF INVENTION: Hepatitis B Virus (HBV) Infection
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: Davidson, Davidson and Kappel, LLC
STREET: 1140 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: MS-DOS EDITOR
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/439,856
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/795,473
FILING DATE: 11-FEB-1997
ATTORNEY/AGENT INFORMATION:
NAME: Davidson, Clifford M.
REGISTRATION NUMBER: 32,728
REFERENCE/DOCKET NUMBER: 963.1007
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212)-997-1028
TELEFAX: (212)-997-1037
INFORMATION FOR SEQ. ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 3085 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: unknown
US-09-439-856-4
Alignment Scores:
Pred. No.: 5.08e-65 Length: 3085
Score: 683.00 Matches: 186
Percent Similarity: 46.48% Conservative: 118
Best Local Similarity: 28.44% Mismatches: 280
Query Match: 19.36% Indels: 70
Gaps: 21
US-10-006-265-17 (1-662) x US-09-439-856-4 (1-3085)
Qy 35 ProAlaLysProGluAsnIleSerCysValIleThrArgIleLeuSerCysThr 54
Db 631 CCGAAAAAACTTAATAATTTGAGTTGATGTGAACAGGAGGAGAAATGAGGTGAG 650
Qy 55 TrpSerProGlyLysGluThrSerTyr---ThrGlnTyrThrValys-----Arg 70
Db 691 TGGATGCTGGAAGGAAACACACTTGAGACAACCTTCACTTAAATCGAATGAGCA 750
Qy 71 ThrTyrAlaIleGlu-----LysHisAsp-----AsnCysThrThrAsn 84
Db 751 ACACACAAGTTTGCTGATTCGCAAAAGCAAAACGTGACACCCCACTCATGCTGTGAT 810

Qy 85 SerSerThrSerGluAsnArgIleSerCysSerPhePheLeuProArgIleThrIlePro 104
Db 811 TATTTACT-----GTGATTTTGTG----- 831
Qy 105 AspAsnTyrThrIleGluValGluValAsnGlyAspGlyValIleLysSer---His 123
Db 832 ---AACATTGAAGTCTGGGTGAGAGAGAAATGCTTGGAGAGGTTCATCAGATCAT 888
Qy 124 MetThrTyrThrArgLeuGluAsnIleAlaLysThrGluProLysIlePheArgVal 143
Db 889 ATCAATTTGATCCGTATATATAAGT---AGCCCAATCCGCACATATATTATCAGTG 945
Qy 144 LysProValLeuGlyIleLysArgMetIleGlnIleGluTyrIleLysProGluLeuAla 163
Db 946 ATCAACTGAGAGAACTGCTAGTATCTTAAATGACATGAGACCAACCAAGTATTAG 1005
Qy 164 ProValSerSerAspLeuLysTyrThrLeuArgPheArgThrValAsnSerThrTrp 183
Db 1006 AGTGTTATATA---CTAAATAATTAACATTCATATAGGACCAAGATCCCTCACTTG 1062
Qy 184 MetGluValAsnPheAlaLysAsnArgLysAspLysAsnGlnThrTyrAsnLeuThrGly 203
Db 1063 AGCCAGATTCT---CTGAAAGACAGCATCCACCCGATCTTCATCTGTCAGAC 1119
Qy 204 LeuGlnProPheThrGluTyrValIleAlaLeuArgCysAlaValLysGluSerLys--- 222
Db 1120 CTTAAACCTTTACAGAAATATGTGTTAGATTCGCTGATAGAGAAATGTAAGGA 1179
Qy 223 PheTrpSerAspTrpSerGlnGluLysMetGlyMetThrGluGluGluAlaProCys--- 241
Db 1180 TACTGAGTGAAGTCTGGAGTGAAGAGCAAGTGGATCACCTTAGAAGATGACCATCTAA 1239
Qy 242 GlyLeuGluLeuThrArgValLeuLysProAlaGluAlaAspGlyArgArgProValArg 261
Db 1240 GCACCAAGTTCTGGTATAATAATAGATCCATCCATCTCAAGGCTACAGACTGTACA 1299
Qy 262 LeuLeuTrpLysLysAlaArgGlyAlaProValLeuGluLysThrLeuGlyTyrAsnIle 281
Db 1300 CTGCTGTGAAGACATGCTGCTCCTTTGAGCAACCTGAAGAAATCTGATATAGAGTG 1359
Qy 282 TrpTyrTyrProGluSerAsnThrAsnLeuThrGluThrMetAsnThrThrAsnGln 301
Db 1360 ACTCTCAACAAGATGGAATCAGATTTACAAATTCACAGTTAATGCCCA-----AAA 1413
Qy 302 LeuGluLeuHisLeuGlyGlyGluSerPheTrpValSerMetIleSerTyrAsnSerLeu 321
Db 1414 CTGACAGTAAATCTCAAAATATGCTATCTAGCAACCTTAACGTAAGAAATCTTGT 1473
Qy 322 GlyLysSerProValAlaThrLeuArgIleProAlaIleGlnGluLysSerPheGlnCys 341
Db 1474 GGCAATTCAGATGCAAGCTGTTTAACTATCCCTGCTGATGATTCAGACTCAACCTC 1533
Qy 342 IleGluValMetGlnAlaCysValAlaGluAspGlnLeuValValLysTrpGlnSerSer 361
Db 1534 GTAATGACATCTTAAGATTTCCCAAGAGTAACATGCTTTGGGTGAAGGATCTCCA 1593
Qy 362 AlaLeuAspValAsnThrTrpMetIleGluTyrPheProAspValAspSerGluProThr 381
Db 1594 AGGGAATCTGTAAAGAAATATATCTGAGTGTGTGTCTTATCGATTAAGCACCTGT 1653
Qy 382 ThrLeuSerTrpGluSerValSerGlnAlaThrAsnTrpThrIleGlnGlnAspLysLeu 401
Db 1654 ATCAACGATCGCAACAAAGATGTTACCGGCATCGCACTCATTTAAGAGGAACCTTA 1713
Qy 402 LysProPheTrpCysTyrAsnIleSerValTyrProMetLeuHisAspLysValGlyGlu 421
Db 1714 GCAGAGCAAAATGCTATTGTAACAGTTACTCCAGTATATGCTGATGACACAGAGAAC 1773
Qy 422 ProTyrSerIleGlnAlaTyrAlaLysGluGlyValProSerGlnGlyProGluThrLys 441
Db 1774 CCGAATTCATTAAGGATATCTTAAACAGCTCCACCTTCCAAAGAGACTTACTGTTCG 1833

```

? ? ATTORNEY/AGENT INFORMATION:
? NAME: Seese, Kathryn A.
? REGISTRATION NUMBER: 32,172
? REFERENCE/DOCKET NUMBER: 2607
? TELECOMMUNICATION INFORMATION:
? TELEPHONE: 206-587-0430
? TELEFAX: 206-587-0606
? INFORMATION FOR SEQ ID NO: 1 :
? SEQUENCE CHARACTERISTICS:
? LENGTH: 2369 base pairs
? TYPE: NUCLEIC ACID
? STRANDEDNESS: single
? TOPOLOGY: linear
? MOLECULE TYPE: cDNA to mRNA
? HYPOTHEetical: NO
? ANTI-SENSE: NO
? FRAGMENT TYPE: N-terminal
? ORIGINAL SOURCE:
? TISSUE TYPE: human placenta
? IMMEDIATE SOURCE:
? CLONE: B10g/pdC303
? FEATURE:
? NAME/KEY: CDS
? LOCATION: 244..2369
? FEATURE:
? NAME/KEY: mac_peptide
? LOCATION: 310..2369
? FEATURE:
? NAME/KEY: sig_peptide
? LOCATION: 244...309
US-07-797-556-1

Alignment Scores:
Pred. No.:      1,03e-64          Length:       2369
Score:         678..50           Matches:     169
Percent Similarity:   48.44%    Conservative:  110
Best Local Similarity: 29.34%    Mismatches:  258
Query Match:        19.23%      Indels:       39
                               Gaps:         14

US-10-006-265-17 (1-662) x US-07-797-556-1 (1-2369)

QY      35 ProAlalysPProGluAenIlSeSerCySvalTyTtyTrArGlVsAbnLeurThrCysThr 54
||| |||| |::| ::::::::::::::::::::||| ||| ::| 
Db      619 CCAGAAAAAACCTTAATAATTGTGAATGGCATTTGTAAACGAGCGGAGAAMAATAGAGTGAG 678
QY      55 ThrSerProGlyLvsGIuThSetyr---ThrgInTyRtHValVse-----Arg 70
||||| ::::::::::::::::::::||| ::::::::::::::::::::
Db      679 TGGAATGGTGGMAAGGAAAACAACCCTGGAGCAAAACTTCATTAAATCTGAATGGSCA 738
QY      71 ThryralPaPeegIyglu-----LyshIsAsP-----AscYeThrThzAn 84
||| ::| ::| ::| ||| ||| ||| ||| ||| ||| ||| ||| ::| 
Db      739 ACAACACAAGTTGTCGTATGCAGAACCAAACGTGACACCCCACTCATGTCACTTGAT 798
QY      85 SerSerThrserGIuaAmrAglaSaSerCysSerPhpheleuProrAgIetHrlrePre 104
||||| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| 
Db      799 TATCTACT-----GTGFATTTTTGCC----- 819
QY      105 AspaentTyrrhlleglualGIUALagLUasnGLyaepGIvAlllelseser---His 123
||| ||| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| 
Db      820 ---AACAATTGAAAGCTGGTAGAAGCACAGAGATCCCCCTGGGAAGGTTACATCAGANTAT 876
QY      124 MetThryTYTParGLEugLuAMnlalaYSthrGIUProproLYslEPheArGal 143
::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| 
Db      877 ATCAATTTTGATCCTGTATATAAAGTC---AAGCCCAtccGCCAcATMATTTATCAcGTG 933
QY      144 LysBrovallauengLIelysarMetileglnllegturPIelElysProGUleuala 163
::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| 
Db      934 ATCAACTCAGAGCAAGCTGTAGATATCTTAAAATGTGACATGACCAACCAAGATTAAAG 993
QY      164 ProVALserSerApbleuluPyTYTHleuarGrHeArghTrVaLaensetrThsetirP 183
||| ||| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| 
Db      994 AGTGTVTATAATA--CTTAAAATATAACATTCATATATGTGACCAAGAAGATGCTCAACTTG 1050
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QY 184 MetGluValAsnPhenAlaLysAsnArgLysAspLysAsnGlnThrTrpAsnLeuThrGly 203
 Db 1051 AGCCAGATTCTCT---CCTGAAGACACAGCATCCACCAGATCTTCACTGTCACAGAC 1107
 QY 204 LeuGlnProPheThrGlnTrpValIleAlaLeuArgCysAlaValLysGlnSerLys--- 222
 Db 1108 CTTAAACCTTTTACAGAAATATGTGTATAGATTGCTGTATGAAGAAATGTGTAAGGGA 1167
 QY 223 PheTrpSerAspTrpSerGlnGlnLysMetGlyMetThrGlnGlnGlnAlaProCys--- 241
 Db 1168 TACTGAGTGACTGAGTGAAGCAAGGTGATCACTATGAAGATAGACATCTTAA 1227
 QY 242 GlyLeuGlnLeuThrArgValLysProAlaGlnAlaAspGlyAspArgProValArg 261
 Db 1228 GCACCAAGTTCTGCTATAAATAGATCCATCCATCTCAAGGCTACAGAACTGACAA 1287
 QY 262 LeuLeuTrpLysLysAlaArgGlyAlaProValLeuGlnLysThrLeuGlyTrpAsnIle 281
 Db 1288 CTCGTGTGAAGACATTGCTCTCTTTGAAGCAATGAAATAATCTTGATTTGAAGTG 1347
 QY 282 TrpTrpTrpProGlnSerAsnThrAsnLeuThrGlnThrMetAsnThrThrAsnGln 301
 Db 1348 ACTCTCAAGATGGAATGAAATCAATTTACAAATTAACACACTATATGCCACA-----AA 1401
 QY 302 LeuGlnLeuThrLeuGlyGlnSerPheTrpValSerMetLysSerTrpAsnSerLeu 321
 Db 1402 CTGACAGTAATCTCAAAATGATCGCTATCTAGCAACCTTAACAGTAAGAAATCTTGT 1461
 QY 322 GlyLysSerProValAlaThrLeuArgLysProAlaIleGlnLysSerPheGlnCys 341
 Db 1462 GGCAAAATCAGATGCGCTGTTTAACATATCCCTGCTGATCTTCAAGTACTCAACCT 1521
 QY 342 IleGlnValMetGlnAlaCysValAlaGlnAspGlnLeuValLysTrpGlnSerSer 361
 Db 1522 GATATGATTTAAAGCATTTCCCAAGATTAACATGCTTTGGTGGATGAGTACTCA 1581
 QY 362 AlaLeuAspValAsnThrTrpMetIleGlnTrpPheProAspValAspSerGlnProThr 381
 Db 1582 AGGGATCTCTAAAGAAATATATATCTGATGCTGTCTTATCAAGATAAGACCTCTG 1641
 QY 382 ThrLeuSerTrpGlnSerValSerGlnAlaThrAsnTrpThrIleGlnIleAspLysLeu 401
 Db 1642 ATCAGACTGCGCAACAAAGATGTATCCGTGATGAGGCACTATTTAAGAGGAACCTTA 1701
 QY 402 LysProPheTrpCysTrpAsnIleSerValTrpProMetLeuThrAspValGlyGln 421
 Db 1702 GCAGAGAGCAAAATGCTATTTGATTAACGTTATCTCAATATATGCTGATGACAGCAAGC 1761
 QY 422 ProTrpSerIleGlnAlaTrpAlaLysGlnGlyValProSerGlnGlyProGlnThrLys 441
 Db 1762 CCGATCTCCTAAAGCATCTTAAACAGCTCCACCTTCCAAAGACCTTACTGTTCCG 1821
 QY 442 ValGlnAsnIleGlyValLysThrValThrIleThrTrpLysGlnLysProLysSerGln 461
 Db 1822 ACAAAAAGATAGGAAAGAAAGCAAGCTGCTTGAAGTGGAGCAACTTCTGTTGATGTT 1881
 QY 462 ArgLysGlyIleIleCysAsnTrpThrIlePheTrpGlnAlaGlnGlyLysGlyPhe 481
 Db 1882 CAGAAATGATTTTACAGAAATTTATCTATATTTATTAAGAACCATCATTTGAAATGAAACT 1941
 QY 482 SerLysThrValAsnSerSerIleLeuGlnTrpGlyLeuGlnSerLeuLysArgLysThr 501
 Db 1942 GCTGTGATGTGATTTCTTCCACACAGAAATATATATGCTCTTGTGACTAGTACACAA 2001
 QY 502 SerTrpIleValGlnValMetAlaSerThrSerAlaGlyLysThrAsnGlyThrSerIle 521
 Db 2002 TTGTACATGTGTACGAATGCGATACACAGATGAAGTGGAAAGTGTCCAGAAATTC 2061
 QY 522 AsnPheLysThrLeuSerPheSerValPheGlnIleIleLeuIleThrSerIleGly 541
 Db 2062 ACTTTTACTACCCCAAGATTGCTCAAGAGAAATGAAACCATATGTCGTGCTGTTGC 2121

QY 542 GlyGlyLeuLeuIleLeuIleIleLeuThrValAlaTrpGlyLeuLysLysProAsnLys 561
 Db 2122 TTAGCATCTCTATGTAGCAACTTCTGGAGATGCTGTTCTGTTAATTAAGCGAGACTTA 2181
 QY 562 LeuThrHisLeuCysTrpProThrValProAsnProAlaGlnSerSerIleAlaThrTrp 581
 Db 2182 ATTAATAAACAACATCTGCGCTATGTTCAGATCTCTTCAAAAGATCATTTTCCCGAGTG 2241
 QY 582 -----HisGlyAspAspPheLysAspLysLeu 590
 Db 2242 TCACTCACACTCTCCCAAGGCAATTTTAATTCAAAGATCAATG 2289
 RESULT 8
 US-08-308-881-1
 ; Sequence 1, Application US/08308881
 ; Patent No. 5783672
 ; GENERAL INFORMATION:
 ; APPLICANT: Mosley, Bruce
 ; APPLICANT: Cosman, David J.
 ; TITLE OF INVENTION: Receptor for Oncostatin M
 ; NUMBER OF SEQUENCES: 11
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSES: Immunex Corporation
 ; STREET: 51 University Street
 ; CITY: Seattle
 ; STATE: WA
 ; COUNTRY: USA
 ; ZIP: 98101
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: Apple Macintosh
 ; OPERATING SYSTEM: Apple 7.1
 ; SOFTWARE: Microsoft Word, Version 5.1a
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/308, 881
 ; FILING DATE: 12-SEP-1994
 ; CLASSIFICATION: 435
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 08/249,553
 ; FILING DATE: 26-MAY-1994
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Seese, Kathryn A.
 ; REGISTRATION NUMBER: 32,172
 ; REFERENCE/DOCKET NUMBER: 2614-A
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (206) 587-0430
 ; TELEFAX: (206) 233-0644
 ; TELEX: 756822
 ; INFORMATION FOR SEQ ID NO: 1:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 2369 base pairs
 ; TYPE: nucleic acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: CDNA to mRNA
 ; HYPOTHETICAL: NO
 ; ANTI-SENSE: NO
 ; FRAGMENT TYPE: N-terminal
 ; ORIGINAL SOURCE:
 ; TISSUE TYPE: human placenta
 ; IMMEDIATE SOURCE:
 ; CLONE: B10G/pDC303
 ; FEATURE:
 ; NAME/KEY: CDS
 ; LOCATION: 244..2369
 ; FEATURE:
 ; NAME/KEY: mat_peptide
 ; LOCATION: 310..2369
 ; FEATURE:
 ; NAME/KEY: sig_peptide
 ; LOCATION: 244..309
 ; US-08-308-881-1

Alignment Scores: 1.03e-64 Length: 2369
 Pred. No.: 678.50 Matches: 169
 Score: 48.44% Conservative: 110
 Percent Similarity: 29.34% Mismatches: 258
 Best Local Similarity: 19.23% Indels: 39
 Query Match: 1 Gaps: 14
 DB: 14
 US-10-006-265-17 (1-662) x US-08-308-881-1 (1-2369)

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Qy 35 ProAlaLysProGluAsnIleSerCyseValTyrTyrTyrArgLysAsnLeuThrCysThr 54
Db 619 CCAGAAAAACCTAAATAATTGATTGCAATTGTGAACGAGGGAGAAATAATGAGTGTGAG 678
Qy 55 TrpSerProGlyLysGluThrSerTyr---ThrGlnTyrThrValLys-----Arg 70
Db 679 TGGGATGGTGAGGAGAAACACACTTGAGACAACTTCATTAAATCTGAATGGGCA 738
Qy 71 ThrTyrAlaPheGlyGlu-----LysHisAsp-----AsnCyseThrThrAsn 84
Db 739 ACACACAACTTCTGCTGATTGCAACGAAACCTGACACCCCACTCATGACCTGTGAT 798
Qy 85 SerSerThrSerGluAsnArgAlaSerCyseSerPheLeuProArgIleThrIlePro 104
Db 799 TATTCTACT-----GTGATTTTGTG----- 819
Qy 105 AsnAsnTyrThrIleGluValGluAlaGluAsnGlyValIleLysSer---His 123
Db 820 ---AACATTGAAGTCTGGTAGAGACAGAGATGCCCTTGGAGAGTTACATCAGATCAT 876
Qy 124 MetThrTyrTrpArgGluGluAsnIleAlaLysThrGluProProLysIlePheArgVal 143
Db 877 ATCAATTGATCCTGATATTAAGTG---AAGCCCAATCCGCCCATTAATTATCAGTG 933
Qy 144 LysProValLeuGlyIleLysArgMetIleGlnIleGluTrpIleLysProGluLeuAla 163
Db 934 ATCAACTCAGAGGAACCTCTAGATCTTAATAATGATGACGACCAACCAAGATTAAG 993
Qy 164 ProValSerSerAspLeuLysTyrThrLeuArgPheArgThrValAsnSerThrSerTrp 183
Db 994 AGTGTTAATAATA---CTAAATATATACATTCATATAGACCAAAAGATGCTCAACTGG 1050
Qy 184 MetGluValAsnPheAlaLysAsnArgLysAspLysAsnGlnThrTyrAsnLeuThrLys 203
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Qy 204 LeuGlnProPheThrGluTyrValIleAlaLeuArgCysAlaValLysGluSerLys--- 222
Db 1108 CTTAAACCTTTTACGATATGTGTTTAGATTCGCTGTATGAGAGAAAGATGCTAAGGGA 1167
Qy 223 PheTrpSerAspTrpSerGlnGluLysMetGlyMetThrGluGluGluAlaProCys--- 241
Db 1168 TACTGAGTGAAGTGAAGAGCAAGATGGGATCACTATGAAGATAGACATCTTAA 1227
Qy 242 GlyLeuGluLeuTrpArgValLeuLysProAlaGluAlaAspGlyArgArgProValArg 261
Db 1228 GCACCAAGTTCTGTATTAATAATAGATCATCTCCATCTCAAGGCTACAGAACTGTAA 1287
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Db 1288 CTCGTGTGAGAGACTTGCCTCTTTGAAGCCAAATGAGAAATTTGGATTTAGAACTG 1347
Qy 282 TrpTyrTyrProGluSerAsnThrAsnLeuThrGluThrMetAsnThrThrAsnGlnGln 301
Db 1348 ACTCTCAAGATGAGAAATCACATTTAACAAATTAACACAGTTAATGCCACA-----AAA 1401
Qy 302 LeuGluLeuHisLeuGlyGlyGluSerPheTrpValSerMetIleSerTyrAsnSerLeu 321
Db 1402 CTGACAGTAACTTACAAATAGATGCTATCTAGACCACTTAACAGTAAGAAATCTTGT 1461
Qy 322 GlyLysSerProValAlaThrLeuArgIleProAlaIleGlnGluLysSerPheGlnCys 341
Db 1462 GGCAAAATAGATGACGCTGTTTAACATATCCCTGCTGTGACTTCAAGCTACACACCT 1521

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Qy 342 IleGluValMetGlnAlaCysValAlaGluAsnGlnLeuValValLysTrpGlnSerSer 361
Db 1522 GTAAATGATCTTAAAGCATTTCCCAAGAAATACATGCTTGTGGGTGAATGACCTACCA 1581
Qy 362 AlaLeuAspValAsnThrTrpMetIleGluTrpPheProAspValAspSerGluProThr 381
Db 1582 AGGGAATCTGTAAGAAATATATATCTTACAGTGTGTGTGTTATCAGTAAGAACCCCTGT 1641
Qy 382 ThrLeuSerTrpGluSerValSerGlnAlaThrAsnTrpThrIleGlnGlnAspLysLeu 401
Db 1642 ATCACAGACTGCAACAAGAAAGATGTACCTGATGATGACCACTTTAAAGAGGAACTTA 1701
Qy 402 LysProPheTrpCyseTyrAsnIleSerValTyrProMetLeuHisAspLysValGlyGlu 421
Db 1702 GCAGAGACAAATGCTATTTGATTAACAGTTACTCAGATATATGCTGATGAGACCAAGAAC 1761
Qy 422 ProTyrSerIleGlnAlaTyrAlaLysGluGlyAlaProSerGluGlyProGluThrLys 441
Db 1762 CCGATTCATTAAGCATACCTTAACAGCTCCACCTTCAAGAGACTTACTGCTTGG 1821
Qy 442 ValGluAsnIleGlyValLysThrValThrIleThrTrpLysGluIleProLysSerGlu 461
Db 1822 ACAAAAAAGTAGGAGAAAAAGAGCTGTCTTAGAGTGGACCAACTTCTGTGATGTT 1881
Qy 462 ArgLysGlyIleIleCyseAsnTyrThrIlePheTyrGlnAlaGluGlyLysGlyPhe 481
Db 1882 CAGATGATTTATACAGAAATTAATATATATTTATATGAAACCATCATTTGAAATGAAACT 1941
Qy 482 SerLysThrValAsnSerSerIleLeuGlnTrpGlyLeuGluSerLeuLysArgLysThr 501
Db 1942 GCTGTGAATGTGATTTCTTCCACACAGAAATATACATTTGCTCTTTGACTAGTACACA 2001
Qy 502 SerTyrIleValGlnValMetAlaSerThrSerAlaGlyGlyThrAsnGlyThrSerIle 521
Db 2002 TTGTATACATGTAACAAATGAGCAGATACACAGATGAGGTGGAGAGATGCTCAGAAATTC 2061
Qy 522 AsnPheLysThrLeuSerPheSerValPheGluIleIleLeuIleThrSerLeuIleGly 541
Db 2062 ACTTTTCTACCCCAAGTTTGCTCAAGAGAAATTAAGCCATATGCTGCTGTTGC 2121
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Qy 562 LeuThrHisLeuCyseTrpProThrValProAsnProAlaGluSerSerIleAlaThrTrp 581
Db 2182 ATTAATAAAACATCTGGCTTAATGTTCCAGATCTTCAAAAGATCATATTGCCAGTGG 2241
Qy 582 -----HisGlyAspAspPheLysAspLysLeu 590
Db 2242 TCACCTCACACTCTCCAAAGGCACAATTTTAATCAAAAGATCAAAATG 2289

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RESULT 9
 US-09-058-263-1
 Sequence 1, Application US/09058263
 Patent No. 5891997
 GENERAL INFORMATION:
 APPLICANT: Mosley, Bruce
 APPLICANT: Cosman, David J.
 TITLE OF INVENTION: Receptor for Oncostatin M
 NUMBER OF SEQUENCES: 11
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Immunex Corporation
 STREET: 51 University Street
 CITY: Seattle
 STATE: WA
 COUNTRY: USA
 ZIP: 98101
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: Apple Macintosh
 OPERATING SYSTEM: Apple 7.1

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SOFTWARE: Microsoft Word, Version 5.1a
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/058,263
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/308,881
FILING DATE: 12-SEP-1994
APPLICATION NUMBER: US 08/249,553
FILING DATE: 26-MAY-1994
ATTORNEY/AGENT INFORMATION:
NAME: Seese, Kathryn A.
REGISTRATION NUMBER: 32,172
REFERENCE/DOCKET NUMBER: 2614-A
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 587-0430
TELEFAX: (206) 233-0644
TELEX: 756822
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 2369 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA to mRNA
HYPOTHEICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: N-terminal
ORIGINAL SOURCE:
TISSUE TYPE: human placenta
IMMEDIATE SOURCE:
CLONE: B10G/PDC303
FEATURE:
NAME/KEY: CDS
LOCATION: 244..2369
NAME/KEY: mat_peptide
LOCATION: 310..2369
FEATURE:
NAME/KEY: sig_peptide
LOCATION: 244..309
US-09-058-263-1
US-10-006-265-17 (1-662) x US-09-058-263-1 (1-2369)

Alignment Scores:
Pred. No.: 1,03e-64 Length: 2369
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Query Match: 19.23% Indels: 39
DB: 2 Gaps: 14

US-10-006-265-17 (1-662) x US-09-058-263-1 (1-2369)
QY 35 ProAlaIysProGluAsnIleSerCyValTYrTYrAlaGlyAsnLeuThrCyThr 54
DB 619 CCGAAGAAACCTTAAATTTGAGTTCATGTGACACGAGGGAAGAAATGAGGTGAG 678
QY 55 TrpSerProGlyLysGluThrSerTYr---ThrGluThrValLys-----Arg 70
DB 679 TGGAGTGGTGAAGGAAACACACTTGGAGCAAACTTCATTAAATGTGAATGGCA 738
QY 71 ThrTAlaIleGluGlyLys-----LysHIsAsp-----AsnCyThrThrAsn 84
DB 739 ACACACAGATTCTGTATTCGACAAAGCAAAACGTGACACCCCACTCATGCTTGGAT 798
QY 85 SerSerThrSerGluAsnAlaSerCySerPhePheLeuProArgIleThrIlePro 104
DB 799 TATTCTACT-----GTGATTTTGTG----- 819
QY 105 AspAsnTYrThrIleGluValGluAlaGluAsnGlyAspGlyValIleLysSer---His 123
DB 820 ---AACATTGAAGTCTGGTAGAAGCAGAGAAATGCCCTTGGGAAGTTACATCATCAT 876

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QY 382 ThrLeuSerTrpGluSerValSerGlnAlaThrAsnTrpThrIleGlnIleAspLysLeu 401
DB 1642 ATCACAGACTGGCAACAGAAAGATGTCAGTCCGATCGACCTATTTAAAGAGGAACCTTA 1701
QY 402 LysProPheTrpCySerTyrAsnIleSerValTYrProMetLeuHIsAspLysValGlyGlu 421
DB 1702 GCAGAGAGCAAAATGCTATTTGATTAACAGTTACTCCAGTATATGCTATGACCAAGAAC 1761
QY 422 ProTyrSerIleGlnAlaTyrAlaLysGluGlyValProSerGlnGlyProGluThrLys 441
DB 1762 CCTGAATCCATTAAGGCAATACCTTAAACAAAGCTCCACCTTCAAAAGAACTTACTGTTC 1821
QY 442 ValGluAsnIleGlyValLysThrValThrIleThrTrpLysGluIleProLysSerGlu 461
DB 1822 ACACAAAAGATGAGGAAAAACAAAGCTGTATGAGGTGGACCAACTTCTGTGATGTT 1881
QY 462 ArgLysGlyIleIleCyAsnTYrThrIlePheTYrGluAlaGluGlyLysLysPhe 481
DB 1882 CCAATGAGATTATACGAATTTATCTATATTTTATGAAACATCATCTTGGAAATGAACCT 1941
QY 482 SerLysThrValAsnSerSerIleLeuGlnTYrGlyLeuGluSerLeuLysArgLysThr 501

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Db 1942 GCTGTGAATGTGATCTTCCACACAGATATACATTCTCTTTGACTAGTACACA 2001
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Qy 502 SerTyrIleValGluValMetAlaSerThrSerAlaGlyGlyThrAsnGlyThrSerIle 521
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 2002 TTGTGTACATGTCAGTACGATACATACAGATGAGGAGGAGATGTCACAGAAATTC 2061
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy 522 AsnPheLysThrLeuSerPheSerValPheGluIleIleLeuIleThrSerLeuIleGly 541
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 2062 ACTTTTACTACCCCAAGTTTGTCTCAGAGAAATGAAAGCCATGTCCTGCTGTTGC 2121
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy 542 GlyGlyLeuLeuIleLeuIleLeuThrValAlaTyrGlyLeuLysPheProAsnLys 561
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 2122 TTAGATTCCTTATACAACTCTCTGGAGTGTCTGTCTGTTAATAGGAGACCTA 2181
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy 562 LeuThrIleLeuCysTyrProThrValProAsnProAlaGluSerSerIleAlaThrTyr 581
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
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      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy 582 -----HisGlyAspAspPheLysAspLysLeu 590
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 2242 TCACCTCACACTCTCCAGGACAAATTTTATTCAGAAAGATCAATG 2289
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RESULT 10
US-09-059-099-1
: Sequence 1, Application US/09059099
: Patent No. 5925740
: GENERAL INFORMATION:
: APPLICANT: Mosley, Bruce
: APPLICANT: Cosman, David J.
: TITLE OF INVENTION: Receptor for Oncostatin M
: NUMBER OF SEQUENCES: 11
: CORRESPONDENCE ADDRESS:
: ADDRESS: Immunex Corporation
: STREET: 51 University Street
: CITY: Seattle
: STATE: WA
: COUNTRY: USA
: ZIP: 98101
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: Apple Macintosh
: OPERATING SYSTEM: Apple 7.1
: SOFTWARE: Microsoft Word, Version 5.1a
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/09/059, 099
: FILING DATE:
: CLASSIFICATION:
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US/08/308, 881
: FILING DATE: 12-SEP-1994
: APPLICATION NUMBER: US 08/249, 553
: FILING DATE: 26-MAY-1994
: ATTORNEY/AGENT INFORMATION:
: NAME: Seese, Kathryn A.
: REGISTRATION NUMBER: 32,172
: REFERENCE/DOCKET NUMBER: 2614-A
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (206) 587-0430
: TELEFAX: (206) 233-0644
: TELEX: 756822
: INFORMATION FOR SEQ ID NO: 1:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 2369 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: MOLECULE TYPE: cDNA to mRNA
: HYPOTHEICAL: NO
: ANTI-SENSE: NO
: FRAGMENT TYPE: N-terminal
: ORIGINAL SOURCE:
: TISSUE TYPE: human placenta

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: IMMEDIATE SOURCE:
: CLONE: B106/pDC303
: FEATURE:
: NAME/KEY: CDS
: LOCATION: 244..2369
: FEATURE:
: NAME/KEY: mat_peptide
: LOCATION: 310..2369
: FEATURE:
: NAME/KEY: sig_peptide
: LOCATION: 244..309
: US-09-059-099-1

Alignment Scores:
Pred. No.: 1,03e-64 Length: 2369
Score: 678.50 Matches: 169
Percent Similarity: 48.44% Conservative: 110
Best Local Similarity: 29.34% Mematches: 258
Query Match: 19.23% Indels: 39
DB: 2 Gaps: 14

US-10-006-265-17 (1-662) x US-09-059-099-1 (1-2369)
Qy 35 ProAlaLysProGluAsnIleSerCysValTyrTyrTyrArgLysAsnLeuThrCysThr 54
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Qy 55 TyrSerProGlyLysGluThrSerTyr---ThrGlnTyrThrValLys-----Arg 70
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
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Qy 71 ThrTyrAlaPheGlyGlu-----LysHisAsp-----AsnCysThrThrAsn 84
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Qy 85 SerSerThrSerGluAsnArgAlaSerCysSerPheLeuProArgIleThrIlePro 104
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Qy 105 AspAsnTyrThrIleGluValGluAlaGluAsnGlyValIleLysSer---His 123
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 820 ---AACATTTGAAGCTGGTGTGAAGACAGAAATGCCCTTGGAGGATTAATCATGATCAT 876
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Qy 124 MetThrTyrTyrPheGluGluAsnIleAlaLysThrGluProPheLysIlePheArgVal 143
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Db 877 ATCAATTTTGAATCTGTATATTAAGTG---AAGCCCATCCGCACATTAATTATCATCTG 933
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Qy 144 LysProValLeuGlyIleLysArgMetIleGlnIleGluTyrPheLysProGluLeuAla 163
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Qy 164 ProValSerSerAspLeuLysTyrThrLeuArgPheArgThrValAsnSerThrSerTyr 183
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Db 1051 AGCCAGATTCCT---CCTGAAGACACAGCATCCACCGATCTTATTCACGTCCAAAGAC 1107
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Qy 204 LeuGlnProPheThrGluTyrValIleAlaLeuArgCysAlaValLysGluSerLys--- 222
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Db 1108 CTTAAACCTTTTACAGATATATGTGTTTAGATTTGCTGTATGAAGAAAGATGTAAAGGA 1167
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy 223 PheTyrSerAspTyrSerGlnGluLysMetGlyMetThrGluGluGluAlaProCys--- 241
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1168 TACTGAGTGTACTGTAGTGAAGAAAGCAAGTGGATCACTATGAAGATACCATCTTAAA 1227
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy 242 GlyLeuGluLeuTyrPheValLeuLysProAlaGluLysArgGlyArgProValArg 261
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Db 1228 GCACCAAGTTTCTGTATTAATATGATCATCCCATCACTCAAGGCTCAAGAACTGTCAA 1287
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Qy 262 LeuLeuTyrLysLysAlaArgGlyAlaProValLeuGluLysThrLeuGlyTyrAsnIle 281
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Db      1288 CTCGTGTGAGAGACATGCTCCTTTTGAAGCAATGAGAAAACTTGATTAAGAGTG 1347
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Db      1348 ACTCTCAAGAGATGAGAAATCATTTACAAATAATTAACACTTAATGCCACA-----AAA 1401
Qy      302 LeuGluLeuHleuGlnGlyGlyGluSerPheTrpValSerMetIleSerTyraenSerLeu 321
Db      1402 CTGACAGTAAATCTCACAATGATCGCTACTAGCAACCTTAACAGTAAGAAATCTTGTT 1461
Qy      322 GlyLysSerProValAlaThrLeuArgIleProAlaIleGlnGlySerPheGlnCys 341
Db      1462 GGCAAATTCAGATGACACTGTTTAACTATCCCTGCGCTGACCTTCAAGCTACTCACCT 1521
Qy      342 IleGluValMetGlnAlaCysValAlaGluAspGlnLeuValValIlystrPglInsSer 361
Db      1522 GTAAATGATCTTAAACATCTCCCAAGAAATACATGCTTGGGTGGAATGACTACTCCA 1581
Qy      362 AlaLeuAspValaenThrTrpMetIleGluTrpPheProAspValaLysSerGluProThr 381
Db      1582 AGGGAATCTGTAAAGAAATATATATAGTGTGTGTGTATCAAGTAAGACACCTGT 1641
Qy      382 ThrLeuSerTrpGluSerValSerGlnAlaThrAsnTrpThrIleGlnGlnAspLysLeu 401
Db      1642 ATCAGAGACTGGCAGCAAGAGATGTATCCGTGATCGCACCTATTTAAGAGGAACTTA 1701
Qy      402 LysProPheTrpCysTrpAenIleSerValTrpProMetLeuHleAspLysValaGlyGlu 421
Db      1702 GCAGAGAGCAATGCTTTTGTATACAGTTACTCCAGTATATGCTGATGAGACAGAGAAC 1761
Qy      422 ProTySerIleGlnAlaTrpAlaLysGlyGlyValaProSerGlnGlyProgluTrpLys 441
Db      1762 CTGGAATCCATAAAGCATACCTTAAACAGATCCACCTTCAAGAGACCTACTGTTCCG 1821
Qy      442 ValGluAsnIleGlyValIlystrValThrIleThrTrpLysGluIleProLysSerGlu 461
Db      1822 ACAAAAAGATGGAGAAAAAGAGCTGTCTAGAGGGAGCAACCTCTGTTGATGTT 1881
Qy      462 ArgLysGlyIleIleCysAenTyThrIlePheTyrglnAlaGluGlyGlyLysGlyPhe 481
Db      1882 CAGAAATGATTTATCAGAAATTTATCTATTTTATTAAGAACCATCTGAGAAATGAAACT 1941
Qy      482 SerLysThrValaenSerSerIleLeuGlnTrpGlyLeuGlnSerLeuLysArgLysThr 501
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Qy      502 SerTyIleValaGlnValMetAlaSerThrSerAlaGlyLysThrAsnGlyThrSerIle 521
Db      2002 TTGTACATGTGTAGCAATGATGAGCATACAGATGAAGTGAAGATGTCTCAGAAATTC 2061
Qy      522 AsnPhelyThrLeuSerPheSerValaPheGluIleIleLeuIleThrSerLeuIleGly 541
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Qy      542 GlyGlyLeuLeuLeuIleLeuIleLeuThrValaAlaTrpGlyLeuLysProAsnLys 561
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Qy      562 LeuThrHisLeuCystrpProThrValaProAsnProAlaGluSerSerIleAlaThrTrp 581
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RESULT 11
US-09-058-264-1
; Sequence 1, Application US/09058264
; Patent No. 6010886

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; GENERAL INFORMATION:
; APPLICANT: Mosley, Bruce
; APPLICANT: Cosman, David J.

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; TITLE OF INVENTION: Receptor for Oncostatin M
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSER: Immunex Corporation
; STREET: 51 University Street
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: Apple 7.1
; SOFTWARE: Microsoft Word, Version 5.1a
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/058,264
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/308,881
; FILING DATE: 12-SEP-1994
; APPLICATION NUMBER: US 08/249,553
; FILING DATE: 26-MAY-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Seese, Kathryn A.
; REGISTRATION NUMBER: 32,172
; REFERENCE/DOCKET NUMBER: 2614-A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 587-0430
; TELEFAX: (206) 233-0644
; TELEX: 756822
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2369 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA to mRNA
; HYPOTHEICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE: N-terminal
; ORIGINAL SOURCE:
; TISSUE TYPE: human placenta
; IMMEDIATE SOURCE:
; CLONE: B10G/pDC303
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 244..2369
; FEATURE:
; NAME/KEY: mat_peptide
; LOCATION: 310..2369
; FEATURE:
; NAME/KEY: sig_peptide
; LOCATION: 244..309
; US-09-058-264-1
; Alignment Scores:
; Pred. No.: 1 03e-64 Length: 2369
; Score: 678.50 Matches: 169
; Percent Similarity: 48.44% Conservative: 110
; Best Local Similarity: 29.34% Mismatches: 258
; Query Match: 19.23% Indels: 39
; DB: Gaps: 14
; US-10-006-265-17 (1-662) x US-09-058-264-1 (1-2369)
Qy      35 ProAlaLysProGluAsnIleSerCysValTyTrpYrArgLysAsnLeuThrCysThr 54
Db      619 CCAGAAAACCTTAAATTTGAGTTGATGTAACGAGGAGAAATGAGGTGTAG 678
Qy      55 TrpSerProGlyLysGluThrSerTyR---ThrGlnTyThrValys-----Arg 70
Db      679 TGGGATGTGTGAGGAGAAACACACTTGAGACAACTTAAATCTGAATGGGCA 738

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TELEX: 756822
 INFORMATION FOR SEQ ID NO: 1:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 2369 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: cDNA to mRNA
 HYPOTHEICAL: NO
 ANTI-SENSE: NO
 FRAGMENT TYPE: N-terminal
 ORIGINAL SOURCE:
 TISSUE TYPE: human placenta
 IMMEDIATE SOURCE:
 CLONE: B10G/PDC303
 FEATURE:
 NAME/KEY: CDS
 LOCATION: 244..2369
 FEATURE:
 NAME/KEY: mat_peptide
 LOCATION: 310..2369
 FEATURE:
 NAME/KEY: sig_peptide
 LOCATION: 244..309
 US-09-455-962-1

Alignment Scores:

Pred. No.:	1,03e-64	Length:	2369
Score:	678.50	Matches:	169
Percent Similarity:	48.44%	Conservative:	110
Best Local Similarity:	29.34%	Mismatches:	258
Query Match:	19.23%	Indels:	39
DB:	4	Gaps:	14

US-10-006-265-17 (1-662) x US-09-455-962-1 (1-2369)

QY 35 ProAlaLysProGluAsnIleSerCysValTyrTyrTyrArgLysAsnLeuThrCysThr 54
 Db 619 CCAGAAACCTTAATAATTTGAGTTGTCATGTGAACGAGGAAAGAAATGAGGTGTGAG 678
 QY 55 TrpSerProGluLysGluThrSerTyr--ThrGlnTyrThyValys-----Arg 70
 Db 679 TGGGATGCTGGAGGAAACACACTTGGAGACAACTTCACTTAAATCTGAATGGGCA 738
 QY 71 ThrTyrAlaPheGluGlu-----LysHisAsp-----AsnCysThrThrAsn 84
 Db 739 ACACACAGTTTCTGATTCGAAAGCAACGTCGACCCCACTCATGCTGTTGAT 798
 QY 85 SerSerThrSerGluAsnArgAlaSerCysSerPhePheLeuProArgIleThrIlePro 104
 Db 799 TATTCTACT-----GTGATTTTGTCT----- 819
 QY 105 AspAsnTyrThrIleGluValIgluAlaGluAsnGlyAspGlyValIleLysSer---His 123
 Db 820 ---AACATTGAACTCTGGTGAAGACAGAAATGCCCTTGGAGGTTACATCAGATCAT 876
 QY 124 MetThrTyrTrpArgLeuGluAsnIleAlaLysThrGluProProLysIlePheArgVal 143
 Db 877 ATCAATTTGATCTGTATATAAGT--AAGCCCAATCCGCCAATAATTATATCAGTG 933
 QY 144 LysProValLeuGlyIleLysArgMetIleGlnIleGluTrpIleLysProGluLeuAla 163
 Db 934 ATCAACTCAGAGAACTGCTAGATCTTAAATTTGATGACGCAACCAAGATATTAG 993
 QY 164 ProValSerSerAspLeuLysIlyTrnLeuArgPheArgThrValAsnSerThrSerTrp 183
 Db 994 AGTGTATATATA---CTAAATATATACATTCAATATATGACCAAAAGATGCTCAACTGG 1050
 QY 184 MetGluValAsnPheAlaLysAsnArgLysAspLysAsnGlnIleThrTrpAsnLeuThrGly 203
 Db 1051 AGCCAGATTCTCT--CCTGAAGACACAGCATCCACCGGATCTTCACTGTCACAGAC 1107
 QY 204 LeuGlnProPheThrGluTyrValIleAlaLeuArgCysAlaValLysGluSerLys--- 222

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 QY 223 PheTrpSerAspTrpSerGlnGluLysMetGlyMetThrGluGluAlaProCys--- 241
 Db 1168 TACTGAGTACTGCTGAGAAAGCAAGATGGATCATCTATGAAATGACCATTTAA 1227
 QY 242 GlyLeuGluLeuTrpArgValLeuLysProAlaGluAlaAspGlyArgArgProValArg 261
 Db 1228 GCACCAAGTTTCTGTATATAAATAGATCCATCCATACCTCAAGCTACAGAACTGACAA 1287
 QY 262 LeuLeuTrpLysLysAlaArgGlyAlaProValLeuGluLysThrLeuGlyTyrAsnIle 281
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 QY 282 TrpTyrTyrProGluSerAsnThrAsnLeuThrGluThrMetAsnThrThrAsnGln 301
 Db 1348 ACTTTCACAAAGATGGAATCACATTTTACAAATTTACACAGTTAAATGCCACA----AAA 1401
 QY 302 LeuGluLeuHisLeuGlyLysGluSerPheTrpValSerMetIleSerTyrAsnSerLeu 321
 Db 1402 CTGACAGTAAATCTCAAAATGATCGCTATCTAGCAACCTTAACAGTAAGAAATCTGTT 1461
 QY 322 GlyLysSerProValAlaThrLeuArgIleProAlaIleGlnGluLysSerPheGlnCys 341
 Db 1462 GCGAATCAGATGACAGCTGTTTAACTATCCCTGCTGATCTTCAACCTTCAACCTCCT 1521
 QY 342 IleGluValMetGlnAlaCysValAlaGluAsnArgIleuValValLysTrpGlnSerSer 361
 Db 1522 GTTAATGATCTTAAACATATCCCAAGAAATACATGCTTTGGTGAATGAACTACTCCA 1581
 QY 362 AlaLeuAspValAsnThrTrpMetIleGluTrpPheProAspValAspSerGluProThr 381
 Db 1582 AGGGAATCTGTAAAGAAATATATACTGTGCTGTGTGTATGACATGAAGACCTGT 1641
 QY 382 ThrLeuSerTrpGluSerValSerGlnAlaThrAsnTrpThrIleGlnIleAspLysLeu 401
 Db 1642 ATCACAGACTGCGACAAACAAAGATGGTACCGTCATCGCACTTATTAAGAGGAACCTTA 1701
 QY 402 LysProPheTrpCysTrpAsnIleSerValTyrProMetLeuHisAspLysValGlyGlu 421
 Db 1702 GCAGAGAGCAAAATGCTATTGTAAACAGTTACTCCAGTATATGCTGATGACACCAAGAAC 1761
 QY 422 ProTyrSerIleGlnAlaTyrAlaLysGluGlyValProSerGluGlyProGluThrLys 441
 Db 1762 CCTGAATCATATAAGCATACCTTAACAAGCTCCACTTCCAAAGACCTACTGTCCG 1821
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 Db 1822 ACNAAAAAGTAGGGAATAACAGAGCTGCTTGAAGTGGAGCAACCTTCTGTGATGTT 1881
 QY 462 ArgLysGlyIleIleCysAsnTyrThrIlePheTyrGlnAlaGluGlyLysGlyPhe 481
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 Db 2002 TTGTATCATGTGATGATGACATACACAGATGAAGGAGGAGATGATGTCAGAAATTC 2061
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RESULT 13			
PCT-US95-06530-1			
/ Sequence 1, Application PC/TUS9506530			
/ GENERAL INFORMATION:			
/ APPLICANT: Mosley, Bruce			
/ APPLICANT: Cosman, David J.			
/ TITLE OF INVENTION: Receptor for Oncostratin M			
/ NUMBER OF SEQUENCES: 11			
/ CORRESPONDENCE ADDRESS:			
/ ADDRESSEE: Immunex Corporation			
/ STREET: 51 University Street			
/ CITY: Seattle			
/ STATE: WA			
/ COUNTRY: USA			
/ ZIP: 98101			
/ COMPUTER READABLE FORM:			
/ MEDIUM TYPE: floppy disk			
/ COMPUTER: IBM PC			
/ OPERATING SYSTEM: PC-DOS/MS-DOS			
/ SOFTWARE: Patentin Release #1, Version #1.30			
/ CURRENT APPLICATION DATA:			
/ APPLICATION NUMBER: PCT/US95/06530			
/ FILING DATE:			
/ CLASSIFICATION:			
/ PRIOR APPLICATION DATA:			
/ APPLICATION NUMBER: US 08/308, 881			
/ FILING DATE: 09-SEP-1994			
/ APPLICATION NUMBER: US 08/249,553			
/ FILING DATE: 26-MAY-1994			
/ ATTORNEY/AGENT INFORMATION:			
/ NAME: Anderson, Kathryn A.			
/ REGISTRATION NUMBER: 32,172			
/ REFERENCE/DOCKET NUMBER: 2614-WO			
/ TELECOMMUNICATION INFORMATION:			
/ TELEPHONE: (206) 587-0430			
/ TELEFAX: (206) 233-0644			
/ TELEX: 756822			
/ INFORMATION FOR SEQ ID NO: 1:			
/ SEQUENCE CHARACTERISTICS:			
/ LENGTH: 2369 base pairs			
/ TYPE: nucleic acid			
/ STRANDEDNESS: single			
/ TOPOLOGY: linear			
/ MOLECULE TYPE: cDNA to mRNA			
/ HYPOTHETICAL: NO			
/ ANTI-SENSE: NO			
/ FRAGMENT TYPE: N-terminal			
/ ORIGINAL SOURCE:			
/ TISSUE TYPE: human placenta			
/ IMMEDIATE SOURCE:			
/ CLONE: B10G/pDC303			
/ FEATURE:			
/ NAME/KEY: CDS			
/ LOCATION: 244..2369			
/ FEATURE:			
/ NAME/KEY: mat_peptide			
/ LOCATION: 310..2369			
/ FEATURE:			
/ NAME/KEY: sig_peptide			
/ LOCATION: 244..309			
PCT-US95-06530-1			
Alignment Scores:			
Pctd. No.: 1,03e-64			2369
Score: 678.50			Matches: 169
Percent Similarity: 48.44%			Conservative: 110
Best Local Similarity: 29.34%			Mismatches: 258

[illegible]

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Qy 362 AlaleuapValanThripMetilegUtrPheProAspValaspSerGluProThr 381
Db 1582 AGGAAATCTGTAAAGAAATATATATCTGAGTGAGTGATATACAGATAAGACCTGT 1641
Qy 382 ThleuSerTrpGluSerValSerGlnAlaThrAsnTrpThrileGlnInAspLysleu 401
Db 1642 ATCAGACACTGGGACAAAGAAATGGTACCGTCACTGCCTATATTAAGAGGAACTTA 1701
Qy 402 LysProPheTrpCyTrpAsnIleSerValTrpProMetLeuHisAspLysValGlyGlu 421
Db 1702 GCGAGAGCAAAATGCTATTTGATTAACGTTACTCCAGTATATGCTGATGAGACAGAGAGC 1761
Qy 422 ProTrpSerileGlnAlaTrpAlaLysGluGlyValProSerGluGlyProGluTrpLys 441
Db 1762 CCTGAATCCATAAAGGATATCTTAACAGAGCTCCACCTTCAAGAGACCTACGTTCGG 1821
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; Sequence 3, Application US/08825558
; Patent No. 5965724
; GENERAL INFORMATION:
; APPLICANT: SHARKEY, ANDREW
; APPLICANT: SMITH, STEPHEN K.
; APPLICANT: DELLOW, KIMBERLEY A.
; TITLE OF INVENTION: Gp 130 Lacking the Transmembrane Domain
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX
; STREET: 1100 NEW YORK AVENUE
; CITY: WASHINGTON
; STATE: DC
; COUNTRY: USA
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/825,558
; FILING DATE: 19-MAR-1997

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; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: ESKMOND, ROBERT W.
; REGISTRATION NUMBER: 32,893
; REFERENCE/DOCKET NUMBER: 0623,0530001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)371-2540
; TELEFAX: (202)371-2540
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1977 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..1974
; US-08-825-558-3

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Score: 636.50 Matches: 163
Percent Similarity: 46.53% Conservative: 105
Best Local Similarity: 28.30% Mismatches: 237
Query Match: 18.04% Indels: 72
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OY 322 GlyLysSerProValAlaThrLeuArgIleProAlaIleGlnGluLysSerPheGlnCys 341
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DB 1519 CCTGAATCATTAAGCAATACCTTAACAGACTCCACCTCCAAAGCACTTACTGTTGG 1578
OY 442 ValGluAsnIleGlyValLysThrValThrIleThrTrrPylGluIleProLysSerGlu 461
DB 1579 ACAAAAAGAGTGAAGAAAACGAACCTGCTTAAGTGGGACCACTTCTCTTATGTT 1638
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OY 502 SerTyrIleValAlaGlnValMetAlaSerThrSerAlaGlyGlyThrAsnGlyThrSerIle 521
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DB 1902 TCACCTCACACTCTCCAAAGCACAATTTTAATTCAAAAGATCAAAATG 1949

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RESULT 15
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; Sequence 3, Application US/09312611
; Patent No. 6380160
; GENERAL INFORMATION:
; APPLICANT: SHARKEY, ANDREW
; APPLICANT: SMITH, STEPHEN K.
; APPLICANT: DELLOW, KIMBERLEY A.
; TITLE OF INVENTION: Gp130 Lacking the Transmembrane Domain
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSER: STERN, KESSLER, GOLDSTEIN & FOX
; STREET: 1100 NEW YORK AVENUE
; CITY: WASHINGTON
; STATE: DC
; COUNTRY: USA
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/312,611
; FILING DATE: 17-MAY-1999
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: ESMOND, ROBERT W.
; REGISTRATION NUMBER: 32,893
; REFERENCE/DOCKET NUMBER: 0623_0530002
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)371-2600
; TELEFAX: (202)371-2540
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1977 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..1974
; US-09-312-611-3
;
Alignment Scores:
Pred. No.: 3,596-60 Length: 1977
Score: 636.50 Matches: 163
Percent Similarity: 46.53% Conservative: 105
Best Local Similarity: 28.30% Mismatches: 237
Query Match: 18.04% Indels: 72
DB: 3 Gaps: 15
US-10-006-265-17 (1-662) x US-09-312-611-3 (1-1977)
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 Db 1902 TCACCTCACACTCTCCAAAGGCAAAATTTTAATTCAAAAGATCAAAATG 1949

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 Job time : 349.791 secs

GenCore version 5.1.6
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Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

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Database :

Published Applications NA:*

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Prod. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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6	3518	99.7	2529	10	US-09-892-949-45
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12	3465.5	98.2	2402	10	US-09-892-949-1
13	3465.5	98.2	2402	17	US-10-351-157-110
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40	2606	73.9	2445	14	US-10-227-873-91
41	2606	73.9	2445	14	US-10-227-883-91
42	2606	73.9	2445	14	US-10-219-076-91
43	2606	73.9	2445	14	US-10-230-434-91
44	2606	73.9	2445	14	US-10-219-003-91
45	2606	73.9	2445	14	US-10-219-075-91

ALIGNMENTS

RESULT 1
US-10-006-265-16
; Sequence 16, Application US/1006265
; Publication No. US20030125520A1
; GENERAL INFORMATION:
; APPLICANT: Maeda, Masatsugu
; TITLE OF INVENTION: NOVEL HEMOPHILIN RECEPTOR PROTEIN, NR10
; FILER REFERENCE: 06501-096001
; CURRENT FILING DATE: 2003-01-06
; PRIOR APPLICATION NUMBER: US/10/006-265
; PRIOR FILING DATE: 2000-06-01
; PRIOR APPLICATION NUMBER: JP 11/155797
; PRIOR FILING DATE: 1999-06-02
; PRIOR APPLICATION NUMBER: JP 11/217797
; PRIOR FILING DATE: 1999-07-30
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 16

; LENGTH: 2119
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 ; FEATURE:
 ; NAME/KEY: CDS
 ; LOCATION: (11)...(1996)
 ; US-10-006-265-16

Alignment Scores:

Pred. No.:	0	Length:	2119
Score:	3528.00	Matches:	662
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	15	Gaps:	0

US-10-006-265-17 (1-662) x US-10-006-265-16 (1-2119)

QY 1 MetLysLeuSerProGlnProSerCybValAsnLeuGlyMetMetTrpThrTrpAlaLeu 20
 Db 11 ATGAAGCTCTCTCCAGCCTTCATGTTAACTGGGAGATGATGGACCTGGCACTG 70
 QY 21 TrpMetLeuProSerLeuCybLysPheSerLeuAlaAlaLeuProAlaLysProGluAsn 40
 Db 71 TGGATCTCCCTCCACTGCAATTGACGCTGCGAGCTCTGCGAGCTAAGCCGGAAC 130
 QY 41 LLeSerCybValTyrTyrTyrArgLysAsnLeuThrCybThrTrpSerProGlyLysGlu 60
 Db 131 ATTTCCTGTCTACTACTATAGAAAAATTTCCTGCACTTGGAGTCCAGAAAGAA 190
 QY 61 ThrSerTyrThrGlnTyrThrValLysArgThrTyrAlaPheGlyGluLysHisAspAsn 80
 Db 191 ACAGATTATACCAGTACACAGTTAAGAACTTAACGCTTTGGAGAAAAACATGATAAT 250
 QY 81 CybThrThrAsnSerSerThrSerGluAsnArgAlaSerCybSerPhePheLeuProArg 100
 Db 251 TGTACAAACCAATAGTTCTCAAGTGAATAATCGCTTCGCTCTTTTTCCTTCCAAAG 310
 QY 101 LLeThrLLeProAspAsnTyrThrLLeGluValGluAlaGluAsnGlyAspGlyValLLe 120
 Db 311 ATACACATCCCAATATTTATACATTGAGGTGGAGCTGAAATGGAGATGGGTGAAT 370
 QY 121 LysSerHisMetThrTyrTrpArgLeuGluAsnLLeAlaLysThrGluProProLysLLe 140
 Db 371 AAATCATATGATCATACTGAGATTAAGAAACATAGCGAAACCTGAACCACTTAAGATT 430
 QY 141 PheArgValLysProValLeuGlyLLeLysArgMetLLeGlnLLeGluTrpLLeLysPro 160
 Db 431 TTCGGGTGAACCAAGTTTGGGCATCAACGATGATTCAAAATTGATGGATMAAGCCCT 490
 QY 161 GluLeuAlaProValSerSerAspLeuLysTyrThrLeuArgPheArgThrValAsnSer 180
 Db 491 GAGTTGGCCCTTTTCATCTGATTTAAATATACACTTCGATTTCAGAGACATCAACAGT 550
 QY 181 ThrSerTrpMetGluValAsnPheAlaLysAsnArgLysAspLysAsnGlnThrTyrAsn 200
 Db 551 ACCAGCTGATGGAAGTCAACTTCGCTAAGAACCGTAAGATMAAAACCAACGATCAAC 610
 QY 201 LeuThrGlyLeuGlnProPheThrGluTyrValLLeAlaLeuArgCybAlaValLysGlu 220
 Db 611 CTCACGGGGCTGAGGCTTTTACAAATATGTCATAGCTCTGCGAGTGGGGTCAAGGAG 670
 QY 221 SerLysPheTrpSerAspTrpSerGlnGluLysMetGlyMetThrGluGluGluAlaPro 240
 Db 671 TCBAATTTCTGAGTACTGAGACCAAGAAAAATGGAAATGACTGAGGAAGAGCTCCA 730
 QY 241 CybGlyLeuGlnLeuTrpArgValLLeLysProAlaGluAlaAspGlyArgArgProVal 260
 Db 731 TGTGGCTGGAACACTGTGAGAGTCTGTAACCAAGCTGAGGCGGATGGAAGAGCCAGTG 790
 QY 261 ArgLeuLeuTrpLysLysAlaArgGlyAlaProValLeuGluLysThrLeuGlyTyrAsn 280
 Db 791 CGGTGTGTATGGAAGAGCAAGAGAGGCCCACTGCTTATAGAAAAACACTTGGCTCAAC 850

QY 281 LLeTrpTyrTyrProGluSerAsnThrAsnLeuThrGluThrMetAsnThrThrAsnGln 300
 Db 851 ATATGCTACTATCCAGAAAGCAACTTAACCTTCAGAAACATGAACACTTAACCGAG 910
 QY 301 GlnLeuGluLeuHisLeuGlyGlyGluSerPheTrpValSerMetLLeSerTyrAsnSer 320
 Db 911 CAGCTTGAACCTGATCTGGAGGCGAGAGCTTTTGGGTGTCTATGATTTCTTATATTTCT 970
 QY 321 LeuGlyLysSerProValAlaThrLeuArgLLeProAlaLLeGlnGluLysSerPheGln 340
 Db 971 CTTGGAAATCTTCCAAGTGGCCACCTCGAGAAATTCACGATTTCAAGAAAAATCATTTGAG 1030
 QY 341 CybLLeGluValMetGlnLLeCybValAlaGluAspGlnLeuValValLysTrpGlnSer 360
 Db 1031 TGCATTGAGTCAATGAGGCTCGCTGCTGAGACCACTAGTGTGAAGTGGCAAGC 1090
 QY 361 SerAlaLeuAspValAsnThrTrpMetLLeGluTrpPheProAspValAspSerGluPro 380
 Db 1091 TCTGCTCTAGAGGTGAACCTTGATGATGATGATGATGATGATGATGATGATGATGATGAT 1150
 QY 381 ThrThrLeuSerTrpGluSerValSerGlnAlaThrAsnTrpThrLLeGlnGluAspLys 400
 Db 1151 ACCACCTTTCCTGGGAATCTGTCTCAGGCCACAGACTGACATCCAGCAAGATAAA 1210
 QY 401 LeuLysProPheTrpCybTyrAsnLLeSerValTyrProMetLeuHisAspLysValGly 420
 Db 1211 TTTAAACCTTTCTGGGCTCTTAACATCTGTGTATCCATGTGATGATGATGATGATGATGAT 1270
 QY 421 GluProTyrSerLLeGlnAlaTyrAlaLysGluGlyValProSerGluGlyProGluThr 440
 Db 1271 GAGCCATATTCATCCAGGCTTATGCGCAAGAGGGCTTCCATCAGAAAGTCCCTGAGACC 1330
 QY 441 LysValGluAsnLLeGlyValLysThrValLLeThrTrpLysGluLLeProLysSer 460
 Db 1331 AAGGTGAAGAAATGGCGGTGAAGAGGTGACAGATCAATGAAAGATTTCCCAAGAGT 1390
 QY 461 GluArgLysGlyLLeLLeCybAsnTyrThrLLePheTyrGlnAlaGluGlyLysGly 480
 Db 1391 GAGAGAAAGGTATCTACTCTGCAACTACACACTTTTACCAAGCTGAAAGTGAAGAAAGCA 1450
 QY 481 PheSerLysThrValAsnSerSerLLeLeuGlnTyrGlyLeuGluSerLeuLysArgLys 500
 Db 1451 TTCTCCAGACAGTCAATTCAGACATCTTGACAGTACGGCTGGAGTCCCTGAAACCAAAAG 1510
 QY 501 ThrSerTyrLLeValGlnAlaMetLLeSerThrSerAlaGlyGlyThrAsnGlyThrSer 520
 Db 1511 ACCTTTACATTGTTCAAGTCAATGGCCAGCACAGTGTGGGGGAAACCAACGGGACCGAC 1570
 QY 521 LLeAsnPheLysThrLeuSerPheSerValPheGluLLeLLeLeuLLeThrSerLeuLLe 540
 Db 1571 ATTAATTTCAAGACATTTGATTCATCACTGATGCTTTGAGATTTATCTCTCAATCTTCGATT 1630
 QY 541 GlyGlyGlyLeuLeuLLeLeuLLeLLeLeuThrValAlaTyrGlyLeuLysLysProAsn 560
 Db 1631 GGTGAGGCTCTTATTTCTCATTTCTGACAGATGAGTGTGCTCAAAAAACCAAC 1690
 QY 561 LysLeuThrHisLeuCybTrpProThrValProAsnProAlaGluSerSerLLeAlaThr 580
 Db 1691 AAATTGACTCATCTGTGTGGCCACCGTTCCCAACCTGTGAAAGTGTATGACCA 1750
 QY 581 TrpHisGlyAspAspPheLysAspLysLeuAsnLeuLysGlyLysSerAspSerValAsn 600
 Db 1751 TGGCATGAGATGATTTCAAGATTAAGCTTAACCTGAAGAGTGTGATGATCTGTGAAC 1810
 QY 601 ThrGluAspArgLLeLeuLysProCybSerThrProSerAspLysLeuValLLeAspLys 620
 Db 1811 ACAGAAAGAGATCTTAATAACATGTTCCACCCCAAGTGAAGCAAGTGTGATGATGATGATGAT 1870
 QY 621 LeuValValAsnPheGlyAsnValLeuGlnGlnLLePheThrAspGluLLeArgThrArgLys 640
 Db 1871 TTGGTGTGTAACCTTTGGGATGTCTGCAAGAAATTTTCAAGATGAAGCCAGAAACGGGT 1930

Qy 641 GINGUAENASnLeuG1Yc1Yg1u1yBaenG1YThrArg1LeuSerSerCysPProThr 660
| | | | |
Db 1931 CAGGAAACAAATTTAGAGGAGGAAAAAGATGGAGCTAGAAATCTGCTTCTGCGCAACT 1990
| | | | |
Qy 661 Serile 662
| | | | |
Db 1991 TCAATA 1996
| | | | |
RESULT 2
US-09-892-949-53
; Sequence 53, Application US/09892949
; Publication No. US20030096339A1
; GENERAL INFORMATION:
; APPLICANT: Sprecher, Cindy A.
; APPLICANT: Presnell, Scott R.
; APPLICANT: Gao, Zeren
; APPLICANT: Whitmore, Theodore E.
; APPLICANT: Kujper, Joseph L.
; APPLICANT: Maurer, Mark F.
; TITLE OF INVENTION: CYTOKINE RECEPTOR ZCYTOR17
; FILE REFERENCE: 00-42
; CURRENT APPLICATION NUMBER: US/09/892,949
; CURRENT FILING DATE: 2001-06-26
; PRIOR APPLICATION NUMBER: US 60/214,282
; PRIOR FILING DATE: 2000-06-26
; PRIOR APPLICATION NUMBER: US 60/214,955
; PRIOR FILING DATE: 2000-06-29
; PRIOR APPLICATION NUMBER: US 60/267,963
; NUMBER OF SEQ ID NOS: 93
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 53
; LENGTH: 2903
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (497)...(2482)
US-09-892-949-53
Alignment Scores:
Pred. No.: 0 Length: 2903
Score: 3528.00 Matches: 662
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
Gaps: 0
US-10-006-265-17 (1-662) x US-09-892-949-53 (1-2903)
Qy 1 MetLysLeuSerProGlnProSerCysValAsnLeuGlyMetMetTrpThrTrpAlaLeu 20
| | | | |
Db 497 ATGAAGCTCTCTCCACACCTTCATGTGTAACTGGGAGATGATGTGACCTGGGACACTG 556
| | | | |
Qy 21 TrpMetLeuProSerLeuCysLysPheSerLeuAlaLeuProAlaLeuProGlu 40
| | | | |
Db 557 TGGATGCTCCCTTCACTCTGCAAAATTCAGCCGCGAGCTCTGCCAGCTAAGCTTGAAGC 616
| | | | |
Qy 41 LLeuSerCysValYrTYrTYrArgLysAsnLeuThrCysThrTrpSerProGlyLysGlu 60
| | | | |
Db 617 ATTTCCTGTGTCTACTACTATAGGAAAAATTTAACTGCACCTTGAAGTCCAGAAAGAA 676
| | | | |
Qy 61 ThreSerYrThrGlnTYrTYrValLysArgThrTYrAlaPheGlyGluLysHisAspAsn 80
| | | | |
Db 677 ACCAGTTTACCCTGACACAGTTTAAAGAACTTTCGCTTTTGGGAAAAACATGATATAT 736
| | | | |
Qy 81 CysThrTrpAsnSerSerThreSerGluAsnArgAlaSerCysSerPhePheLeuProArg 100
| | | | |
Db 737 TGTACACCAATAGTCTTCAACAGTAAATCTGCTGTGCTTTTCTTCTTCAAGA 796
| | | | |
Qy 101 LLeuThrLLeuProAspAsnTYrThrLLeuGluValGluAsnGlyAspGlyValLLeu 120
| | | | |
Db 797 ATTAAGATCCCAAGATTAATTAATACATTTAGGTGGAAGCTGAAATGGAAGTGTATAT 856
| | | | |

Qy 121 LysSerHisMetThrTYrTrpArgLeuGluAsnLLeuAlaLysThrGluProProLysLLeu 140
| | | | |
Db 857 AAATCTCATATGACATCTACTAGAGATTAGAAACATAGGAAAACTGAACCACTTAAGATT 916
| | | | |
Qy 141 PheArgValLysProValLeuGlyLLeuLysArgMetLLeuLLeuGluTrpLLeuLysPro 160
| | | | |
Db 917 TTCCGTGTGAACCAAGTTTGGGATCCAAAGAAATGATTCAAAATTTGAATGAATAAGCTT 976
| | | | |
Qy 161 GluLeuAlaProValSerSerAspLeuLysTYrThrLeuArgPheArgThrValAsnSer 180
| | | | |
Db 977 GAGTTGGCGCCGTGTTTCATCTGATTTAAATACACACTTCATTCAGGACAGTCAACAGT 1036
| | | | |
Qy 181 ThrSerTrpMetGluValAsnPheAlaLysPheArgLysAspLysAsnGlyThrTYrAsn 200
| | | | |
Db 1037 ACCAGCTGATGAAGTAACTGCTGTAAGAACGTAAGATTAATAACCAACGTAACAC 1096
| | | | |
Qy 201 LeuThrGlyLeuGlnProPheThrGluTYrValLLeuAlaLeuArgCysAlaValLysGlu 220
| | | | |
Db 1097 CTCACGGGGCTGCACTTTTACAGAAATATGTCATAGCTTGCAGATGTGCGGTCAAGAG 1156
| | | | |
Qy 221 SerLysPheTrpSerAspTrpSerGlnGluLysMetGlyMetThrGluGluGluAlaPro 240
| | | | |
Db 1157 TCAAAATTCTGAGAGTGAAGAGCCAAAGAAAAATGGGAATGACTGAGGAAGAGCTCCA 1216
| | | | |
Qy 241 CysGlyLeuGluLeuTrpArgValLeuLysProAlaGluAlaAspGlyArgArgProVal 260
| | | | |
Db 1217 TGTGGCTGTGAACGTGTGAAGTCTCTTAACCACTGAGGCGAGTGAAGAGGCAAGTGTG 1276
| | | | |
Qy 261 ArgLeuLeuTrpLysValArgGlyValaProValLeuGluLysThrLeuGlyTYrAsn 280
| | | | |
Db 1277 CGGTGTTATGGAAGAAAGCAAGAGAGCCCAAGTCCAGAAACAACTTGCTGCTACAAAC 1336
| | | | |
Qy 281 LLeuTYrTYrProGluSerAsnThrAsnLeuThrGluThrMetAsnThrThrAsnGln 300
| | | | |
Db 1337 ATATGTACTACTACCAAGAAAGCAACACTAACCTCAGAAACAAATGAACATACTAACAG 1396
| | | | |
Qy 301 GlnLeuGluLeuHisLeuGlyGlyGluSerPheTrpValSerMetLLeuSerTYrAsnSer 320
| | | | |
Db 1397 CAGCTTGAACGTCACTGGAGGCGAAGCTTTTGGGTGTGTATGATTTCTTAATAATCT 1456
| | | | |
Qy 321 LeuGlyLysSerProValAlaThrLeuArgLLeuProAlaLLeuGlnLysSerPheGln 340
| | | | |
Db 1457 CTGGGAAGTCTCCAGTGGCCACCTGAGAGTTTCCAGCTATTCAAAGAAAAATCATTTGAG 1516
| | | | |
Qy 341 CysLLeuGluValMetGlnAlaCysValAlaGluAspGlnLeuValLysTrpGlnSer 360
| | | | |
Db 1517 TGCATTGAGGTCAATGCAAGGCTGCGTTGCTGAGGACCAAGTATGTGAAGTGGCAAGC 1576
| | | | |
Qy 361 SerAlaLeuAspValAsnThrTrpMetLLeuLLeuTrpPheProAspValAspSerGluPro 380
| | | | |
Db 1577 TCTGCTTACAGCGTAACACTTGATGATTAAGTTTCCGGAATGTGGACTCAGAGCC 1636
| | | | |
Qy 381 ThrThrLeuSerTrpGluSerValSerGlnAlaThrAsnTrpThrLLeuGlnLAspLys 400
| | | | |
Db 1637 ACCACCTTTCTGGGAATCTGTCTCTCAGGCCAGAACTGAGATCCAGCAAGATATAA 1696
| | | | |
Qy 401 LeuLysProPheTrpCysTYrAsnLLeuSerValTYrProMetLeuHisAspLysValGly 420
| | | | |
Db 1697 TTAACACCTTTCTGTGCTATTAACATCTGTGATCAATGTTGATGACAAAGTTGGC 1756
| | | | |
Qy 421 GluProTYrSerLLeuGlnAlaTYrAlaLysGluGlyValaProSerGluGlyProGluThr 440
| | | | |
Db 1757 GAGCCATATTCACATCCAGGCTTAATGCAAAAGAGCGTTCATAGAAAGTCTGAGAGCC 1816
| | | | |
Qy 441 LysValGluAsnLLeuGlyValLysThrValThrLLeuTrpLysGluLLeuProLysSer 460
| | | | |
Db 1817 AAGGTGAAGAACTTGGCGTGAACAGCTCACATCACTGAAAGAGATTCCCAAGAGT 1876
| | | | |
Qy 461 GluArgLysGlyLLeuLLeuCysAsnTYrThrLLeuPheTYrGlnAlaGluGlyLysGly 480
| | | | |
Db 1877 GAGAGAAAGGTATCATCTGCACTCAACCATTTTAACCAAGCTGAAGGTGGAAGAAAGGA 1936
| | | | |

Qy	481	PheserYsThrValaenSesSerileuengInYrGlyLeuGUsrLeuLyAsPrlys	500
Db	1937	TTCTCCAGACAGATGCATTTCCAGCATCTTGACGTAAGCCCTCGAGATCCCTTAACGAAAG	1996
Qy	501	ThsSerYrIleValaGlnValaMeaLaserThsSerIaGlyGlyThrsAnGlyThsSer	520
Db	1997	ACCTCTTAACATGTTCAAGGTCATGAGCCACGACCAAGTGCTGGGGGAACCAACGGGACGAC	2056
Qy	521	IlAsenPelysThrLeuSerPheserValaPheGUnlelleleuIleThsSerLeuIle	540
Db	2057	ATAAATTTCAAGACATGTCATTCAGGTCTTTGAGATATCCCATNAACCTTCTCGATT	2116
Qy	541	GlyGlyGlyLeuLeuIleleuIleIleleuThrValaIaYrGlyLeuLyAsProAn	560
Db	2117	GGTGGAGGCCCTCTTATATCTCATTAATCCTGACAGTGGCATGTGGCTCAAAAAACCCAC	2176
Qy	561	LysLeuThrHisLeuCySTrPProThrValaProAnPoaIaGUsrSerIleAlaThr	580
Db	2177	AAATTTGACTCATCTGTGTGTGGCCCAACCCGTCGCCAACCTGCTGAAGATGATGCCACA	2236
Qy	581	TrpHisGlyAspAspPheLyAspLyLeuAnmLeuLyGUsrAspAspSerValaAn	600
Db	2237	TGGCATGAGATGATTTTCAGAGATAGCTTAACCTGGAAGGCTCTGATGACTCTGTGAAC	2296
Qy	601	ThrsIuAsPaRgIleLeuLySProCySerThrProSerAspLySLeuValIleAsPrlys	620
Db	2297	ACAGAAAGCAGATGCTTTAAACCATGTTGCCACCCCACTGACAGATGCTGATTGACAAAG	2356
Qy	621	LeuValValaAnPheGlyAsnValaLeuGlnIuIlePheThrAspGUnIaIaGThrGly	640
Db	2357	TTGTGTGGGAATCTTGGGAATGTTCTGCAAAATAATTTTCACAGATGAAGAACCAAGACGGGT	2416
Qy	641	GlnIuAsnAenLeuGlyGlyGlyLyAsnGlyThrsArgIleLeuSerSerCySProThr	660
Db	2417	CAGAAAAACATTTTAGAGGAGGGAAGAAATGGAGCTAGAAATTCGTCTCTGCCCACT	2476
Qy	661	SerIle 662	
Db	2477	TCAATA 2482	
RESULT 3			
US-10-351-157-4			
Sequence 4, Application US/10351157			
Publication No. US20030215838A1			
GENERAL INFORMATION:			
APPLICANT: Sprecher, Cindy A.			
APPLICANT: Gao, Zeren			
APPLICANT: Kujper, Joseph L.			
APPLICANT: Dasovich, Maria M.			
APPLICANT: Grant, Francis J.			
APPLICANT: Presnell, Scott R.			
APPLICANT: Whitmore, Theodore E.			
APPLICANT: Hammond, Angela K.			
APPLICANT: No. US20030215838A1ak, Julia E.			
APPLICANT: Gross, Jane A.			
APPLICANT: Dillon, Stacey R.			
TITLE OF INVENTION: CYTOKINE RECEPTOR ZCYTOR17 MULTIMERS			
FILE REFERENCE: 02-02			
CURRENT APPLICATION NUMBER: US/10/351,157			
CURRENT FILING DATE: 2003-01-21			
PRIOR APPLICATION NUMBER: US 60/435,361			
PRIOR FILING DATE: 2002-12-19			
PRIOR APPLICATION NUMBER: US 60/389,108			
PRIOR FILING DATE: 2002-06-14			
PRIOR APPLICATION NUMBER: US 60/350,325			
PRIOR FILING DATE: 2002-01-18			
NUMBER OF SEQ ID NOS: 183			
SOFTWARE: FastSeq for Windows Version 4.0			
SEQ ID NO 4			
LENGTH: 2903			
TYPE: DNA			
ORGANISM: Homo sapiens			
FEATURE:			

:	NAME/KEY:	CDS
:	LOCATION:	(497)...(2482)
US-10-351-157-4		
 Alignment Scores:		
Pred. No.:	0	Length: 2903
Score:	3528.00	Matches: 662
Percent Similarity:	100.00%	Conservative: 0
Best Local Similarity:	100.00%	Mismatches: 0
Query Match:	100.00%	Indels: 0
DB:	17	Gaps: 0
US-10-006-265-17 (1-662) x US-10-351-157-4 (1-2903)		
OY	1 MetIysLeuSerP-roGInP-roSeR-CyValAsnLeuGIyMeTTrpThrAlaLeu	20
Dd	497 ATGAAGCTCTCTCCCAAGCCTTCATGTGTAACTGGAGGATGATGACCTGGCACTG	556
OY	21 TrpMetLeuProSerLeuCySLysPheSerLeuAlaLeuProAlaLysProGIuaSn	40
Dd	557 TGGATTGCCTCCCTTACTCTCGAATAATTACGCTGGCACTCTGCCAGCTTAAGCCTGAAC	616
OY	41 ILeserCySValTYrTYrFargLYsAsnLeuThrcYSthrTriPser-ProGLyVSGlu	60
Dd	617 ATTTCCTGTGCTACTACTATAGAAAAAATTTAACCGCACTGGACTCCAGGAAGAAGAA	676
OY	61 ThrseryTrpThrGIuTYrThrValLyArgThrTYrAlaPheGIuLYSH;ASPAsn	80
Dd	677 ACCAGTTATACCAGTACACAGATTAAAGAACTTACGCTTTTGAGAAAACAATGATAT	736
OY	81 CystrThrAnSerSerThrSerGIuAsnArgALasercYsserPhePheLeuProArg	100
Dd	737 TGTCACACCAATAGTCTTACAAAGTAAACCTGGCTTCGTCTCTTTTCCCTTCCAAGA	796
OY	101 ILehrtLIeP-roASpAenTYrThrLIaGIuValGIuAlaGIuSenGIyaSPGIValILE	120
Dd	797 ATAACGATCCCAGATATTTATACCATTAGAGGTGAGACCTGAAAATGGAGATGGTAAAT	856
OY	121 LysSerHisMetThrTYrTParGLEuGIuAsnIIeaIalystHrgIuProProlysILE	140
Dd	857 AAATCTCATNTGACATATCTGGAGATTAGAGAACATACGAAACCTGAACCACTTAAGATT	916
OY	141 PheaArgValLysP-roValleuGLyILEyArqMetILEgNIleGIuTPILelysPro	160
Dd	917 TTCGGTGTGAACCAAGATTTGGGGCATMAACGAATGATTCAMATGATGATTAACCT	976
OY	161 GIuLeuAlaP-roVALSerSerASPLeuLYSTyrThrLeuArgPheArgThrValAsnSer	180
Dd	977 GAGTTGGCGGCTGTTTCATCTGATTTAAATATACACTTCGATTACGACAGCTAACAGT	1036
OY	181 ThrSerTrpMetGIuAlaasnPheAlaLYsaSnArgLYsApLYsaSnGIntHrTYrAsn	200
Dd	1037 ACCAGCTGGATGGAAGTCAACTTGGCTPAGAACCGTAAAGATTAATAAACCAACCTAAC	1096
OY	201 LeuHrGIyLeuGInP-roPheThrcGIuTYrValIIeAlaLeuArgCySAIaValLySGlu	220
Dd	1097 CTCACGGGGCGTGCACCTTTTACGAATATGTCACTACTCTGCGATGGCGGTAAAGAG	1156
OY	221 SerIysPheTriPserASPTrPserGIuGIuLYsMetGIyMetThrGIuGIuAlaPro	240
Dd	1157 TCAAAGTTCTTGGATGACTGGAGCCCAAGAAAAATGGGAATGACTGAGGAAGAAGCTCCA	1216
OY	241 CysGLyLeuGIuLeuTPARgValLeuLYsProAlaGIuAlaaSpGIyaArgP-roVal	260
Dd	1217 TGTGGCCTCGGAACGTGGAGAGTCTTAAACCAAGCTAGGCGGATGGAAAGAAGGCCAGTG	1276
OY	261 ArgLeuLeuTPryLSySaIaArgVALAProValLeuGIuYsrThrLeuGLITYrAsn	280
Dd	1277 CGGTTGTTATGGAAGAAGCCAGAGAGGCCCACTCTTAAGAAAAACACTTGCTTAACA	1336
OY	281 IleTPryTYrProGIuSerAsnThrAsnLeuThrGIuThrMetAsnThrThrAsnGIu	300
Dd	1337 ATATGATGATCATTCAGAAAGCAACATCTACCTCACAAACAAATGAACATCACTAACAG	1396

QY	301	GINLEUGIULNEHISLEUGIYGLYGLUSERPHETRPVALSERMELISERTYRANSEN	320
Db	1397	CAGCTTGAACTGCACATCGGAGGCGCAGAGCTTTGGGTCGTATGATATTTCTATATATCTT	1456
QY	321	LEUGIYLSERPROVALATHIRLEUKYGLIEPROVALIEGINGLUDYSERPHEGIN	340
Db	1457	CTTGGAAGTCTCCAGTGGCCACCCTGAGGATTCAGACGATTCAGAAAATCATTTCCAG	1511
QY	341	CYBIIIEGLUVALMERGLINALCYVALAGIUAERGINLEUVALIYSTRPGLINER	360
Db	1517	TGCATTGAGGTCATGACAGCCCTGCCTGTGAGACCGACTAGTGTGMAAGCGMAAGC	1576
QY	361	SERIALAUAERVALASMTHTTRPHECTIEGILUTRPHEPROAERVALASERGIUPRO	380
Db	1577	TCTGCTCTAGACGTGACACCTTGATGATGATTAATGATTTCCGAGTGTGACTCAAGACC	1633
QY	381	THRTHLEUSERTRIPGLUSERVALSERGINALATHANSTRPTHIEGININAPLYS	400
Db	1637	ACCACCCCTTCTCGTGGGAATCTGTGCTCAGGCCGAACTGGACGATCCAGCAATATAA	1696
QY	401	LEULYSPROPHETTRPCYSTRANMISEERVALTYRPROMETLEHISAPRYSPALGILY	420
Db	1697	TTAAACCTTTCTGTGCTATTAACACTCTGTGTATCCAAATGTTCAATGACAAATTTGGC	1756
QY	421	GLUPROTYRSERIEGINALATYRVALSPYSGIUYVALPROSERGIUGIYPROGLUTHR	440
Db	1757	GAGCATATTCATCCATCAGGCTTAATGCCAAAGAGCGTTCCATCAGAAAGTCTTAGACC	1811
QY	441	LYSVALGIUANMIEGLIYVALIYSTRYVALTHRIETHTRPLYEGLUILEPROLYSER	460
Db	1817	AAGGTGGGAACATTTGGCGTGMAAGCGGTCCAGATCAATGMAAGAGATTTCCAAAGAT	1876
QY	461	GLUARGLYSGIYIEILECYASMTYRTHRIIEPETHYRGINALIGIUGIYGLYSGIY	480
Db	1877	GAGGAAAGGATATCATCTGCACATCAACCATTTTACCAAGCTGMAAGTGGAAAAGGA	1933
QY	481	PHESERYTRHVALASNSERSERIIELEUGINTYRGILEUGIUSERIEULYSPRYYS	500
Db	1937	TTCTCCAAAGACATGCAATTTCCAGCATCTTGACATCGGCTGGAATGCCCTGAAACGAAG	1996
QY	501	THREERTYRILEVALGINVALMERLASEERTHSERIALGIYGLYTHRANGIYTHSER	520
Db	1997	ACCTCTTACATTTGTCAGTCAATGGCCAGCACCACTGTGGGGAAACCAACGGACCAAC	2056
QY	521	ILEASNPELYSTRLEUSERPHESEVALPHEGIUIEILELEUIETHERSERLEUIE	540
Db	2057	ATTAATTTCCAGACATTTGCTCATCTCACTGCTTTGATGATTAATTCCTATTAATCTTGATT	2116
QY	541	GLIYGLIYLEULEUIEILEUIEILELEUTHRVALATYRGILEULYSYLEPROASN	560
Db	2117	GGTGAGGCTCTTCTTATCTCATTTATCTGTGACAGTGGCATGTGCTCAAAAAAACCCAAC	2176
QY	561	LYSELEUTHRHSLEUCYSTRIPROTHRALPROANPROALAGUSERSERIIELEATHR	580
Db	2177	AAATTTGACTCATCTGTGTGTGGCCACCGTTCCCAACCTGTGAAAGTAGTATCCACA	2233
QY	581	TRPHISGLIYASERPHELYASPLYLEUASNLEULYSGIUSERASERVALASN	600
Db	2237	TGCGATGGAGATGATTTCCAGGATTAAGCTTAAACCTGAAGGAGTGTGATGACTGTGAAAC	2296
QY	601	THRTGLUAPRAGIILEULIYSPROCYSEERTHRPROSERASPLYLEUVALIIEAPLYS	620
Db	2297	ACAGAAAGCAGAGATTTTAAACCAATTTCCACCCCACTGACAAATTTGTATGTGACAAG	2356
QY	621	LEUVALVALASNPHEGIYASNVALIEUGINGIUIIEPETHRASPGIUALASRTHRGLY	640
Db	2357	TTGGTGGTGAACTTTGGGAAATGTTCTGCAGAAATTTTCACAGATGAAGCCAGAACGGGT	2416
QY	641	GINGLUASNANLEUGIYGLIYULYASNGIYTHRAGIILEUSERSERCYSPROTHR	660
Db	2417	CAGGAAACAAATTTAGAGGGGAAAGATGGGACTGAATATTCGTCTTCTCGCCCAACT	2476

QY	661	Seqfile 662	
Db	2477	TCMAAT 2482	
		RESULT 4	
		US-10-352-554-4	
		/ Sequence 4, Application US/10352554	
		/ Publication No. US20030224487A1	
		GENERAL INFORMATION:	
		/ APPLICANT: Sprecher, Cindy A.	
		/ APPLICANT: Kuiper, Joseph L.	
		/ APPLICANT: Dasovich, Maria M.	
		/ APPLICANT: Grant, Francis J.	
		/ APPLICANT: Hammond, Angela K.	
		/ APPLICANT: Novak, Julia E.	
		/ APPLICANT: Gross, Jane A.	
		/ APPLICANT: Dillon, Stacey R.	
		/ TITLE OF INVENTION: NOVEL CYTOKINE ZCYTOR17 LIGAND	
		/ FILE REFERENCE: 02-01	
		/ CURRENT APPLICATION NUMBER: US/10/352,554	
		/ CURRENT FILING DATE: 2003-01-21	
		/ PRIOR APPLICATION NUMBER: US 60/350,325	
		/ PRIOR FILING DATE: 2002-01-18	
		/ PRIOR APPLICATION NUMBER: US 60/375,323	
		/ PRIOR FILING DATE: 2002-04-25	
		/ PRIOR APPLICATION NUMBER: US 60/435,315	
		/ PRIOR FILING DATE: 2002-12-19	
		/ NUMBER OF SEQ ID NOS: 168	
		/ SOFTWARE: FastSeq for Windows Version 3.0	
		/ SEQ ID NO 4	
		/ LENGTH: 2903	
		/ TYPE: DNA	
		/ ORGANISM: Homo sapiens	
		/ FEATURE:	
		/ NAME/KEY: CDS	
		/ LOCATION: (497)...(2482)	
		US-10-352-554-4	
		Alignment Scores:	
		Pred. No.: 0	Length: 2903
		Score: 3528.00	Matches: 662
		Percent Similarity: 100.00%	Conservative: 0
		Best Local Similarity: 100.00%	Mismatches: 0
		Query Match: 100.00%	Indels: 0
		DB: 17	Gaps: 0
		US-10-006-265-17 (1-662) x US-10-352-554-4 (1-2903)	
QY	1	MethylSeuSerProGlnProSerCysValaIenLeuGlyMetNetrThrTPalaleu 20	
Db	497	ATGAAGCTCTCTCCCCAGCCTTCATGTGTAACTGGGATGATGTGAGCACTGGCACTG 556	
QY	21	TrpMetLeuProSerLeuCysAluBheSerLeuAlaLeuProAlaLysProGluAen 40	
Db	557	TGGAGTCCCTCTCACTCGCAAAATTCACCTGGCAGCTCTGCACACTAAGCCTGAGAAC 616	
QY	41	IleSerCysValTyrTyrTyrArgTysAenLeuThrCysThrTrpSerProGlyLysGlu 60	
Db	617	ATTTCCTGTGTACTACTCATATGAAAAATTTAACTGCACCTTGAGCTCCAGAAAGGAA 676	
QY	61	ThrSerTyrThrGlnTyrThrValLysArgThrTyrAlaPheGlyGluLysHisAepAen 80	
Db	677	ACCAAGTTAAACCAAGTACAGATTAAAGAACTTACGCTTTGGAGAAAAACATGATAT 736	
QY	81	CysThrThrAenSerSerThrsSerGluAenAlaSerCysSerPheLeuProArg 100	
Db	737	TGTAAACCAAAAGTTCTCAACAAGTAAATCTGTGCTCTTTTTCCTTCCAAAGA 796	
QY	101	IleThrIleProAspAsnTyrThrIleGluValGluAlaGluLysGlyValIle 120	
Db	797	ATAACGATCCCAAGATATTTATTCATTGAGCTGGAGAACTGAAAATGAGATGATATT 856	
QY	121	LysSerHisMetThrTyrTrpArgLeuGluAenIleAlaLysThrGluProLysIle 140	

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Db      857  AAATCTCATGTAGACATATCGAGATTAGAGAAACATAGCGAAACCTAGGATT 916
Qy      141  PhaaArgVallySerProValLeuGlyIlelyAspMetIleGlnIleGluTyrPileysPro 160
Db      917  TTCGGTGTAAACACAGTTTGGGCATCAACGAAATGATTCAATATGATGATGAAAGCC 976
Qy      161  GluLeuAlaProValSerSerAspLeuLeuYrThrLeuArgPheArgThrValAsnSer 180
Db      977  GAGTTGGCGCTTTCATCTGATTTTAAATACACACTTCGATTCAGAGACAGTCACAG 1036
Qy      181  ThrSerTrpMetGluValAsnPheAlaYAsnArgYAspIlyAsnGlnThrYrAsn 200
Db      1037  ACCAGCTGAGTGAATGCAACTTCGCTAAGAACCGTAAGATGATGATGATGATGATG 1096
Qy      201  LeuThrGlyLeuGlnInProPheThrGluYrValIleAlaLeuArgCysAlaValIlyGlu 220
Db      1097  CTCACGGGGCTGAGCCCTTTTACAGAAATGTCATAGCTTCGCAATGTGGCTCAAGAG 1156
Qy      221  SerIlyPheTrpSerAspTrpSerGlnGluYMetThrGluGluGluAlaPro 240
Db      1157  TCAAATTTCTCGAGTGTACTGAGCCCAAGAAATGGGAATGACTGAGAGAAAGACTCCA 1216
Qy      241  CysGlyLeuGluLeuTrpArgValIleuYsProAlaGluAlaAspGlyArgArgProVal 260
Db      1217  TGTGGCCTGGAACCTGAGAGAGTCTGAAACACAGCTGAGGCGGATGGAAGAGCCAGTG 1276
Qy      261  ArgLeuLeuTrpIlySerIlyAsnArgGlyAlaProValLeuGluYrThrLeuGlyYrAsn 280
Db      1277  CGGTGTGTATGAGAGAGGAGGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1336
Qy      281  IletTrpYrTrpProGluSerAsnThrAsnLeuThrGluThrMetAsnThrTrpAsnGln 300
Db      1337  ATATGTACTATCTCAGAAAGCAACACTAATCTCAGAAAGCAATGAACTACTAATCCAG 1396
Qy      301  GlnLeuGluLeuHisLeuGlyIlyGluSerPheTrpValSerMetIleSerYrAsnSer 320
Db      1397  CAGCTTGAACCTGCATCTGGAGGCGGAGAGCTTTGGGTGTCTATGATTTCTTAATTC 1456
Qy      321  LeuGlyIlySerProValAlaThrLeuArgIleProAlaIleGlnGluYrSerPheGln 340
Db      1457  CTTGGAGAGCTCCAGTGGCCACCTGAGAGATTCCAGCTATTTCAAGAAATATATTTCA 1516
Qy      341  CysIleGluValMetGlnAlaCysValAlaGluAspGlnLeuValIlyTrpGlnSer 360
Db      1517  TGCATTGAGGTCTATGACAGGCTCTGCTTCGTCGAGAGACCACTATGCTGAAGTGGCAA 1576
Qy      361  SerAlaLeuAspValAsnThrTrpMetIleGluTrpPheProAspValAspSerGluPro 380
Db      1577  TCTGCTCTAGACGCTGAACACTTGATGATGATGATGATGATGATGATGATGATGATG 1636
Qy      381  ThrThrLeuSerTrpGluSerValSerGlnAlaThrAsnTrpThrIleGlnGlnAspIly 400
Db      1637  ACCACCCCTTCCCGGAAATCTGTCTCAGGCCACAGACGAGTCGACGATCCGCAAGATAA 1696
Qy      401  LeuIlyProPheTrpCysIlyrAsnIleSerValYrProMetLeuHisAspIlyValGly 420
Db      1697  TTAAACCTTTCGTGGCTATTAACATCTCTGTGTATCCAAATGTTGATGACAAAGTTGG 1756
Qy      421  GluProYrSerIleGlnAlaYrAlaYleGluGlyValProSerGluGlyProGluThr 440
Db      1757  GAGCCATATTCATCCACAGGCTTATGCCAAAGAGGCTTCATCAGAGGCTCTGAGACC 1816
Qy      441  IlyValGluAsnIleGlyValIlySerValThrIleThrTrpIlySerGluIleProIlySer 460
Db      1817  AAGGTGAAGAACTTGGCGGTGAAGACGTCACATCACAAGAAAGATTTCCCAAGAGT 1876
Qy      461  GluArgIlyGlyIleIleCysAsnYrThrIlePheTrpGlnAlaGluGlyIlyGly 480
Db      1877  GAGAGAAAGGTATCATCTGCACTACACCATCTTTTACCAAGCTGAGGTGAGAAAGGA 1936
Qy      481  PheSerIlyThrValAsnSerSerIleLeuGlnYrGlyLeuGluSerLeuYsArgIly 500

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Db      1937  TTCTCCAGACAGCATATTCAGACATCTTGACATCGGCGCTGAGTCCCTGAAACGAAAG 1996
Qy      501  ThrSerTrpIleValGlnValMetAlaSerTrpSerAlaGlyIlyThrAsnGlyThrSer 520
Db      1997  ACCTCTTACATTTGTCAGGTCAATGGCCAGACACAGGCTGGAGGAAACCAAGGACAC 2056
Qy      521  IleAsnPheIlyThrLeuSerPheSerValPheGluIleIleLeuIleThrSerLeuIle 540
Db      2057  ATTAATTTCAAGCATTGTCATTGACGTGTCTTGAGATTATCTGTAACTTCTTGATT 2116
Qy      541  GlyIlyGlyLeuLeuIleLeuIleIleLeuThrValAlaYrGlyLeuIlySlyProAsn 560
Db      2117  GGTGGAGGCTTCTTATTTCTATTTCTTCAATGTCGACAGTGGCATATGTCTCAAAAA 2176
Qy      561  IlyLeuThrHisLeuCysTrpProThrValProAsnProAlaGluSerSerIleAlaThr 580
Db      2177  AAATGTACTATCTGTGTGGCCACCGTTCACCACTCTGCAAGTGTGATGATGATGATG 2236
Qy      581  TrpHisGlyAspAspPheIlyAspIlySleuAsnLeuYsGluSerAspAspSerValAsn 600
Db      2237  TGGCATGAGAGATTTTCAAGGATTAAGCTAAACCTGAAAGAGTCTGATGATGATG 2296
Qy      601  ThrGluAspArgIleLeuIlyProCysSerThrProSerAspIlyLeuValIleAspIly 620
Db      2297  ACAGAAAGACAGATCTTAAACCATGTCTCACCCCAAGTGAAGTGTGATGATGATG 2356
Qy      621  LeuValValAsnPheGlyAsnValIleuGlnIlePheThrAspGluAlaArgThrGly 640
Db      2357  TTGGTGTGTAACCTTGGGAATGTTCTGCAAGAAATTTTACAGATGAAACCGAGAGG 2416
Qy      641  GlnGluAsnAsnLeuGlyIlyGlyIlySlyAsnGlyThrArgIleLeuSerSerCysProThr 660
Db      2417  CAGGAAACAAATTTGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 2476
Qy      661  SerIle 662
Db      2477  TCATA 2482

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RESULT 5

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US-10-772-531-53
; Sequence 53, Application US/10772531
; Publication No. US2004014242A1
; GENERAL INFORMATION:
; APPLICANT: Sprecher, Cindy A.
; APPLICANT: Preenell, Scott R.
; APPLICANT: Gao, Zeren
; APPLICANT: Whitmore, Theodore E.
; APPLICANT: Kuljper, Joseph L.
; APPLICANT: Maurer, Mark F.
; TITLE OF INVENTION: CYTOKINE RECEPTOR ZCYTOR17
; FILE REFERENCE: 00-42
; CURRENT APPLICATION NUMBER: US/10/772, 531
; CURRENT FILING DATE: 2004-02-05
; PRIOR APPLICATION NUMBER: US/09/892, 949
; PRIOR FILING DATE: 2001-06-26
; PRIOR APPLICATION NUMBER: US 60/214, 282
; PRIOR FILING DATE: 2000-06-26
; PRIOR APPLICATION NUMBER: US 60/214, 955
; PRIOR FILING DATE: 2000-06-29
; PRIOR APPLICATION NUMBER: US 60/267, 963
; PRIOR FILING DATE: 2001-08-02
; NUMBER OF SEQ ID NOS: 93
; SOFTWARE: PaateSeq for Windows Version 3.0
; SEQ ID NO 53
; LENGTH: 2903
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (497) ... (2482)
US-10-772-531-53
Alignment Scores:

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Pred. No.: 0 Length: 2903
 Score: 3528.00 Matches: 662
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 Gaps: 0

US-10-006-265-17 (1-662) x US-10-772-531-53 (1-2903)

QY 1 MetLysLeuSerProGlnProSerCyValAaenLeuGlyMeuMetTrpThrTrpAlaLeu 20
 Db 497 ATGAAGCTCTCCACAGCCTTCATGTGTTAACTGGGGATGATGTGACCTGGGCACCTG 556
 QY 21 TrpMetLeuProSerLeuCyValyPheSerLeuAlaAlaLeuProAlaLysProGluLeu 40
 Db 557 TGGAGTCTCCCTTCACTGCAAAATTCAGCCCTGGAGCTTCGCAAGCTTAAGCTTAGAAC 616
 QY 41 LLeSerCyValTyTrpTyArgLysAenLeuThrCyThrTrpSerProGlyLysGlu 60
 Db 617 ATTTCCTGTCTACTACTATAGAAAATTTAACTGCACTTGAGAGTCCAGAAAGAA 676
 QY 61 ThrSerTyTrpGlnTyTrpValLysArgTrpTyraLapheGlyLysHisAapAan 80
 Db 677 ACCAGTTATACCAAGTACAGTAAAGAACTTAAGCTTTGGAGAAAACATGATATAT 736
 QY 81 CySerThrAenSerSerThrSerGluAenAgaLaseCySerPhePheLeuProArg 100
 Db 737 TGTACAAACCAATAGTCTTACAAAGTAAATCGTCTGCTCTTTTTCCTTCAAGA 796
 QY 101 LLeThrIleProAspAenTyThrIleGluValGluAgaAenGlyAaspGlyValIle 120
 Db 797 ATTAAGATCCCAAGATTAATTAACATTGAGGTGAAAGCTGAAAATGGAGATGCTTAAT 856
 QY 121 LysSerHisMetThrTyTrpArgLeuGluAenIleAlaLysThrGluProProLysIle 140
 Db 857 AAATCTCATATGACACTACTGAGATTAGAAACATAGGAAAACGAAACCACTAAGATT 916
 QY 141 PheArgValLysProValLeuGlyLysLysArgMetIleGlnIleGluTrpLysPro 160
 Db 917 TTCCTGTGAAACCAAGTTCGATCAAAACCAATGATTCAAATGGATGATAAGCTT 976
 QY 161 GluLeuAlaProValSerSerAspLeuLysTyThrLeuArgPheArgThrValAenSer 180
 Db 977 GAGTTGGCGCTGTTTCACTGATTTAAATACACACTTCGATTCAGGACGTCACAGT 1036
 QY 181 ThrSerTrpMetGluValAaenPheAlaLysAenArgLysAapLysAenGlnThrTyraAan 200
 Db 1037 ACCAGCTGATGGAAGTCAACTGCTTAAGAAACGTTAAGATTAABAAACCAACGTAAC 1096
 QY 201 LeuThrGlyLeuGlnProPheThrGluTyraIleAlaLeuArgCyAlaValLysGlu 220
 Db 1097 CTCACGGGGCTGACGCTTTTAAACAAATATGTCATAGCTTCGCGATGCGCTCAAGAG 1156
 QY 221 SerLysPheTrpSerAspTrpSerGlnLysMetGlyMetThrGluGluGluAlaPro 240
 Db 1157 TCAAAAGTCTGAGTGAAGTGAAGCCAAAGAAAATGGAAATGACTGAGAGAAAGCTCA 1216
 QY 241 CyseGlyLeuGluLeuTrpArgValLeuLysProAlaGluAlaAapGlyAArgArgProVal 260
 Db 1217 TGTGGCCTGGAAGCTGAGAGTCTGAAACCAAGTGAAGGCGGATGGAAGAAAGCAATG 1276
 QY 261 ArgLeuLeuTrpLysValAaenArgValAaProValLeuGlnLysThrLeuGlyTyraAan 280
 Db 1277 CGGTGTGATGAGAAAGCAAGAGAGAGCCCAAGCTTCAAGAAAACCTTGGCTACAAAC 1336
 QY 281 LLeTrpTyTrpProGluSerAaenThrAenLeuThrGluThrMetAaenThrThraAanGln 300
 Db 1337 ATATGATCTATCCAGAAAGCAACATACTCAAGAAACATGAAACATACCTAACAG 1396
 QY 301 GlnLeuGluLeuHisLeuGlyGlyLysSerPheTrpValSerMetLLeSerTyraAanSer 320
 Db 1397 CAGCTTGAACCTGCACTCTGGAAGGCGAGGCTTTTGGGTGTATGATTTCTTATATCT 1456

QY 321 LeuGlyLysSerProValAlaThrLeuArgIleProAlaIleGlnGluLysSerPheGln 340
 Db 1457 CTGGGAAGTCTCCAGTGGCCACCTGAGATTCAGCTATTCAGAAAATCATTTTCAG 1516
 QY 341 CysIleGluValMetGlnAlaCyValAlaGluAaenGlnLeuValLysTrpGlnSer 360
 Db 1517 TGCATTGAGGTCAATGCAAGCCCTGGCTGCTAGAGACCAAGTATGATGATGCAAGTGGCAAAAGC 1576
 QY 361 SerAlaLeuAaenValAaenThrTrpMetIleGluTrpPheProAaenValAapSerGluPro 380
 Db 1577 TCTGCTTACAGAGTGAACACTGATGATTAATGTTCCGAGATGTGAGCTCAGAGCC 1636
 QY 381 ThrThrLeuSerTrpGluSerValSerGlnAlaThrAaenTrpThrIleGlnGluAapLys 400
 Db 1637 ACCACCTTCTCTGGAAATCTGTGCTCAGGCCAAGAACTGAGATCAGACAGATTA 1696
 QY 401 LeuLysProPheTrpCyTrpAaenLLeSerValTyProMetLeuHisAapLysValGly 420
 Db 1697 TTTAAACCTTCTGGTGTATTAACATCTCTGTGATCCAAATGTTGCAAGACAAAGTTGGC 1756
 QY 421 GluProTySerIleGlnAlaTyraLalysGluGlyValProSerGlyGlyProGluThr 440
 Db 1757 GAGCCATATTCATCCAGGCTTAAGCCAAAGAGCGCTTCATCAGAAAGTCTGAGAAC 1816
 QY 441 LysValGluAenIleGlyValLysThrValThrIleTrpTrpLysGluIleProLysSer 460
 Db 1817 AAGGTGAGAACTGGGCTGAAGACGCTACGATACATGAAAGAAAGATTTCCAAAGGT 1876
 QY 461 GluArgLysGlyIleLLeCyAaenTyThrIlePheTyTrpGlnAlaGluGlyLysGly 480
 Db 1877 GAGGAAAGGCTATCATCTGCACTACACACTCTTTTACCAAGCTGAAGGTGGAAGAAAG 1936
 QY 481 PheSerLysThrValAaenSerSerIleLeuGlnTyTrpGlyLeuGlnSerLeuLysArgLys 500
 Db 1937 TTCCTCAAGACAGTCAATTCAGCATCTTCAGATGAGCGCTGAGAGTCCCTGAAACGAAG 1996
 QY 501 ThrSerTyTrpIleValGlnValMetAlaSerThrSerAlaGlyLysThrAaenGlyThraSer 520
 Db 1997 ACCCTTACATGTTTCAGGTATGAGCCAGCAACGAGTGGGGAAACCAACGGAACCAAGC 2056
 QY 521 LLeAaenPheLysThrLeuSerPheSerValPheGluIleIleLeuIleThrSerLeuIle 540
 Db 2057 ATTAATTTCAAGACATTCATCTCATGAGTCTTTAGATTAATCCATACATCTCTGATTT 2116
 QY 541 GlyGlyLeuLeuLeuIleIleLeuThrValAlaTyrglyLeuLysLysProAan 560
 Db 2117 GGTGAGGCGCTTCTTATTTCTCATATCTGACAGTGGCATGTGCTCAAAAACCCAAAC 2176
 QY 561 LysLeuThrHisLeuCyTrpProThrValProAaenProAlaGluSerSerIleAlaThr 580
 Db 2177 AAATTTGACTCATCTGTGTGGCCCAAGCTTCCCAACCTGTGAAAGTATAGCCACA 2236
 QY 581 TrpHisGlyAaenPheLysAapLysLeuAaenLeuLysGluSerAaenPheSerValAaen 600
 Db 2237 TGGCATGGAATGATTTTCAAGATTAAGCTTAACCTGAAGAGTCTGATCTGTGAAC 2296
 QY 601 ThrGluAaenArgIleLeuLysProCySerThrProSerAapLysLeuValIleAapLys 620
 Db 2297 ACAGAAAGCAGGATCTTAAACCATGTTCCACCCCAAGTGAAGTGTGATGAGCAAG 2356
 QY 621 LeuValValAaenPheGlyAaenValLeuGlnGluIlePheThrAaenGluAlaArgThrGly 640
 Db 2357 TTGGTGTGAACTTGTGGAAATGTTCTCAAGAAATTTTTCAGATGTAAGCCAGAACGGGT 2416
 QY 641 GlnGluAaenLeuGlyGlyLysAaenGlyThraArgIleLeuSerSerCyProThr 660
 Db 2417 CAGAAAACAAATTTTGAAGGGAAGAAAGAAATGGACATGAATTCGTCTTCTGCCCAACT 2476
 QY 661 SerIle 662
 Db 2477 TCAATA 2482

RESULT 6

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US-09-892-949-45
; Sequence 45, Application US/09892949
; Publication No. US20030096339A1
; GENERAL INFORMATION:
; APPLICANT: Sprecher, Cindy A.
; APPLICANT: Presnell, Scott R.
; APPLICANT: Gao, Zeren
; APPLICANT: Whitmore, Theodore E.
; APPLICANT: Knipper, Joseph L.
; APPLICANT: Maurer, Mark F.
; TITLE OF INVENTION: CYTOKINE RECEPTOR ZCYTOR17
; FILE REFERENCE: 00-42
; CURRENT APPLICATION NUMBER: US/09/892,949
; CURRENT FILING DATE: 2001-06-26
; PRIOR APPLICATION NUMBER: US 60/214,282
; PRIOR FILING DATE: 2000-06-26
; PRIOR APPLICATION NUMBER: US 60/214,955
; PRIOR FILING DATE: 2000-06-29
; PRIOR APPLICATION NUMBER: US 60/267,963
; PRIOR FILING DATE: 2001-08-02
; NUMBER OF SEQ ID NOS: 93
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 45
; LENGTH: 2529
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (162)...(2108)
US-09-892-949-45

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Alignment Scores:

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Pred. No.: 0 Length: 2529
Score: 3518.00 Matches: 660
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 99.72% Indels: 0
Gaps: 0

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US-10-006-265-17 (1-662) x US-09-892-949-45 (1-2529)

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QY 3 LeuSerProGlnProSerCysValAsnLeuGlyMetMetTrpThrTrpAlaLeuTrpMet 22
DB 129 CTCTCTCCCGACGCTTCATGTGTAACTGGGATGATGTGACCTGGGCACCTGTGATG 188
QY 23 LeuProSerLeuGlySerPheSerLeuAlaLeuProAlaSerProGlyLysGluThrSer 42
DB 189 CTCCTCTCAGCTGCAATTCAGCTGGCAGCTCTGCAAGCTAAGCCTGAACATTTCC 248
QY 43 CysValTyrTyrTyrArgLysAsnLeuThrCysThrTrpSerProGlyLysGluThrSer 62
DB 249 TGTGTCTACTACTATGAGAAATTTAACTGCACTTGGAGTCCAGGAAAGAAACCACT 308
QY 63 TyrThrGlnTyrThrValLysArgThrTyrAlaPheGlyGlyLysHisAspAsnCysThr 82
DB 309 TATAACCAAGACAGATTAGAACTTACGCTTTTGAAGAAAAACATGATTAATTGACA 368
QY 83 ThrAsnSerSerThrSerGluAsnArgAlaSerCysSerPhePheLeuProArgLysThr 102
DB 369 ACCAATAGTTCTCAAGTGAATTCGCTTCGCTCTTTTCCCTCCAGAAATPACG 428
QY 103 IleProAspAsnTyrThrIleGluValGluAlaGluAsnGlyAspGlyValIleLysSer 122
DB 429 ATCCGATATTAATTAACCATTTGAGCTGGAGCTGAAATGAGATGCTGTAATTAATCT 488
QY 123 HisMetThrTyrTrpArgLeuGluAsnIleAlaLysThrGlnProProLysIlePheArg 142
DB 489 CATATACATACATGAGATTAGAGAAACATAGCAAAACCTAACCACTTAAGATTTCCGT 548
QY 143 ValLysProValLeuGlyIleLysArgMetIleGlnIleGluTrpIleLysProGluLeu 162
DB 549 GTGAAACCAAGTTTGGGCATCAACGATGATTCAAATGAATGAATGAATGAAGCTGAGTTG 608

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QY 163 AlaProValSerSerAspLeuLysTyrThrLeuArgPheArgThrValAsnSerThrSer 182
DB 609 GCGCCGTTCATCTGATTAATAATACACATTCATTCAGGACAGTCAACAGTACCAAGC 668
QY 183 TrpMetGluValAsnPheAlaLysAsnArgLysAspLysAsnGlnThrTyrAsnLeuThr 202
DB 669 TGGATGGAAGTCAACCTTGCTAAGAACCTTAAGATTAATAAACCAACGTAACCTCACG 728
QY 203 GlyLeuGlnProPheThrGluTyrValIleAlaLeuArgCysAlaValLysGluSerLys 222
DB 729 GGGCTGCACCTTTTACGAATATGTCTAGCTCTGCGATGCGCGTCAAGAGTCAAAAG 788
QY 223 PheTrpSerAspTrpSerGlnGluLysMetThrGlnGluAlaProCysGly 242
DB 789 TTCTGGAGTACTGGAGCCAAAGAAATGGAAATGAGTACGAGGAAGAGCTCATGTGCGC 848
QY 243 LeuGluLeuTrpArgValLeuLysProAlaGluAlaAspGlyArgArgProValArgLeu 262
DB 849 CTGGAACCTGTGAGAGTCTGAAACCACTGAGGCGGATGGAAGAGGCACTGCGGTTG 908
QY 263 LeuTrpLysLysAlaArgGlyAlaProValLeuGluLysThrLeuGlyTyrAsnIleTrp 282
DB 909 TTATGGAAGAGGCAAGAGAGCCCACTGCTAGAGAAACCTTGCTACAACTATGCG 968
QY 283 TyrTyrProGluSerAsnThrAsnLeuThrGluThrMetAsnThrThrAsnGlnLeu 302
DB 969 TACTATCCAGAAAGCAACTAATCTACAGAAACATGACATCACTAACAGCAGCTT 1028
QY 303 GluLeuHisLeuGlyGlyLysSerPheTrpValSerMetIleSerTyrAsnSerLeuGly 322
DB 1029 GAACGTCATCTGGAGGCGAGGCTTTGGGTCTATGATTTCTTAATTTCTCTGGG 1088
QY 323 LysSerProValAlaThrLeuArgIleProAlaIleGlnGluLysSerPheGlnCysIle 342
DB 1089 AAGTCTCCAGTGGCCACCTTGAGATTCACGCTATTCAGAAATAATCATTTAGTGCATT 1148
QY 343 GluValMetGlnAlaCysValAlaGluSerGluLeuValLysTrpGlnSerSerAla 362
DB 1149 GAGGTATCAGGCGCTGCTGCTGAGGACCACTAGTGTGAATGGCAAGCTCTGCT 1208
QY 363 LeuAspValAsnThrTrpMetIleGluTrpPheProAspValAspSerGluProThrThr 382
DB 1209 CTAGAGCTGAACACTGATGATTAATGATTTCCGAGTGGACTCAAGGCCACCACTC 1268
QY 383 LeuSerTrpGluSerValSerGlnAlaThrAsnTrpThrIleGlnGlnAspLysLeuLys 402
DB 1269 CTTTCTGGGAATCTGTGCTCAGGCCACGAACTGGACATCCAGCAGATTAATTAATA 1328
QY 403 ProPheTrpCysTyrAsnIleSerValTyrProMetLeuHisAspLysValGlyLysPro 422
DB 1329 CTTTCTGGTGTATTAACATCTCTGTGATCCAAATGTCATGACAAAGTTGGCAGGCA 1388
QY 423 TyrSerIleGlnAlaTyrAlaLysGluGlyValProSerGluGlyProGluThrLysVal 442
DB 1389 TATTCATCCAGCTTATGCCAAAGAGCGTTTCATCAAGAGGCTCTGAAGCAAGGTG 1448
QY 443 GluAsnIleGlyValLysThrValThrIleTrpLysGluIleProLysSerGluArg 462
DB 1449 GAGAACATTTGGCTGAAGCGCTCAGATCAATGAAAGAAATTCCTCAAGAGTGAAGA 1508
QY 463 LysGlyIleIleCysAsnTyrThrIlePheTyrGlnAlaGluGlyLysGlyPheSer 482
DB 1509 AAGGGTATCATCTGCAACTACACATCTTTTACCAAGCTGAAGGTGGAAGAAAGATTCTCC 1568
QY 483 LysThrValAsnSerSerIleLeuGlnTyrGlyLeuGluSerLeuLysArgLysThrSer 502
DB 1569 AAGACAGTCAATTCAGCACTTTCAGTACGCTGAGTCCCTGAAACGAAAGACCTCT 1628
QY 503 TyrIleValGlnValMetAlaSerThrSerAlaGlyGlyThrAsnGlyThrSerIleAsn 522
DB 1629 TACATTTGTCAGTCTGCGCACCAAGTGTGGGGGAACCAAGGACGACATTAAT 1688
QY 523 PheLysThrLeuSerPheSerValPheGluIleIleLeuIleThrSerLeuIleGlyGly 542

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Db      1689 TTCAAGACATTGTCTAGTGTCTTTGAGATTATCCATCACTTCTGTGTTGTGGA 1748
Qy      543 GtyleuleuileuileuileuileuThValaIaYrglyleuylasProbauleu 562
Db      1749 GGCCTTCTTATTTCTATTATCTGACAGTGGCATGTGCTCAAAAAACCAAAATTG 1808
Qy      563 ThrHleuCySerProThrValaProbaProaIaGuserSerIlealathrTrrHis 582
Db      1809 ACTCATCTGTGTGGCCCAACCGTCCCAACCTGTGAAAGTATGATGCCCATGGCAT 1868
Qy      583 GtlyAspAspPheLysAspLysleuAsnleuLysGtLysSerAspAspSerValaAsnThrGlu 602
Db      1869 GGAGATGATTTCAAGATTAAGCTTAACCTGAAGAGCTGTGATCTGTGTAACACAGA 1928
Qy      603 AsparGtIleuLysProCysSerThrProSerAspLysleuValIleAspLysleuVal 622
Db      1929 GACAGGATCTTAAAAACCAATGTTCCACCCCAAGTGAACAAGTTGATTCAGCAAGTTGGTG 1988
Qy      623 ValaAspPheGtLysAsnValaLeuGlnGluIlePheThrAspGluAlaArgThrGtLysGlnGlu 642
Db      1989 GTGAACCTTGGGAATGTTCTGTCAAGAAATTTTCAAGATGAAGCCAGAACGGGTACAGAA 2048
Qy      643 AsnAsnleuGtLysGtLysleuAsnGtLysThrArgIleLeuSerSerCysProThrSerIle 662
Db      2049 AACCAATTTAGAGAGGGGAAAAAGATGGACATGAATTTCTGTCTTCTGCCCAACTTCATA 2108

RESULT 7
US-10-351-157-108
: Sequence 108, Application US/10351157
: Publication No. US20030215838A1
: GENERAL INFORMATION:
: APPLICANT: Sprecher, Cindy A.
: APPLICANT: Gao, Zeren
: APPLICANT: Kujiiper, Joseph L.
: APPLICANT: Daseovich, Maria M.
: APPLICANT: Grant, Francis J.
: APPLICANT: Presnell, Scott R.
: APPLICANT: Whitmore, Theodore E.
: APPLICANT: Hammond, Angela K.
: APPLICANT: No. US20030215838A1ak, Julia E.
: APPLICANT: Gross, Jane A.
: APPLICANT: Dillon, Stacey R.
: TITLE OF INVENTION: CYTOKINE RECEPTOR ZCYTOR17 MULTIMERS
: FILE REFERENCE: 02-02
: CURRENT APPLICATION NUMBER: US/10/351,157
: PRIOR FILING DATE: 2003-01-21
: PRIOR APPLICATION NUMBER: US 60/435,361
: PRIOR FILING DATE: 2002-12-19
: PRIOR APPLICATION NUMBER: US 60/389,108
: PRIOR FILING DATE: 2002-06-14
: PRIOR APPLICATION NUMBER: US 60/350,325
: NUMBER OF SEQ ID NOS: 2002-01-18
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO 108
: LENGTH: 2529
: TYPE: DNA
: ORGANISM: Homo sapiens
: FEATURE:
: NAME/KEY: CDS
: LOCATION: (162)...(2108)
: US-10-351-157-108

Alignment Scores:
Pred. No.: 0 Length: 2529
Score: 3518.00 Matches: 660
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 99.72% Indels: 0
DB: 17 Gaps: 0
US-10-006-265-17 (1-662) x US-10-351-157-108 (1-2529)

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Qy      3 LeuSerProGlnProSerCysValaAsnleuGtLysMetTrpThrTrpAlaLeuTrpMet 22
Db      129 CTCTCTCCCAAGCCTTCAATGTTTAACTGGAGATGATGTAAGTGGCACTGGAGATG 188
Qy      23 LeuProSerLeuCysLysPheSerLeuAlaIleuProAlaLysProGlnLysIleSer 42
Db      189 CTCCCTACTCTGTGAATTTACGCTGGCACTCTGCCAGCTTAAGCTTGAGAACATTTCC 248
Qy      43 CysValIlyrTyrrArgLysAsnleuThrCysThrTrpSerProGtLysGtLysSer 62
Db      249 TGTGTCTACTACTATAGAAAAATTTAACTGCACTTGGATGCAAGAAAGAAACCACT 308
Qy      63 TyrThrGlnTyrrThrValaArgThrTyrrAlaPheGtLysLysAspAspCysThr 82
Db      309 TATACCCAGTACACAGTTAAGAACTTACCTTTGAGAAAAACATGATTAATTGTACA 368
Qy      83 ThrAsnSerSerThrSerGtLysAsnArgLysSerCysSerPhePheLeuProArgIleThr 102
Db      369 ACCAATAGTTCTACAGTGAABATGCTGCTCTTCTTTCTTCCCAAGAAATACG 428
Qy      103 IleProAspAsnTyrrThrIleGtLysAlaGluAsnGtLysAspGtLysValIleLysSer 122
Db      429 ATCCAGATTAATTATACCATGAGGTGGAAGCTGAATAAGAGATGTGTATTAATCT 488
Qy      123 HisMetThrTyrrThrArgLeuGluAsnIleAlaLysThrGluProProLysIlePheArg 142
Db      489 CATATGACATCTGAGATTGAGAAACATACGAAACATGAACCACTTAAGATTTTCCGT 548
Qy      143 ValLysProValaLeuGtLysIleLysArgMetIleGlnIleGtLysIleLysProGtLys 162
Db      549 GTGAACCAAGTTTGGGCATCAACGATGATTTCAATTTGATGATTAACCTGAGTTG 608
Qy      163 AlaProValSerSerAspLysTyrrThrLeuArgPheArgThrValaAsnSerThrSer 182
Db      609 GCGCCTGTTTCATCTGATTTAAATATACACTTGATTCAGAGACAGTCAACAGTACAGC 668
Qy      183 TrpMetGtLysAsnPheAlaLysAsnArgLysAspLysAsnGlnThrTyrrAsnLeuThr 202
Db      669 TGGATGGAATCAACTTCGTCAAGAACCGTAAAGATGAATAAAACCAACCTTAACCTCAG 728
Qy      203 GtLysleuGlnProPheThrGtLysTyrrValIleAlaLeuArgCysAlaValLysGtLys 222
Db      729 GGGCTGAGCCTTTTACAGATATGTCATAGCTCTGCGATGTGGGTCAAGAGTCAAG 788
Qy      223 PheTrpSerAspTrpSerGlnGtLysMetGtLysMetThrGtLysGtLysAlaProCysGtLys 242
Db      789 TTCTGAGTGACTGAGCCAAAGAAATGGAATGACTGAGAAAGCTCCATGTGGC 848
Qy      243 LeuGtLysLeuTrpArgValaLeuLysProAlaGluAlaAspGtLysArgProValaArgLeu 262
Db      849 CTGAACCTGTGAGAACGCTCGAAACCAAGCTGAGCGGATGAAGAAAGCCAGTCCGCTG 908
Qy      263 LeuTrpLysLysAlaArgGtLysAlaProValleuGtLysThrLysGtLysTyrrAsnIleTrp 282
Db      909 TTATGAGAGAGGCAAGAGAGGCCCTCTTAAGAAACACTTGGCTACAAATATAG 968
Qy      283 TyrTyrrProGtLysAsnThrAsnLeuThrGtLysMetAsnThrAsnGlnLeu 302
Db      969 TACTATCCAGAAACCACTTAACCTCAAGAAACATGAACACTTAACCAAGCTT 1028
Qy      303 GtLysleuHsleuGtLysGtLysSerPheTrpValaSerMetIleSerTyrrAsnSerLeuGtLys 322
Db      1029 GAACCTGATCTGGAGAGCGAGAGCTTTGGTGTCTATGATTTCTTAATTTCTTGGG 1088
Qy      323 LysSerProValaIaThrLysArgIleProAlaIleGlnGtLysSerPheGtLysIle 342
Db      1089 AAGTCTCAAGTGGCCACCTGAGGATTCAGACTTTCAGAAAAATCATTTCAATGCAATT 1148
Qy      343 GluValaMetGlnAlaCysValaIaGluAspGlnLeuValaLysTrpGlnSerSerAla 362
Db      1149 GAGGTCATGACAGGCTCGTGTGTCAGAGACAGCTAGGTGGAGAGTGGCAAAAGCTGTGCT 1208

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QY 363 LeuAspValAsnThrTrpMetIleGluTrpPheProAspValAspSerGluProThrThr 382
Db 1209 CTGACGCTGAACCTTGATGATTTGATGATGATTTCCGAGATGTGACCTCAGAGCCACCA 1268
QY 383 LeuSerTrpGluSerValSerGlnAlaThrAsnTrpThrIleGlnGlnAspIleLeuVal 402
Db 1269 CTTTCTGGGAATCTGTCTCGAGCCAGAACGTGACGATCCAGACAGATTAATTAATAA 1328
QY 403 ProPheTrpCysTrpAsnIleSerValTyrProMetLeuHisAspIleValGlyGluPro 422
Db 1329 CCTTTCTGGTGTCTATACATCTCTGTGTATCCAAATGTTGATACAAAGTTGGCGAGCA 1388
QY 423 TyrSerIleGlnAlaTyrAlaValGluGluValProSerGluGluProGluThrVal 442
Db 1389 TATTCCATCCAGGCTTATGCGCAAGAGGCGTTCCATCAGAAAGTCTCTGAGACCAAGTGT 1448
QY 443 GluAsnIleGlyValIleThrValIleThrIleThrIleThrIleProIleSerGluVal 462
Db 1449 GAGAACATTTGGCTGGAAGACGGTCCAGCATCAGTAAGAAAGATTCCTCAAGATGAGAGA 1508
QY 463 LysGlyIleIleCysAsnTyrThrIlePheTyrGlnAlaGluGlyLysGlyPheSer 482
Db 1509 AAGGATATCATCTCGCAACTRACCATCTTTTACCAAGCTGAGGTGAGAAAGATTTCTCC 1568
QY 483 LysThrValAsnSerSerIleLeuGlnTyrGlyLeuGluSerLeuLysArgLysThrSer 502
Db 1569 AAGACAGTCATCTCCAGCATCTTGAGTACGGCTGAGAGTCCCTGAAACGAAAGACTCTCT 1628
QY 503 TyrIleValGlnValMetAlaSerThrSerAlaGlyGlyThrAsnGlyThrSerIleAsn 522
Db 1629 TACATTTGTTCAGGTATGCGCACGACACGATGCTGGGGGAAACCAAGGACACATTAAT 1688
QY 523 PheLysThrLeuSerPheSerValPheGluIleIleLeuIleThrSerLeuIleGlyGly 542
Db 1689 TTCAACACATTTGATTCATTCAGTGTCTTGAGATTATCTCTCAATCTCTCGATGGTGA 1748
QY 543 GlyLeuLeuIleLeuIleIleLeuThrValAlaTyrGlyLeuLysLysProAsnLysLeu 562
Db 1749 GGCCTTCTATTTCTCATTTATCTGACAGTGGCATATGTGTCTCAAAAACCAATATTTG 1808
QY 563 ThrHisLeuCysTrpProThrValProAsnProAlaGluSerSerIleAlaThrTrpHis 582
Db 1809 ACTCATCTGTGTGGCCACCGTTCACCACTGTGAAAGTATGACATGACATGGCAT 1868
QY 583 GlyAspAspPheLysAspLysLeuAsnLeuLysGlySerAspAspSerValAsnThrGlu 602
Db 1869 GGGAGATGATTTCAAGATTAAGCTTAACCTGAAAGAGTGTGATCTGTGAAACACAGAA 1928
QY 603 AspArgIleLeuLysProCysSerThrProSerAspLysLeuValIleAspLysLeuVal 622
Db 1929 GACAGATCTTAAACCATGTTCCACCCAGTGAACAGTTGTGATTCAGATTTGGTGTG 1988
QY 623 ValAsnPheGlyAsnValLeuGlnGlnIlePheThrAspGluAlaArgThrGlyGlnGlu 642
Db 1989 GTGAACCTTTGGGAAATGTTCTGCAAGAAATTTTTCACAGATGAACCCAGAAAGGCTCGGAA 2048
QY 643 AsnAsnLeuGlyGlyGluLysAsnGlyThrArgIleLeuSerSerCysProThrSerIle 662
Db 2049 AACAAATTTAGAGAGGAGAAAGAAATGGGACTAGAAATTTCTGTCTTCCGCAATTCATA 2108

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RESULT 8
US-10-772-531-45
; Sequence 45, Application US/10772531
; Publication No. US200401422A1
; GENERAL INFORMATION:
; APPLICANT: Sprecher, Cindy A.
; APPLICANT: Gao, Zeren
; APPLICANT: Presnell, Scott R.
; APPLICANT: Whitmore, Theodore E.
; APPLICANT: Kuiper, Joseph L.
; APPLICANT: Maurer, Mark F.
; TITLE OF INVENTION: CYTOKINE RECEPTOR ZCYTOR17
; FILE REFERENCE: 00-42

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; CURRENT APPLICATION NUMBER: US/10/772,531
; CURRENT FILING DATE: 2004-02-05
; PRIOR APPLICATION NUMBER: US/09/892,949
; PRIOR FILING DATE: 2001-06-26
; PRIOR APPLICATION NUMBER: US 60/214,282
; PRIOR FILING DATE: 2000-06-26
; PRIOR APPLICATION NUMBER: US 60/214,955
; PRIOR FILING DATE: 2000-06-29
; PRIOR APPLICATION NUMBER: US 60/267,963
; PRIOR FILING DATE: 2001-08-02
; NUMBER OF SEQ ID NOS: 93
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 45
; LENGTH: 2529
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (162) ... (2108)
US-10-772-531-45

Alignment Scores:
Pred. No.: 0 Length: 2529
Score: 3518.00 Matches: 660
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 99.72% Indels: 0
DB: 18 Gaps: 0

US-10-006-265-17 (1-662) x US-10-772-531-45 (1-2529)
QY 3 LeuSerProGlnProSerCysValAsnLeuGlyMetMetTrpThrTyrAlaLeuTrpMet 22
Db 129 CTCTCTCCCACTTCATGATGTTAACTCGGGAGATGTGACCTGGGCACTGTGAGAT 188
QY 23 LeuProSerLeuCysLysPheSerLeuAlaLeuProAlaLysProGluAsnIleSer 42
Db 189 CTCCTCTCATCTCGCAAAATTCAGCTGCGAGCTCTGCCAGCTTAAGCTGAGAACTTTCC 248
QY 43 CysValTyrTyrTyrArgLysAsnLeuThrCysThrTrpSerProGlyLysGluThrSer 62
Db 249 TGTGTCTACTACTATAGAAAATTTTAACTCTCACTTGAGTCCAGAGAGAAACCACT 308
QY 63 TyrThrGlnTyrThrValLysArgThrTyrAlaPheGlyGlyLysHisAspAsnCysThr 82
Db 309 TATACCACTATACAGTTTAAGAACTTACGCTTTTGAGAGAAACATGATATTGTACA 368
QY 83 ThrAsnSerSerThrSerGluAsnArgAlaSerCysSerPhePheLeuProArgIleThr 102
Db 369 ACCCAATAGTTCTTCAAGTAAATCGTGTCTGTCTTTTCTTCCCAAGAAATTAACG 428
QY 103 IleProAspAsnTyrThrIleGluValGluAlaGluAsnGlyAspGlyValIleLysSer 122
Db 429 ATCCCAATATATTAACATTAAGGTGAGAGCTGAAATGAGATGATTAATTAATCT 488
QY 123 HisMetThrTyrTrpArgLeuGluAsnIleAlaLysThrGluProProLysIlePheArg 142
Db 489 CATATGACATATCTCGAGATTAAGAAACATGAGAAACCTTAAGATTTTCCGT 548
QY 143 ValLysProValLeuGlyIleLysArgMetIleGlnIleGluTrpIleLysProGluLeu 162
Db 549 GTGAACCACTTTTGGGCACTCAACAGATTCATTAATGAATGATTAAGCTGTGTG 608
QY 163 AlaProValSerSerAspLeuLysTyrThrIleAspPheArgThrValAsnSerThrSer 182
Db 609 GGCCTGTTTCATCTGATTTAAATACACTTCGATTCAGACACGTCAACGTACAC 668
QY 183 TrpMetGluValAsnPheAlaLysAsnArgLysAspLysAsnGlnThrTyrAsnLeuThr 202
Db 669 TGGATGGAAGTCACTTCCTGTAAGAACCTTAAGATTAAGAAACCAACGTACACCTCAG 728
QY 203 GlyLeuGlnProPheThrGluTyrValIleAlaLeuArgCysAlaValLysGluSerLys 222

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Db 729 GGGCTGACAGCTTTTACAGAAATATGTCATAGCTCTGCATGTGGGTCAAGAGTCAAG 788
Qy 223 PheTPSerAspTPTrpSerGlnGluyswMetGlyMetThrGluGluAlaProCysGly 242
Db 789 TTCGTGAGTGAATCGAGCCAGAAAAAAGGGAAATGACGAGAGAAAGAGCTTCATGTGGC 848
Qy 243 LeuGluLeuTPArGValLeuAspProAlaGluAlaAspGlyArgArgProValArgLeu 262
Db 849 CTGGAACGTGGAGAGTCTCTGAACCACTGAGCGGATGAGAAAGGCCCATGGCGGTG 908
Qy 263 LeuTPLyValArgGlyValArgValLeuGluGlyThrLeuGlyTyrAsnIleTP 282
Db 909 TTATGAGAAAGAGGCAAGAGAGAGCCCACTGAGAAAAACCTTGGGTACAACTATGG 968
Qy 283 TyrTPProGluSerAsnThrAsnLeuThrGluThrMetAsnThrThrAsnGlnLeu 302
Db 969 TACTATCCAGAAAGAACACTAACCCTCACAGAAACATGACACTAACCAGAGCTT 1028
Qy 303 GluLeuHsLeuGlyGlyGluSerPheTPValSerMetIleSerTyrAsnSerLeuGly 322
Db 1029 GAACCTGATCTGGAGGCGAGAGCTTTTGGGTGCTATGATTTCTTATATTTCTTGGG 1088
Qy 323 LysSerProValAlaThrLeuArgIleProAlaIleGlnGluLysSerPheGlnCysIle 342
Db 1089 AAGTCTCCAGTGGCCACCCTGAGATTCAGCTATTCAGAAAAATCATTTTCAGTGCATT 1148
Qy 343 GluValMetGlnAlaCysValAlaGluAspGlnLeuValValLysTPGlnSerSerAla 362
Db 1149 GAGGTCAAGCAGGCGCTGGCTGCTAGAGACCAAGCTAGGTGGAAGTGGCAAGCTCTGCT 1208
Qy 363 LeuAspValAsnThrCTPTrpMetIleGluTPPheProAspValAspSerGluProThr 382
Db 1209 CTAGACGTAACACTGGATGATTAATGATGTTCCGAGATGGACTCAGAGCCCAACACC 1268
Qy 383 LeuSerTPGluSerValSerGlnAlaThrAsnTPTrIleGlnGlnAspLysLeuLys 402
Db 1269 CTTTCTCGGAATCTGTGCTCAGGCCCAAGACTGAGATCCAGACATTAATTAATAA 1328
Qy 403 ProPheTPCyETyrAsnIleSerValTyrProMetLeuHsAspLysValGlyGluPro 422
Db 1329 CTTTCTGTGTATTAACATCTCTGTATCAATGTTGATGACAAAGTGGCCAGACCA 1388
Qy 423 TyrSerIleGlnAlaTyrAlaLysGluGlyValProSerGluGlyProGluThrLysVal 442
Db 1389 TATTCATCCAGAGCTTATGCCAAAGAGGCGTTCATCAAGAAAGCTCTGAGCCAGAGT 1448
Qy 443 GluAsnIleGlyValLysThrValThrIleThrTPLyGluIleProLysSerGluArg 462
Db 1449 GAGAAACATTTGGCGTGAAGACGCTCAGATCAATGAAAGAGATTCCCAAGAGTGAAGA 1508
Qy 463 LysGlyIleIleCysAsnTyrThrIlePheTyrGlnAlaGluGlyLysGlyPheSer 482
Db 1509 AAGGTATACATCTGCACTACACCATCTTTTACCAAGCTGAAGGAGAAAGATTCCTCC 1568
Qy 483 LysThrValAsnSerSerIleLeuGlnTyrGlyLeuGluSerLeuLysArgLysThrSer 502
Db 1569 AAGAGAGTCAATTCAGACATCTGCAATGAGGCGCTGAGAGTCCCTGAAAGCAAGACCTCT 1628
Qy 503 TyrIleValGlnValMetAlaSerThrSerAlaGlyGlyThrAsnGlyThrSerIleAsn 522
Db 1629 TACATTTGTTAGGTATGCGCAGACCAAGTGTGGGGAACCAACGGGACCAAGCAATTAAT 1688
Qy 523 PheLysThrLeuSerPheSerValPheGluIleIleLeuIleThrSerLeuIleGlyGly 542
Db 1689 TTCAGAGACATTTGTCATTCAGTCTTTGAGATTATCCCATTAACCTCTCTGATGGTGA 1748
Qy 543 GlyLeuLeuIleLeuIleIleLeuThrValAlaTyrGlyLeuLysLysProAsnLysLeu 562
Db 1749 GGCCTTTTATTTCTATTTCTGACAGTGGCATATGGTCTCAAAAACCCCAACAATTTG 1808
Qy 563 ThrHisLeuCyETPProTPThrValProAsnProAlaGluSerSerIleAlaThrTPHis 582
Db 1809 ACTATCTGTGTGGCCACCGTTCCAAACCTGTGTAAAGTAAATAGTACCAATGGCAT 1868

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Qy 583 GluAspAspPheLysAspLysLeuAsnLeuysGluSerAspAspSerValAsnThrGlu 602
Db 1869 GAGATGATTTTCAAGAGTAACCTTAACCTGAAGAGTGTAGTACTGTGAACACAGAA 1928
Qy 603 AspArgIleLeuLysProCysSerThrProSerAspLysLeuValIleAspLysLeuVal 622
Db 1929 GACAGATCTTAAACATGTTCCACCCCGTACACAAAGTTGGTATGACAAGTTGGTG 1988
Qy 623 ValAsnPheGlyAsnValLeuGlnGluIlePheThrAspGluAlaArgThrGlyGlnGlu 642
Db 1989 GTGAACCTTTGGGAATGTCTCTCAAGAAATTTTCAACAGTGAAGCCAGAACCGGTCA 2048
Qy 643 AsnLeuLeuGlyGlyGlyLysAsnGlyThrArgIleLeuSerSerCysProThrSerIle 662
Db 2049 AACCAATTTAGAGAGGGAGAAAGATGAGACTAGAAATTCGTCTCTGCCCAATTCATA 2108

RESULT 9
US-10-006-265-1
; Sequence 1, Application US/10006265
; Publication No. US20030125520A1
; GENERAL INFORMATION:
; APPLICANT: Maeda, Masatsugu
; APPLICANT: Yaguchi, No. US20030125520A1ko
; TITLE OF INVENTION: NOVEL HEMOPOIETIN RECEPTOR PROTEIN, NR10
; FILE REFERENCE: 06501-096001
; CURRENT APPLICATION NUMBER: US/10/006, 265
; CURRENT FILING DATE: 2003-01-06
; PRIOR APPLICATION NUMBER: PCT/JP00/03556
; PRIOR FILING DATE: 2000-06-01
; PRIOR APPLICATION NUMBER: JP 11/155797
; PRIOR FILING DATE: 1999-06-02
; PRIOR APPLICATION NUMBER: JP 11/217797
; PRIOR FILING DATE: 1999-07-30
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 2969
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (523) ... (2478)
US-10-006-265-1

Alignment Scores:
Pred. No.: 0 Length: 2969
Score: 3512.00 Matches: 661
Percent Similarity: 99.85% Conservative: 1
Best Local Similarity: 99.70% Mismatches: 0
Query Match: 99.55% Indels: 1
DB: 15 Gaps: 0

US-10-006-265-17 (1-662) x US-10-006-265-1 (1-2969)
Qy 1 MelLysLeuSerProGlnProSerCysValAsnLeuGlyMetMetTPTrnTPAlaLeu 20
Db 523 ATGAAGCTCTCTCCCGAGCTTCAATGTTAACTGGGAGTGAAGTGAACCTGGGACATG 582
Qy 21 TrpMetLeuProSerLeuAspLysPheSerLeuAlaIleuProAlaLysProGluAsn 40
Db 583 TGAATGCTCCCTTACTCTGCAATTCAGCTGACCTGACACTTGCAGCTTACGCTGAAGAC 642
Qy 41 IleserCysValTyrTyrTyrArgLysAsnLeuThrCysThrTPTrpSerProGlyLysGlu 60
Db 643 ATTTCTGTGTCTACTACTATAGAAATAATTAACTGCACCTTGAAGTCCAGAGAAAGAA 702
Qy 61 ThrSerTyrThrGlnTyrThrValLysArgThrTyrAlaPheGlyGlyLysHisAspAsn 80
Db 703 ACCAGTTATACCCGATACAGACATTAAGAGAACTTAACCTTTCGAGAAAAACATGATTAAT 762
Qy 81 CysThrAsnSerSerThrSerGluAsnArgAlaSerCysSerPhePheLeuProArg 100

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Db 763 TGTACAAACCAATAGTCTACAGTGAATAATCGTCTTGCTCTTTTCTTCCACAAG 822
 QY 11eThrl1eProspAseNtYrThrl1eGluVal1aGluAsnGlyAspGlyVal11le 120
 Db 823 ATACACATCCCAATATATTTACCATTTGAGGTGGAAGCTGAAAATGGAGATGGTGAATT 882
 QY 121 LysSerHisMetThrYrTPaTgLeuGluAsn11eAlaLysThrGluProProlYs11le 140
 Db 883 AAATTCATATGACATTCGAGATTAGAAACATAGCCGAAACCTGAACCACTTAAGATT 942
 QY 141 PheArgValLysProValLeuGly11leValArgMet11leGluTrp11leYsPro 160
 Db 943 TTCGGTGAACACAGTTTGGGCATCAACGAATGATTCAATTAATGATGAAGCCCT 1002
 QY 161 GluLeuAlaProValSerSerAspLeuYsYrThrLeuArgPheArgThrVal1AsnSer 180
 Db 1003 GAGTTGGCCGCTTTTCATCTGATTTAAATACACACTTCGATTCAGAGACAGCAACAGT 1062
 QY 181 ThrSerTrpMetGluValAsnPheAlaLysAsnArgLysAspLysAsnGluThrYrAsn 200
 Db 1063 ACCAGCTGATGAGAGTCAACTTCGCTAAGAACCGTAAAGATTAACCAACGTAACAC 1122
 QY 201 LeuThGlyLeuGluProPheThrGluYrVal11leAlaLeuArgCysAlaVal11leGlu 220
 Db 1123 CTCACGGGCTGACAGCTTTTACAGAAATGTCATAGCTCTGCGATGTGGCTCAAGAG 1182
 QY 221 SerLysPheTrpSerAspTrpSerGluGluYsMetGlyMetThrGluGluGluAlaPro 240
 Db 1183 TCAAAGTTCCTGGAGTGACTGAGACCCAAAGAAAATGGGAATGACTGAGAGAAAGCTCCA 1242
 QY 241 CysGlyLeuGluLeuTrpArgVal11leuYsProAlaGluAlaAspGlyArgArgProVal 260
 Db 1243 TGTGGCTGGAACTGTGAGAGAGTCTGAAACCACTGAGCGGATGGAAGAGCCAGTG 1302
 QY 261 ArgLeuLeuTrpLysLysAlaArgGlyAlaProValLeuGluLysThrLeuGlyYrAsn 280
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 QY 281 IleTrpYrTrpProGluSerAsnThrAsnLeuThrGluThrMetAsnThrTrpAsnGln 300
 Db 1363 ATATGTGATCATCTCAAGAAACCAACTAACCTCAAGAAACAACTACTTAACAG 1422
 QY 301 GlnLeuGluLeuHisLeuGlyGlyGluSerPheTrpValSerMet11leSerYrAsnSer 320
 Db 1423 CAGCTTGAACCTGATCTGGAGGCGAGAGCTTTGGGTGCTATGATTTCTTAATTTCT 1482
 QY 321 LeuGlyLysSerProValAlaThrLeuArg11leProAla11leGluGluYsSerPheGln 340
 Db 1483 CTGGGAGAGTCTCAGTGGCCACCTGAGGATTCAGCTAATTCAGAAAATCATTTTCAG 1542
 QY 341 Cys11leGluValMetGlnAlaCysValAlaGluAspGluLeuVal11leYsTrpGlnSer 360
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 QY 361 SerAlaLeuAspValAsnThrTrpMet11leGluTrpPheProAspValAspSerGluPro 380
 Db 1603 TCTGCTCTAGACGTGAACCTTGATGATGATGATGTTCCGATGTCAGCTCAGAGCCC 1662
 QY 381 ThrThrLeuSerTrpGluSerValSerGlnAlaThrAsnTrpThr11leGluGlnAspLys 400
 Db 1663 ACCACCTTTTCCCTGGGAATCTGTCTCAGAGCCAGCAAGTCCGACGAAGTAA 1722
 QY 401 LeuLysProPheTrpCysYrAsn11leSerValYrProMetLeuHisAspLysVal11leGly 420
 Db 1723 TTAAACCTTTCTGGTCTATTAACATCTCTGTGTAATTCATGTTGCAATGCAAAAGTTGGC 1782
 QY 421 GluProTrpSer11leGlnAlaYrAlaLysGluGlyValProSerGluGlyProGluThr 440
 Db 1783 GAGCCATATTCATCCAGGCTTATGCCAAGAAAGGCGTTCCATCAGAGGTCTCGAGAGCC 1842
 QY 441 LysValGluAsn11leGlyVal11leYsThrVal11leThrl1eThrTrpLysGlu11leProlYsSer 460
 Db 1843 AAGGTGAGAAATTTGGCTGGAAGCGGTCAAGATCATGAGAAAGATTTCCCAAGAGT 1902

QY 461 GluArgLysGly11le11eCysAsnYrThrl1ePheYrGlnAlaGluGly11leYsGly 480
 Db 1903 GAGAGAAAGGTATATCATCTGCAACTACACCATCTTTTACCAAGCTGGAAGTGAAGGA 1962
 QY 481 PheSerLysTrpVal1AsnSerSer11leLeuGlnYrGlyLeuGluSerLeuLysArgLys 500
 Db 1963 TTCTCCAGACAGTCAATTTCCAGCATTTTGCAAGTACAGGCTGGAATCCCTGAAAGCAAG 2022
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 Db 2083 ATTAATTTCAAGACATTTGTCATTCAGTGTCTTGAGATTATCTCATATCTCTGATTT 2142
 QY 541 GlyGlyGlyLeuLeu11leLeu11le11leuThrVal11leYrGlyLeuLysLysProAsn 560
 Db 2143 GGTGGAGGCTCTTAATTTCTCATTTCTCGACAGTGGCATATGTGCTCAAAAAACCAAC 2202
 QY 561 LysLeuThrHisLeuCysTrpProThrValProAsnProAlaGluSerSer11leAlaThr 580
 Db 2203 AAATTTGACTCATCTGTGTGGCCACCGTTCCCAACCTGCTGAATGTTATGTTAGCCACA 2262
 QY 581 TrpHisGlyAspAspPheLysAspLysLeuAsnLeuLysGluSerAspAspSerValAsn 600
 Db 2263 TGGCATGAGATGATTTCAAGATTAAGCTAAACCTGAAGAGATCTGATGATCTGTGAAC 2322
 QY 601 ThrGluAspArg11leLeuLysProCysSerThrProSerAspLysLeuVal11leAspLys 620
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 QY 621 LeuValValAsnPheGluValAsnVal11leuGluGlu11lePheThrAspGluAlaArgThrGly 640
 Db 2383 TTGGTGTAACTTTGGGAATGTTCTGCAAGAAATTTTCACAGATGAACCGAAGCGGT 2442
 QY 641 GlnGlu-AsnAsnLeuGlyGlyGlyLysAsnGlyThrArg11leLeuSerSerCysProThr 660
 Db 2443 CAGGAAAAACAAATTTTGAAGGCGGAAAAAGAAATGGAGATTAATTCGTCTTCTGCCAAC 2502
 QY 660 rSer11le 662
 Db 2503 TTCAATA 2509

RESULT 10
 US-09-972-708-5
 / Sequence 5, Application US/09972708
 / Publication No. US20030059871A1
 / GENERAL INFORMATION:
 / APPLICANT: Immunex Corporation
 / APPLICANT: Cosman, David J.
 / APPLICANT: Mosley, Bruce A.
 / APPLICANT: Bird, Timothy A.
 / APPLICANT: DuBoise, Robert F.
 / APPLICANT: Wiley, Steven R.
 / TITLE OF INVENTION: HEMATOPOIETIN RECEPTORS HPR1 AND HPR2
 / FILE REFERENCE: 3160-B
 / CURRENT APPLICATION NUMBER: US/09/972,708
 / CURRENT FILING DATE: 2001-10-05
 / NUMBER OF SEQ ID NOS: 29
 / SOFTWARE: PatentIn version 3.1
 / SEQ ID NO 5
 / LENGTH: 2238
 / TYPE: DNA
 / ORGANISM: Homo sapiens
 / US-09-972-708-5

Alignment Scores:
 Score: 0
 Percent Similarity: 3465.50
 Best Local Similarity: 98.79%

Length: 2238
 Matches: 651
 Conservative: 2
 Mismatches: 3

Query Match: 98.23% Indels: 3
 DB: 10 Gaps: 1
 US-10-006-265-17 (1-662) x US-09-972-708-5 (1-2238)

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 Db 1 ATGAAGCTCTCTCCACGCTTCACTGTGTAACTGGGGATGATGTGACCTGGGCACTG 60
 QY 21 TrpMetLeuProSerLeuCysAlaPheSerLeuAlaAlaLeuProAlaLysProGln 40
 Db 61 TGGATGCTCCCTTCACTCTGCAAAATTCAGCTGGAGCTCTCCAGCTAAAGCTGAGAAC 120
 QY 41 LLeSerCysValTyrrTyrrTyrrArgLysAsnLeuTrpCysThrTrpSerProGlyLysGlu 60
 Db 121 ATTTCCTGTCTACTACTATAGGAAAAATTTAACTTCACTTGAAGTCCAGGAAAGGAA 180
 QY 61 ThrSerTyrrThrGlnTyrrThrValLysArgThrTyrrAlaPheGlyGlyLysHisAspAsn 80
 Db 181 ACCAGTTATACCCAGTACACAGTTAAGAACTTACGCTTTGGAGAAAAACATGATATAT 240
 QY 81 CysThrThrAsnSerSerThrSerGluAsnArgAlaSerCysSerPhePheLeuProArg 100
 Db 241 TGTACAAACCAATAGTTCTACAAAGTAAATCGTCTGCTCTTTTCTTCTCCAGAGA 300
 QY 101 LLeThrLLeProAspAsnTyrrThrLLeGluValGluAlaGluAsnGlyAspGlyValLLe 120
 Db 301 ATAAAGATCCAGATTAATTAATCAATGAGTGAAGCTGAAATGAGATGTGTAAAT 360
 QY 121 LysSerHisMetThrTyrrTrpArgLeuGluAsnLLeAlaLysThrGluProProLysLLe 140
 Db 361 AAAATCTCATGACACTACTGAGATTAGAAACATAGCGMAAACGAAACACACTTAAGATT 420
 QY 141 PheArgValLysProValLeuGlyLLeLysArgMetLLeGlnLLeGluTrpLLeLysPro 160
 Db 421 TTCGGTGAACACGATTTTGGGCATCAACGAATGATTCAAAATGAAATGATAAGCT 480
 QY 161 GluLeuAlaProValSerSerAspLeuLysTyrrThrLLeuArgPheArgThrValAsnSer 180
 Db 481 GAGTTGGGCGCTGTTTCATCTGATTTAAATACACACTTCGATTCAGACAGTCAACGCT 540
 QY 181 ThrSerTrpMetGluValAsnPheAlaLysAsnArgLysAspLysAsnGlyLLeThrTyrrAsn 200
 Db 541 ACCAGCTGATGAGAGTCACTTCGCTAAGAACGTAAGATTAACCAACCAACGTAACAC 600
 QY 201 LeuThrGlyLeuGlnProPheThrGluTyrrValLLeAlaLeuArgCysAlaValLysGlu 220
 Db 601 CTCACGGGGCTGCAGCCTTTTACAGAAATATGTCATAGCTCTGCGATGTGCGTCAAGAG 660
 QY 221 SerLysPheTrpSerAspTrpSerGlnGluLysMetGlyMetThrGluGluGluAlaPro 240
 Db 661 TCAAAATCTGAGAGTGAAGTGAAGCCMAAAAAAGGAAATGATGAGAGAAAGAGCTTCA 720
 QY 241 CysGlyLeuGluLeuTrpArgValLeuLysProAlaGluAlaAspGlyArgArgProVal 260
 Db 721 TGTGGCTTGAAGTGTGAGAGTCTTGAACCAAGCTGAGCGAGTGAAGAGGCCAATG 780
 QY 261 ArgLeuLeuTrpLysLysAlaArgLysAlaProValLeuGluLysThrLeuGlyTyrrAsn 280
 Db 781 CGGTTGTTATGGAAGAAAGCAAGAGAGCCCAAGCTTCAAGAAAAACATTGGCTACAAAC 840
 QY 281 LLeTrpTyrrTyrrProGluSerAsnThrAsnLeuThrGluTrpMetAsnThrThrAsnGln 300
 Db 841 ATAAAGTACTATCAAGAAAGCAACATTAACCTCAAGAAACAAATGAACATCAACACAG 900
 QY 301 GlnLeuGluLeuHisLLeuGlyGlyLysSerPheTrpValSerMetLLeSerTyrrAsnSer 320
 Db 901 CAGCTTGAACCTGATCTGGAGGCGAAGCTTTTGGGTGTCTATGATTTCTTAATATCT 960
 QY 321 LeuGlyLysSerProValAlaThrLeuArgLLeProAlaLLeGlnGluLysSerPheGln 340
 Db 961 CTGGGAAGTCTCCAGTGGCCACCTGAGGATTCACAGTATTTCAAGAAAAATCATTTGAG 1020

QY 341 CysLLeGluValMetGlnAlaCysValAlaGluAspGlnLeuValLLeTyrrTrpGlnSer 360
 Db 1021 TGCATTGAGTCAATGACAGGCTTGCCTTGTCTAGGACCAAGCTAGTGTATAGTGGCAAGC 1080
 QY 361 SerAlaLeuAspValAsnThrTrpMetLLeGluTrpPheProAspValAspSerGluPro 380
 Db 1081 CCGTCTTACAGAGTGAACACTTGGATGATGAATGTTTCCGATGTGTGACTCAGAGCC 1140
 QY 381 ThrThrLeuSerTrpGluSerValSerGlnAlaThrAsnTrpThrLLeGlnGluAspLys 400
 Db 1141 ACCACCTTCTCTGGGAATGTGTCTCAGGCCCAAGACTGAGATCCACCAAGATTA 1200
 QY 401 LeuLysProPheTrpCysTyrrAsnLLeSerValTyrrProMetLeuHisAspLysValGly 420
 Db 1201 TTAAACCTTTCTGGTCTATTAACATCTGTGTATCCAAATGTTGATGACAAAGTTGGC 1260
 QY 421 GluProTyrrSerLLeGlnAlaTyrrAlaLysGluGlyValProSerGluGlyProGluTrp 440
 Db 1261 GAGCATATTCATCCAGCTTATGCCAAAGAGGCGTTCCATCAGAAAGTCTGAGAGC 1320
 QY 441 LysValGluAsnLLeGlyValLysThrValThrLLeThrTrpLysGluLLeProLysSer 460
 Db 1321 AAGGTGGAACATTTGGCGTGAAGACGGTCAAGATCACTGAAAGAGATTCCCAAGAT 1380
 QY 461 GluArgLysGlyLLeLLeCysAsnTyrrThrLLePheTyrrGlnAlaGluGlyLysGly 480
 Db 1381 GAGGAAAGGGTATCATCTGCACTACCACTTTTACCAAGCTGAAGGTGAAGAAAGGA 1440
 QY 481 PheSerLysThrValAsnSerSerLLeuGlnTyrrGlyLeuGlnSerLeuLysArgLys 500
 Db 1441 TTCCTCAAGACAGTCATTCAGCATCTTGAGATACGGCTCGAGTCCCTCAAAAGAAAG 1500
 QY 501 ThrSerTyrrLLeValGlnValMetAlaSerThrSerAlaGlyLLeThrAsnGlyThrSer 520
 Db 1501 ACCCTTACATTTGTCAGTGTATGCGCAGACCGAGTGGGGGAACCGAGCGGACAGC 1560
 QY 521 LLeAsnPheLysThrLLeSerSerPheSerValPheGluLLeLLeuLLeThrSerLeuLLe 540
 Db 1561 ATAAATTCCAAGACATTTGTCATGATGTTTAAATTAATCACTTCATTAATCTTCTGATT 1620
 QY 541 GlyLysGlyLeuLeuLLeLLeLLeuThrValAlaTyrrGlyLLeuLysLysProAsn 560
 Db 1621 GGTGAGGCGCTTCTTATTCATTAATCTGACAGATGAGTATGTCTCAAAAACCCCAAC 1680
 QY 561 LysLeuThrHisLeuCysTrpProThrValProAsnProAlaGluSerSerLLeAlaThr 580
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 QY 581 TrpHisGlyAspAspPheLysAspLysLeuAsnLeuLysGluSerAspAspSerValAsn 600
 Db 1741 TGGCATGAGATGATTTCAAGATTAAGTAACTTAAGAGAGTGTGATGACTCTGTGAAC 1800
 QY 601 ThrGluAspArgLLeLeuLysProCysSerThrProSerAspLysLeuValLLeAspLys 620
 Db 1801 ACAGAAAGACGAGATCTTAACATTAATTCACCCCAAGTACAGAGTGTGATATGACAG 1860
 QY 621 LeuValValAsnPheGlyAsnValLeuGlnGluLLePheThrAspGluAlaArgThrGly 640
 Db 1861 TTGGTGTGAACCTTTGGGAATGTTCTGCAAGAAATTTTCAAGATGAAGCAGAACGGGT 1920
 QY 641 GlnGluAsnAsnLeuGlyGlyLysLysAsnGlyThrArgLLeLeuSerSerCysPro 659
 Db 1921 CAGGAAACCAATTTAAGAGGGGAAAGAAATGGG-----TATGTGACTGTGCC 1968

RESULT 11
 US-10-715-667-5
 ; Sequence 5, Application US/10715667
 ; Publication No. US20040152161A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Immunex Corporation
 ; APPLICANT: Cosman, David J.
 ; APPLICANT: Mosley, Bruce A.
 ; APPLICANT: Bird, Timothy A.


```

; APPLICANT: DuBoise, Robert F.
; APPLICANT: Wiley, Steven R.
; TITLE OF INVENTION: HEMATOPOIETIN RECEPTORS HPR1 AND HPR2
; FILE REFERENCE: 3160-B
; CURRENT APPLICATION NUMBER: US/10/715,667
; CURRENT FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: US/09/972,708
; PRIOR FILING DATE: 2001-10-05
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 5
; LENGTH: 2238
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-10-715-667-5

Alignment Scores:
Pred. No.: 0 Length: 2238
Score: 3465.50 Matches: 651
Percent Similarity: 99.09% Conservative: 2
Best Local Similarity: 98.79% Mismatches: 3
Query Match: 98.23% Indels: 3
DB: 18 Gaps: 1

US-10-006-265-17 (1-662) x US-10-715-667-5 (1-2238)
QY 1 MetLysLeuSerProGlnProSerCysValAsnLeuGlyWcMetTrpThrTrpAlaLeu 20
DB 1 ATAAAGCTCTCTCCCAAGCCTTCATGTGTAACTGGGAGTGAATGTGGACCTGGGAC 60
QY 21 TrpMetLeuProSerLeuCysLysPheSerLeuAlaAlaLeuProAlaLysProGlnAsn 40
DB 61 TGTAGTGCTCCTTCACCTGCAATTCAGCCTGGAGCTGTCGACGTAAGCTGGAAC 120
QY 41 LLeSerCysValLysTrpTrpArgLysAsnLeuThrCysThrTrpSerProGlyLysGlu 60
DB 121 ATTTCCTGTGTCTACCTATAGAAAAAATTAACTGCCTGTGAGTCCAGAAAAAGAA 180
QY 61 ThrSerTrpThrGlnTrpThrValLysArgThrTyrAlaPheGlyGluLysHisAspAsn 80
DB 181 AACAGTTATACCAAGTACACAGTTAAAGAACTTACGCTTTTGGAGAAAAACATGATAT 240
QY 81 CysThrThrAsnSerSerThrSerGluAsnArgAlaSerCysSerPhePheLeuProArg 100
DB 241 TGTACAAACCAATAGTTCTACAGTGAATAATCGTCTCGTCTTTTCCCTCCAAAG 300
QY 101 LLeThrLLeProAspAsnTrpThrLLeGluValGluAlaGluAsnGlyAspGlyValLLe 120
DB 301 ATTAACGATCCCAATATAATTATACCATTTGAGTGAAGCTGAAAAATGAGATGCTGTAATT 360
QY 121 LysSerHisMetThrTyrTrpArgLeuGluAsnLLeAlaLysThrGluProProLysHis 140
DB 361 AAATCTCATATGACATCTGAGAAATTAGAAACATACGCCAAACCTGAACCTTAAGATT 420
QY 141 PheArgValLysProValLeuGlyLLeLysArgMetLLeGlnLLeGluTrpLLeLysPro 160
DB 421 TTCGGTGTAAACCAAGTTTGGGATCAACGAATGATTCAAAATTGATGATGAAGCCT 480
QY 161 GluLeuAlaProValSerSerAspLeuLysTrpThrLeuArgPheArgThrValAsnSer 180
DB 481 GAGTTGGCGGCTTTTCATCTGATTTAAATATACACCTTCGATTCAGGACAGCAACAGT 540
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DB 541 AACAGCTGGATGGAAGTCAACTTCGCTTAAGAACCGTAAGATAAAAACCAAGTCAAC 600
QY 201 LeuThrGlyLeuGlnProPheThrGluLysValLLeAlaLeuArgCysAlaValLysGlu 220
DB 601 CTCACGGGGCTGACGCTTTTACAGATATGTCATAGCTCTGGAGATGTGGCTCAAGAG 660
QY 221 SerLysPheTrpSerAspTrpSerGlnGluLysMetGlyWcThrGluGluAlaPro 240
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DB 781 CGTTGTATGGAAGAGCAAGAGAGCCCAAGTCTTAGAATAAAACCTTGGCTTACAAAC 840
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DB 841 ATATGTTACTATCCAGAAAGCAACCTAACCTCACAGAAACATATACCTAACCCAG 900
QY 301 GlnLeuGluLeuHisLLeuGlyLysGluSerPheTrpValSerMetLLeSerTrpAsnSer 320
DB 901 CAGCTTGAAGTCACTCGGAGGCGAGAGCTTTTGGGTCTCATGATTTCTTATATATCT 960
QY 321 LeuGlyLysSerProValAlaThrLeuArgLLeProAlaLLeGlnGluLysSerPheGln 340
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DB 1441 TTCTCCAAACAGTCAATTCACGATCTTGCAGTACGCTGAGTCCCTGAAACGAAAG 1500
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DB 1501 ACCCTTTCATGTTCAAGTCAAGTCCAGCACAGGCTGGGGGAAACCAACCGGACCAAC 1560
QY 521 LLeAsnPheLysThrLeuSerPheSerValPheGluLLeLLeLeuLLeThrSerLeuLLe 540
DB 1561 ATTAATTTTAAACATATTCATTCAGTGTCTTTGAGATTATCTCATTAATCTTCTGATT 1620
QY 541 GlyGlyLysLeuLLeuLLeLLeLLeLLeuThrValAlaTrpGlyLLeuLysLysProAsn 560
DB 1621 GGTGAGAGGCTTCTTATTTCTATTATCTCGAAGAGTGGCATATGCTCAAAAAACCAAC 1680
QY 561 LysLeuThrHisLLeuCysTrpProThrValProAsnProAlaGluSerSerLLeAlaThr 580
DB 1681 AAATTGACTCATCTGTGTGGCCACCGTTCCAAACCTGCTGAAGATGATAGCACCA 1740
QY 581 TrpHisGlyLysAspAspPheLysAspLysLeuAsnLeuLysGluLysAspAspSerValAsn 600
DB 1741 TGCATGAGAGATGATTTCAAGATTAAGCTAAACCTGAAGAGATGTGATGATCTGTGAAC 1800

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Qy 601 ThrGIuAaPArGjIleLeuLySerProCySerThrProSerAaPlyLeuValIleAspIys 620
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Qy 621 LeuValIaAaPheGlyAsnValIeugIingIiIephethrAspGIuAaArgThrGly 640
Db 1861 TTGGGTGGAACCTTGGGAATGTTCTGCAGAAATTTTACAGATGAAAGCCGAAGCGGT 1920
Qy 641 GInGIuAaAaAenLeuGIyGlyIyAsnGlyThraGjIleLeuSerSerCyPro 659
Db 1921 CAGGAAACAAATTTAGAGAGGAGGAAAGAAATGGG-----TATGTACCTGCCCC 1968
RESULT 12
US-09-892-949-1
; Sequence 1, Application US/09892949
; Publication No. US2003009639A1
; GENERAL INFORMATION:
; APPLICANT: Sprecher, Cindy A.
; APPLICANT: Preenell, Scott R.
; APPLICANT: Geo. Zeren
; APPLICANT: Whitmore, Theodore E.
; APPLICANT: Kuljper, Joseph L.
; APPLICANT: Maurer, Mark F.
; TITLE OF INVENTION: CYTOKINE RECEPTOR ZCYTOR17
; FILE REFERENCE: 00-42
; CURRENT APPLICATION NUMBER: US/09/892,949
; CURRENT FILING DATE: 2001-06-26
; PRIOR APPLICATION NUMBER: US 60/214,282
; PRIOR FILING DATE: 2000-06-26
; PRIOR APPLICATION NUMBER: US 60/214,955
; PRIOR FILING DATE: 2000-06-29
; PRIOR APPLICATION NUMBER: US 60/267,963
; PRIOR FILING DATE: 2001-08-02
; NUMBER OF SEQ ID NOS: 93
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1
; LENGTH: 2402
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (171)...(2366)
US-09-892-949-1
Alignment Scores:
Pred. No.: 0 Length: 2402
Score: 3465.50 Matches: 651
Percent Similarity: 99.24% Conservative: 1
Best Local Similarity: 99.09% Mismatches: 2
Query Match: 98.23% Indels: 3
DB: 10 Gaps: 1
US-10-006-265-17 (1-662) x US-09-892-949-1 (1-2402)
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Db 138 CTCCTCTCCCAAGCCTTCAATGTGTAACTGGGAGATGATGTGACCTGGGCACTGTGAGTG 197
Qy 23 LeuProSerLeuCyLyPheSerLeuAlaIaLeuProAlaIyPProGIuAaSnIleSer 42
Db 198 CTCCTCTCACTCTGCAATTTCAAGCTGGCAAGCTCTGCAGAGCTAAAGCTGAAACATTTCC 257
Qy 43 CysValIyTrpTrpArgLyAsnLeuThrCyThrTrpSerProGlyLyGluThrSer 62
Db 258 TGTGCTCTACTACTATAGGAAATTTAACTGCACTTGGAGTCCAGAAAGGAAACAGT 317
Qy 63 TyrThrGInTrpThrValIyAaArgThrTrpAlaPheGlyIyIyAaAaAspCyThr 82
Db 318 TATACCCAGTACACAGTAAAGAACTTACGCTTTTGAAGAAACATGATTAATTGACA 377
Qy 83 ThrAaSerSerThrSerGIuAaAaArgIaSerCySerPhePheLeuProArgIleThr 102
Db 378 ACCAATAGTCTTACAAAGTAAATGCTGCTGCTCTTTTCTTCTTCCAAGATAACG 437

Qy 103 IleProAaAenTrpThrIleGlyValIaGIuAaenGIyAspGIyValIleIySer 122
Db 438 ATCCAGATTAATTAATACATTTAGAGTGAACCTGAATAAGAGATGGTAAATTAATCT 497
Qy 123 HisMetThrTrpTrpArgLeuGIuAaSnIleAlaIySerThrGIuProProIyIlePheArg 142
Db 498 CATATGACATCTGAGATTTAGAGACATAGCGAAATCGAACCACTTAATATTTCCGT 557
Qy 143 ValIyProValIeugIyIleIyAaArgMetIleGInIleGIuTrpIleIyPProGIuLeu 162
Db 558 GTGAACACCACTTTGGGCATCAACGAATGATTCAAATGTGAATGATTAAGCTGAGTTG 617
Qy 163 AlaProValSerSerAaPlyLeuTrpThrIeunArgPheArgTrpValIaSerThrSer 182
Db 618 GCGCCTGTTTATCTGATTTAAATACACTTGTGATTCAGGACGTCACAGTACCAAGC 677
Qy 183 TrpMetGIuValIaAaPheAlaIyAaAaArgIyAspIyAaenGIuTrpTrpValIaSerLeuThr 202
Db 678 TGGATGGAAGTCACTTCGCTAAAGACCTTAAGATTAAGAAACCAACCTACACTCAG 737
Qy 203 GlyLeuGInProPheThrGlyTrpValIleAlaLeuArgCyAlaValIyGluSerIyS 222
Db 738 GGGCTGACGCTTTTACAGATATGTCATAGCTCTGCGATGTGCGTCAAGAGACTCAAG 797
Qy 223 PheTrpSerAaPTrpSerGIuIyIyMetGlyMetThrGIuGIuGIuAlaProCyGly 242
Db 798 TTCTGGAGTACTGAGCCAAAGAAATGGAAATGACTGGAGAAAGACTCCATGTGGC 857
Qy 243 LeuGIuLeuTrpArgValIleuLyPProAlaGIuAlaAaPgyAaArgPProValArgLeu 262
Db 858 CTGGAACCTGTGAAGATCTGAACCAAGCTGAGCGATGGAAGAAGCCAGTCCGCTTG 917
Qy 263 LeuTrpLyIyAaArgIyAlaProValIeugIyIySerThrLeuGIyTrpAsnIleTrp 282
Db 918 TTATGAAAGAAAGCAAGAGAGGCCCACTGCTAGAGAAACACTGCTCAACATATAGG 977
Qy 283 TyrTrpProGInSerAaenThrAsnLeuThrGIuIyMetAaenThrTrpAsnGIuLeu 302
Db 978 TACTATCCAGAAACCAACACTTAACCTCAAGAAACAAATGAACCTACTTAACCAAGCTT 1037
Qy 303 GIuLeuHisLeuGIyGIyGlySerPheTrpValSerMetIleSerTrpAsnSerLeuGIy 322
Db 1038 GAAGTCAATCTGGAGGCGAGAGCTTTGGGTGCTATGATTTCTTATTAATCTCTTGGG 1097
Qy 323 LysSerProValAlaTrpLeuArgIleProAlaIleGIuIySerPheGInCysIle 342
Db 1098 AAGTCTCAAGTGGCCACCCCTGAGGATTCAGCTATTCAGAAATAATCATTTCACTGCAAT 1157
Qy 343 GIuValMetGInAlaCyValAlaGIuAaPInLeuValIyTrpGIuInSerSerAla 362
Db 1158 GAGGTCAATGACGCTCGTGTGAGAGACCAAGCTAGTGTGAAGTGGCAAAAGCTCTGCT 1217
Qy 363 LeuAaPValAaenThrTrpMetIleGIuTrpPheProAaPValAaSerGIuProThrThr 382
Db 1218 CTAGACGTGAACCTTGAATGATTAATGATTTCCGATGTGAGCTAGAGCCCAACACC 1277
Qy 383 LeuSerTrpGluSerValIeGIuAlaIyAsnTrpThrIleGIuIyAspLyLeuIyS 402
Db 1278 CTTTCTCGGGAATGTGTCTCAGGCCAGCAAGTCAAGCAAGTAAATTTAAAA 1337
Qy 403 ProPheTrpCyIyTrpAsnIleSerValIyProMetLeuHisAaPlyValGIyGIuPro 422
Db 1338 CCTTTCTGGGTCTTAACATCTGTGTATCAATGTGTGATGCAAAAGTGGGAGCCCA 1397
Qy 423 TyrSerIleGIuAlaIyAlaIyGlyGIuValProSerGIuGIuProGIuTrpIyVal 442
Db 1398 TATTCATTCAGGCTTTATGCCAAGAAAGGCTTCAATCAAGAGCTCTGAGACCAAGTG 1457
Qy 443 GIuAaSnIleGIyValIySerThrValIleThrTrpLyGIuIleProLySerGIuArg 462
Db 1458 GAGAACTTGGCGGAGAGAGGTGACATGATCAATGAGAAAGATTTCCAAAGATGAGAGA 1517

QY 303 GILUEUHLSEUIGLYGLUSERPHERPVALSERMELLESERTYRASNSEUENGLY 322
DB 1038 GAACTGCACTTGGGAGGAGAGCTTTGGGCTTAATGATTTCTTAATATCTCTTGG 1097
QY 323 LYSERPROVALAATHREUARGILEPROALILEGINGULYSESPHEGINSYALLE 342
DB 1098 AAGCTCCAGTGGCCACCTGAGATTCCAGCTATTCAGAAATAATCTTCAAGTCATT 1157
QY 343 GLUVALMETGINALCYEVALAAGLUABPGLNLEUVALVALYETPGINSERIALA 362
DB 1158 GAGGACGACAGGCGCTGCTGCTAGAGACGAGTAGTGGAAGTGCAAAAGCTCTGCT 1217
QY 363 LEUASPVLAENHTTRMELILEGLUVRPHEPROASPVLAASPSGLUPROTHRTHR 382
DB 1218 CTAGACGGAACACTTGATGATTAAGTTCCGGAATGGACTCCAGCCCAACC 1277
QY 383 LEUSERTPGLUSERVALSERGINALATHRAENTRPTNILEGINLASPYLEUYS 402
DB 1278 CTTTCTGGGAATCTGTCTCAAGCCACGAAGTGAAGTCCAGCAATTAATTAATA 1337
QY 403 PROPHETPYCYSTRASNNLESERVALYRPROWELUEHLSASPYLEVALGLYGLUPRO 422
DB 1338 CTTTCTGCTGCTAATACATCTCTGTATCCAAATGTTGACATGACAAAGTTGGCGAGCCA 1397
QY 423 TYRSERIIEGINALATYRVALALYGLUVALYPROSERGIUGLYPROGLUTHRILYSEVAL 442
DB 1398 TATTCATCCAGGCTTATGCAAGAGAGCGCTTCATAGAAAGCTCGAAGCCAAAGGTG 1457
QY 443 GLUASNNILEGLYVALYSETHRVALTHRIETHRTPLYSGULILEPROLYSESGULYRG 462
DB 1458 GAGAAACATGGCGTGAACGCGTCAAGTCAATGGAAGAGATTCCCAAGAGTAGAGA 1517
QY 463 LYSGLYILLECYEASNTYRTHRIEPEHYRGINALGLYGLYLYSEGLYPHESESER 482
DB 1518 AAGGATATCATCTCAATACCAATCTTTACCAAGCTGAAGGTGAAAGATTTCTCC 1577
QY 483 LYSRTHRVALAENSESERILEUENLNTYRGLYLEUGLUSERLEUVALYRHYETHRSE 502
DB 1578 AAGACAGCAATTCAGCATCTTGAGTAGAGCGCTGAGGTCCCTGAAAGCAAGCTCT 1637
QY 503 TYRILEVALGINVALMETALASERTHSEVALGLYTHRAENGLYTHSERILEASN 522
DB 1638 TACATTTGTCAGTCATGCGACGACGAGTGTGGGGAACCAACGGAACCACTTAAT 1697
QY 523 PHELYRTHRLEUSERPHESESERVALPHEGLNILELEUJLETHSERLEUILEGLYGLY 542
DB 1698 TTCAAGACATGTCATTCAGTGTCTTGAGATTATCTCATNACTTCTGATTGTGGA 1757
QY 543 GLYLEUENLILEUJLELEUJLEUJLEUJLEUJLEUJLEUJLEUJLEUJLEUJLEU 562
DB 1758 GGCCTTCTTATTCATTCATTCATTCATTCATTCATTCATTCATTCATTCATTCAT 1817
QY 563 THRISLEUCYSTRPPTROTHRVALPROASNPROALAGUSERSERILEALATHRTPHIS 582
DB 1818 ACTATCTGTGTGGCCCACTGCTCCCAACCTGCTGAAAGTAGATATGCCAATGGCAT 1877
QY 583 GLYASHPAPHELYASPLYSELEUASNNLEUJSEGLUSERASPSERVALASNTHRGU 602
DB 1878 GGAATGATTTCAAGATTAACCTAAGAGAGGTCTGATGACTGCTGAAACACAGAA 1937
QY 603 ASHPARGILEUJLEUJLEUJLEUJLEUJLEUJLEUJLEUJLEUJLEUJLEUJLEU 622
DB 1938 GACAGGATCTTAAACATGTTCCACCCAGTGAAGATTTGATTAAGTGGTGTG 1997
QY 623 VALASNPHAGLYASNVALLEUGLNTJLEPHERTHRAPGLUALAARGTHGLYGLNGLU 642
DB 1998 GTGAACCTTGGGATTTCTGCAAGAAATTTTCAAGATGAAGCAAGAGGCTCAGGAA 2057
QY 643 ASNANLEUGLYGLYGLYASNNGLYTHRARGILEUSERSERCYSPRO 659
DB 2058 AACCAATTTAGAGAGGAGAAAGAAATGG-----TATGTGACCTGCCCC 2099

RESULT 14
US-10-772-531-1
; Sequence 1, Application US/10772531
; Publication No. US20040142422A1
; GENERAL INFORMATION:
; APPLICANT: Sprecher, Cindy A.
; APPLICANT: Presnell, Scott R.
; APPLICANT: Gao, Zeren
; APPLICANT: Whitmore, Theodore E.
; APPLICANT: Maurer, Mark F.
; TITLE OF INVENTION: CYTOKINE RECEPTOR ZCYTOR17
; FILE REFERENCE: 00-42
; CURRENT APPLICATION NUMBER: US/10/772,531
; CURRENT FILING DATE: 2004-02-05
; PRIOR APPLICATION NUMBER: US/09/892,949
; PRIOR FILING DATE: 2001-06-26
; PRIOR APPLICATION NUMBER: US 60/214,282
; PRIOR FILING DATE: 2000-06-26
; PRIOR APPLICATION NUMBER: US 60/214,955
; PRIOR FILING DATE: 2000-06-29
; PRIOR APPLICATION NUMBER: US 60/267,963
; PRIOR FILING DATE: 2001-08-02
; NUMBER OF SEQ ID NOS: 93
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1
; LENGTH: 2402
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (171)...(2366)
US-10-772-531-1
Alignment Scores:
Pred. No.: 0 Length: 2402
Score: 3465.50 Matches: 651
Percent Similarity: 99.24% Conservative: 1
Best Local Similarity: 99.09% Mismatches: 2
Query Match: 98.23% Indels: 3
DB: 18 Gaps: 1
US-10-006-265-17 (1-662) x US-10-772-531-1 (1-2402)
QY 3 LEUSERPROGLUPROSERCYEVALASNLEUGLYMETRTPRTHRTPALALEUTRPMET 22
DB 138 CTCTCTCCCAAGCCTTATGATGTTAACCTGGGATGATGAGACCTGGCACTGTGATG 197
QY 23 LEUPROSERLEUCYLYSPHESESERLEUALALEUPROALALYSPROGLUASNNILESER 42
DB 198 CTCCCTCACCTGCAAAATTCAGCTGAGCTCTGACAGTAAAGCTGAGAACATTTCC 257
QY 43 CYSEVALTYRTRARGLYASNNLEUJLEUJLEUJLEUJLEUJLEUJLEUJLEUJLEUJLEU 62
DB 258 TGTGTCTACACTATGAGAAATTTAACTGCACTTGAGATCCAGAAAGAAACCACT 317
QY 63 TYRTHRGINTYRTHRVALYARGTHRTYRVALPHEGLYGLYUJYVHLSASPASNCEYTHR 82
DB 318 TATACCCAGTACACAGTTAAGAGAACTTACGCTTTTGAAGAAACATGATTAATGTACA 377
QY 83 THRASNSESERTHRSERGIUASNARGALASERCYSESPHEPHELEUPROARGILETHR 102
DB 378 ACCAATGTTCTTAACATGAAATCGTGCTTCGCTCTTTTCCCTTCCAAAGAAATACG 437
QY 103 ILEPROASPVNTYRTHRIIEGLUVALAGLUASNNGLYASPGLYVALJILEYSESER 122
DB 438 ATCCCAATATAATTAACATTTGAGAGTGAAGCTGAAGATGAGATGCTAATTAATCT 497
QY 123 HISMETRTHRTYRTPARGLEUGLUAENLLEALALYSETHRGUUPROPROLYSILEPHEARG 142
DB 498 CATATGACATATTCGAGATTAAGAAACATAGCCAAACCTAAGATTTTCCGT 557
QY 143 VALYSPROVALLEUGLYLILEYARGMETILEGINLILEGLUVRPHELYSPROGLUJLEU 162

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Db      558 GTGAAACCGATTGGGACATCAAAACGAATGATTCATTAAGCTGAGTTG 617
Qy      163 AIAProValSerSerAspLeuLysTrpThrLeuArgPheArgThrValAsnSerTrpSer 182
Db      618 GGCCCTGTTTCATCTGATTTAAATAACACTTCGATTCAGGACAGTCAACATACAG 677
Qy      183 TrpMetGluValAsnPheAlaLysAsnArgLysAspLysAsnGlnThrTrpAsnLeuThr 202
Db      678 TGGATGGAAGTCAACTTCGCTTAAGAACCGTAAGGATTAACCAACGTAACACTCAAG 737
Qy      203 GlyLeuGlnProPheThrGluTrpValIleAlaLeuArgCysAlaValLysGluSerLys 222
Db      738 GGCCCTCAGCTTTTCAGAAATATGTCATAGCTCTCGATGTGCGGTCAAGGAGTCAAAAG 797
Qy      223 PheTrpSerAspTrpSerGlnLysMetGluMetThrGluGlnGluAlaProCysGly 242
Db      798 TTCTGGAGTGAATCTGGAGCCCAAGAAAAATGGGAATGACTGAGGAAGAGCTCCATGTGGC 857
Qy      243 LeuGluLeuTrpArgValLeuLysProAlaGluAlaAspGlyArgArgProValArgLeu 262
Db      858 CTGGAACGTGGAGAGTCCCTGAAACAGCTGAGCGGATGGAAAGGCGCAGTGGCGTTG 917
Qy      263 LeuTrpLysLysAlaArgGlyAlaProValLeuGluLysThrLeuGlyTrpAsnIleTrp 282
Db      918 TTATGAGAGAGGCAAGAGAGGCCCAAGTCTAGAGAAAAACACTTGGCTAACATATGG 977
Qy      283 TyrTrpProGluSerAsnThrAsnLeuThrGluThrMetAsnThrThrAsnGlnGlnLeu 302
Db      978 TACTATTCAGAAAGCAACACTAACCTCACAGAAACATGAACACTCAACCGACGACTT 1037
Qy      303 GluLeuHisLeuGlyGlyGluSerPheTrpValSerMetIleSerTrpAsnSerLeuGly 322
Db      1038 GAACCTCATCTGGAGAGCGAGACCTTTTGGGTCTCATATGATTTCTTATATTTCTTGGG 1097
Qy      323 LysSerProValAlaThrLeuArgIleProAlaIleGlnGluLysSerPheGlnCysIle 342
Db      1098 AAGTCTCCAGTGGCCCAACCTGAGAGATTCACAGTATTCAGAAAAATCATTTTCAGTGCATT 1157
Qy      343 GluValMetGlnAlaCysValAlaGluAspGlnLeuValValLysTrpGlnSerSerAla 362
Db      1158 GAGGTATGAGAGCGCTGGCTGTGTGAGAGCACACTGATGTGTAAGGCGCAACCTGTGCT 1217
Qy      363 LeuAspValAsnThrTrpMetIleGluTrpPheProAspValAspSerGluProThrThr 382
Db      1218 CTAGAGCTGAACACTTGGATGATTTGAATGTTTCCGATGTGGAATCTCAGAGCCCAACACC 1277
Qy      383 LeuSerTrpGluSerValSerGlnAlaThrAsnTrpThrIleGlnGlnAspLysLeuLys 402
Db      1278 CTTTCTGGGAATCTGTGTCTCAGGCCACGAACTGACATCCAGCAAGATAATTAAAA 1337
Qy      403 ProPheTrpCysTrpAsnIleSerValLysProMetLeuHisAspLysValGlyGluPro 422
Db      1338 CTTTCTGGGTCTATTAACATCTGTGTATCCAAATGTGATACAAAGTTGGCGAGCCA 1397
Qy      423 TyrSerIleGlnAlaTrpAlaLysGluGlyValProSerGluGlyProGluTrpLysVal 442
Db      1398 TATTCATCCAGGCTTATGCAAGAAAGCGTTCCATCAGAAAGCTCTGAGACCAAGGTTG 1457
Qy      443 GluAsnIleGlyValLysThrValThrIleThrTrpLysGluIleProLysSerGluArg 462
Db      1458 GAAACAATGGCGCTGAAGACGCTCAGCATCACATGAAAGAGATTCCCAAGATGAGAGA 1517
Qy      463 LysGlyIleIleLysAsnTrpThrIlePheTrpGlnAlaGluGlyLysGlyPheSer 482
Db      1518 AAGGGATATCATCTGCAACTACACATCTTTTACCAAGCTGAAGGTGAAAAAGGATTCCTCC 1577
Qy      483 LysThrValAsnSerSerIleLeuGlnTrpGlyLeuGluSerLeuLysArgLysTrpSer 502
Db      1578 ABAACAGTCAATTCAGCATCTTGGAGTACGCGCTGGAAGTCCCTGAAACCAAGAACTCT 1637
Qy      503 TyrIleValGlnValMetAlaSerThrSerAlaGlyLysThrAsnGlyThrSerIleAsn 522

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Db      1638 TACATTTGTCAGTCAATGCGCAGCACCAAGTGTGGGGGAAACCAACGGACCATTAAT 1697
Qy      523 PheLysThrLeuSerPheSerValPheGluIleIleLeuIleThrSerLeuIleGly 542
Db      1698 TTCAGACATTTTCATTCATTCAGTGTCTTTGAGATTATCCCTATTAATCTTCTGATGGTGA 1757
Qy      543 GlyLeuLeuIleLeuIleIleLeuThrValAlaTrpGlyLysLysLeuProAsnLysLeu 562
Db      1758 GGCCTTCTTATTCATATTCATATTCCTGACAGTGCATATGTGCTCAAAAAACCCAACAAAATTG 1817
Qy      563 ThrHisLeuCysTrpProThrValProAsnProAlaGluSerSerIleAlaThrTrpHis 582
Db      1818 ACTCATCTGTGTGTGGCCCACTGTCCCAACCTGTGTAAGATGATACCATGCGCAT 1877
Qy      583 GlyAspAspPheLysAspLysLeuAsnLeuLysGluSerAspAspSerValAsnThrGlu 602
Db      1878 GAGATGATTTCAAGATTAAGTAACTGAAGAGAGTCTGATGATCTGTGAACACAGAA 1937
Qy      603 AspArgIleLeuLysProCysSerThrProSerAspLysLeuValIleAspLysLeuVal 622
Db      1938 GACAGATCTTAAACCATGTTCCACCCCACTGACCAAGTTGATGACAAAGTTGGTG 1997
Qy      623 ValAsnPheGlyAsnValLeuGlnGluIlePheThrAspGluAlaArgThrGlyGlnGlu 642
Db      1998 GTGAACCTTGGGAATGTTCTGCAGAAATTTTCAAGATGAAGCCAGAAACGGGTCAAGAA 2057
Qy      643 AsnAsnLeuGlyGlyLysAsnGlyThrArgIleLeuSerSerCysPro 659
Db      2058 AACCAATTTTGAAGGGGAAAGAAATGGG-----TATGTACCTGCCCC 2099

RESULT 15
US-09-972-708-3
; Sequence 3, Application US/09972708
; Publication No. US20030059671A1
; GENERAL INFORMATION:
; APPLICANT: Immune Corporation
; APPLICANT: Cosman, David J.
; APPLICANT: Mosley, Bruce A.
; APPLICANT: Bird, Timothy A.
; APPLICANT: DuBoise, Robert F.
; APPLICANT: Wiley, Steven R.
; TITLE OF INVENTION: HEMATOPOIETIN RECEPTORS HPRI AND HPR2
; FILE REFERENCE: 3160-B
; CURRENT APPLICATION NUMBER: US/09/972,708
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3
; LENGTH: 2480
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-972-708-3

Alignment Scores:
Pred. No.: 0 Length: 2480
Score: 3465.50 Matches: 651
Percent Similarity: 99.09% Conservative: 2
Best Local Similarity: 98.79% Mismatches: 3
Query Match: 98.23% Indels: 3
DB: 10 Gaps: 1

US-10-006-265-17 (1-662) x US-09-972-708-3 (1-2480)
Qy      1 MetLysLeuSerProGluProSerCysValAsnLeuGlyMetMetTrpThrTrpAlaLeu 20
Db      132 ATGAAGCTCTCTCCCGAGCTTCATGTGTAACTGGGGATATGATGAGCTGGGGACTG 191
Qy      21 TrpMetLeuProSerLeuCysLysPheSerLeuAlaAlaLeuProAlaLysProGluAsn 40
Db      192 TGGATGCTCCCTTCACTCTGCAAAATTCAGCTTGGAGAGCTCTCCAGCTAAGCTGAGAA 251
Qy      41 IleSerCysValTyrTrpTrpArgLysAsnLeuThrCysThrTrpSerProGlyLysGlu 60

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Db 252 ATTCTGTCGTACTACTAGTAAATAATTAACTGCATTCGATCGAGAAAGAA 311
 Qy 61 ThrSerTyrThrGlnTyrThrValIysaGthrTyrAlaPheGlyGluLysHisAspAsn 80
 Db 312 ACCAGTTATACCCAGTACACAGTTAAGAACTTACGCTTTTGGAGAAAAACATATAT 371
 Qy 81 CysThrTrpAsnSerSerThrSerGluAsnArgAlaSerCysSerPhePheLeuProArg 100
 Db 372 TGTACACCAATAGTCTTCAAGTGAATTCGCTGCTGCTCTTTTCTTCTTCCAGCA 431
 Qy 101 IleThrIleProAspAsnTyrThrIleGluValGluAlaGluAsnGlyAspGlyValIle 120
 Db 432 ATAAAGATCCCGATATATATATACATTCATTCGATGAGTGAAGTGAATAATGAGATGCTGAAT 491
 Qy 121 LysSerHisMetThrTyrThrArgLeuGluAsnIleAlaLysThrGluProProLysIle 140
 Db 492 AAATTCATATGACATCTAGTACGAGATTAGAACATAGCGMAAACCTGAACACCTTAGATT 551
 Qy 141 PheArgValLysProValLeuGlyIleLysArgMetIleGlnIleGluTrpIleLysPro 160
 Db 552 TTCCTGTGAACACAGTTTGGGCATCAACAGAAATGATTCMAATGATGATTAAGCT 611
 Qy 161 GluLeuAlaProValSerSerAspLeuLysTyrThrLeuArgPheArgThrValAsnSer 180
 Db 612 GAGTTGGCGCTGTTTCATCTGATTTAAATACACACTTCGATTCAGGACAGTCAACAGT 671
 Qy 181 ThrSerTrpMetGluValAsnPheAlaLysAsnArgLysAspLysAsnGlnThrTyrAsn 200
 Db 672 ACCAGCTGATGAGAGTCAACTTCCTAAGAACCTTAAGATMAAACCAACCTACAC 731
 Qy 201 LeuThrGlyLeuGlnProPheThrGluTyrValIleAlaLeuArgCysAlaValLysGlu 220
 Db 732 CTCACGGGAGCTGACCTTTTACAAATATGTCATAGCTTCGCAATGCGGCTCAAGAG 791
 Qy 221 SerLysPheTrpSerAspTrpSerGlnLysMetGlyMetThrGluGluGluAlaPro 240
 Db 792 TCAAAAGTCTGGAGTGAAGTGGAGCAAGAAAAATGGGATGATCGAGGAAGAACTCCA 851
 Qy 241 CysGlyLeuGluLeuTrpArgValLeuLysProAlaGluAlaAspGlyValArgProVal 260
 Db 852 TGTGGCTCGGAACGTGAGAGTCTCTGAACCCAGCTGAGCGGATGAGAAAGGCACTG 911
 Qy 261 ArgLeuLeuTrpLysLysAlaArgLysAlaProValLeuGluLysThrLeuGlyTyrAsn 280
 Db 912 CGGTTGTTATGGAAGAACAGAGAGAGCCCAAGTCTAGAGAAAAACCTTGCTACAC 971
 Qy 281 IleTrpTyrTyrProGluSerAsnThrAsnLeuThrGluThrMetAsnThrThrAsnGln 300
 Db 972 ATATGGTACTATCCAGAAAGCACTAACCTCACAGAAACATGACACTACACAG 1031
 Qy 301 GlnLeuGluLeuHisLeuGlyGlyGluSerPheTrpValSerMetIleSerTyrAsnSer 320
 Db 1032 CAGCTTGAACGTGACTGTGGAGGCGAGAGCTTTTGGTGTATGATTTCTATATCT 1091
 Qy 321 LeuGlyLysSerProValAlaThrLeuArgIleProAlaIleGlnGluLysSerPheGln 340
 Db 1092 CTGGGAAGTCTCCAGTGGCCACCTGAGAGATCCAGCTATTCAGAAAAAATCATTTGAG 1151
 Qy 341 CysIleGluValMetGlnAlaCysValAlaGluAspGlnLeuValValLysTrpGlnSer 360
 Db 1152 TGCATTTGAGTCAATGCAAGCGCTGCTGAGACCAAGCTAGTGTGAAGTGGCAAGC 1211
 Qy 361 SerAlaLeuAspValAsnThrTrpMetIleGluTrpPheProAspValAspSerGluPro 380
 Db 1212 CCGTCTTAGACGTGAACATGATGATGATGATGATGATGATGATGATGATGATGAT 1271
 Qy 381 ThrThrLeuSerTrpGluSerValSerGlnAlaThrAsnTrpThrIleGlnGluAspLys 400
 Db 1272 ACCACCTTCTCTGGGAATCTGTGTCTCAAGGCGACGAAGTGGACGATCCAGAGATAAA 1331
 Qy 401 LeuLysProPheTrpCysTyrAsnIleSerValTyrProMetLeuHisAspLysValGly 420
 Db 1332 TTTAAACCTTCTGTGTGTATACATCTCTGTGTATCCAAATGTTGCAAGAAAGTTGGC 1391

Qy 421 GluProTyrSerIleGlnAlaTyrAlaLysGluGlyValProSerGluGlyProGluThr 440
 Db 1392 GAGCCATATTCATCCAGGCTTATGCCAAAGAGCGTTCCATCCAGAAAGTCTGAGACC 1451
 Qy 441 LysValGluAsnIleGlyValLysThrValThrIleThrTrpLysGluIleProLysSer 460
 Db 1452 AAGGTGAGAACTTGGCGTGAAGACGCTCACGATCATGGAAGAGATCCCAAGAGT 1511
 Qy 461 GluArgLysGlyIleIleCysAsnTyrThrIlePheTyrGlnAlaGluGlyLysGly 480
 Db 1512 GAGAGAAAGGATATCATCTGCACACTACACATCTTTTACCAAGCTGAAGGTGGAAGAGA 1571
 Qy 481 PheSerLysThrValAsnSerSerIleLeuGlnTyrGlyLeuGluSerLeuLysArgLys 500
 Db 1572 TTCCTCAAGACATCAATTCAGCATCTTGACATGAGCGCTGAGAGTCCCTGAACGGAAG 1631
 Qy 501 ThrSerTyrIleValGlnValMetAlaSerThrSerAlaGlyTyrAsnGlyThrSer 520
 Db 1632 ACCTTTCATTTGTCAGTCAATGCGCACGACACAGTCTGGGGGAACCGACGGACACG 1691
 Qy 521 IleAsnPheLysThrLeuSerPheSerValPheGluIleIleLeuIleThrSerLeuIle 540
 Db 1692 ATAAATTCAGACATTCATTCAGTGTCTTGAGATTATCTCATATTAATCTCTGATT 1751
 Qy 541 GlyGlyGlyLeuLeuIleIleLeuThrValAlaTyrGlyLeuLysLysProAsn 560
 Db 1752 GGTGAGGCTTCTTATTTCTATTATCTGACAGTGGCATATGATCTCAAAAAACCCAAC 1811
 Qy 561 LysLeuThrHisLeuCysTrpProThrValProAsnProAlaGluSerSerIleAlaThr 580
 Db 1812 AAATTTGACTCATCTGTGTGGCCACCGTTCCAACTCTGTAAGAGTATGACCA 1871
 Qy 581 TrpHisGlyAspAspPheLysAspLysLeuAsnLeuLysGluSerAspAspSerValAsn 600
 Db 1872 TGGCATGAGATGATTTCAAGATTAAGCTAACTGAAGAGTCTGATGACTCTGTGAC 1931
 Qy 601 ThrGluAspArgIleLeuLysProCysSerThrProSerAspLysLeuValIleAspLys 620
 Db 1932 ACAGAAAGCAGGATCTTAAACCATGTTCCACCCCGAGTCAAGTTGGTGAATTGACAA 1991
 Qy 621 LeuValValAsnPheGlyAsnValLeuGlnGluIlePheThrAspGluAlaArgThrGly 640
 Db 1992 TTGGTGTGAACCTTGGGAATGTTCTGCAAGAAATTTTCACAGATGAAGCCGAACGGGT 2051
 Qy 641 GlnGluAsnAsnLeuGlyGlyLysAsnGlyThrArgIleLeuSerSerCysPro 659
 Db 2052 CAGGAAAACAATTTAGAGGGGGAAGAAAGATGG-----TATGTGACCTGCCCC 2099

Search completed: February 23, 2005, 20:18:25
 Job time : 1102.62 secs

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GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Run on: February 23, 2005, 08:54:07 ; Search time 6085.24 Seconds
(without alignments)
4140.927 Million cell updates/sec

Title: US-10-006-265-17

Perfect score: 3528
Sequence: 1 MKSLPQPSQVNLGMMWTAL.....NNLGEKXKXTRILLSCPTSI 662

Scoring table:
BLOSUM62
Xgapop 10.0, Xgapext 0.5
Ygapop 10.0, Ygapext 0.5
Fgapop 6.0, Fgapext 7.0
Delop 6.0, Delext 7.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:

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Database :

EST:
1: gb_est1:
2: gb_est2:
3: gb_hc:
4: gb_est3:
5: gb_est4:
6: gb_est5:
7: gb_est6:
8: gb_gss1:
9: gb_gss2:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	735.5	20.8	2232	3	AK030512 Mus muscu
2	661	18.7	5264	3	BC071555 Homo sapi
3	657	18.6	3055	3	AY110138 Rattus no
4	529	15.0	663	2	BB617934 BB617934
5	473.5	13.4	653	5	BU455838 BU455838
6	468.5	13.3	637	7	CF174021 CF174021
7	465.5	13.2	2804	3	AK089305 Mus muscu
8	462.5	13.1	2592	9	AY412152 Homo sapi
9	426.5	12.1	2792	3	BC040954 Homo sapi

10	397	11.3	651	7	CF915066
11	396.5	11.2	2535	9	AY412154
12	392	11.1	1931	3	CF610771
13	355	10.1	1512	3	BC020454
14	347	9.8	592	6	CA561173
15	342	9.7	479	6	CA560924
16	326	9.2	828	5	BU271003
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21	308.5	8.7	1131	5	EX380515
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29	294	8.3	642	6	CB512958
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34	286	8.1	1577	3	CB613729
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ALIGNMENTS

RESULT 1	LOCUS	DEFINITION	ACCESSION	VERSION	KEYWORDS	SOURCE	ORGANISM	REFERENCE	AUTHORS	TITLE	JOURNAL	MEDLINE	PUBMED	REFERENCE	AUTHORS
AK030512	AK030512	2232 bp mRNA linear HTC 03-APR-2004	AK030512	1	GI:26326508	HTC; CAP trapper.	Mus musculus (house mouse)	1	Carninci, P. and Hayashizaki, Y.	High-efficiency full-length cDNA cloning	Mech. Enzymol. 303, 19-44 (1999)	99279253	10349636	2	Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Kono, H., Okazaki, Y., Muramatsu, M., and Hayashizaki, Y.
AK030512	AK030512	Mus musculus adult male pituitary gland cDNA, RIKEN full-length	AK030512	1	GI:26326508	HTC; CAP trapper.	Mus musculus (house mouse)	1	Carninci, P. and Hayashizaki, Y.	High-efficiency full-length cDNA cloning	Mech. Enzymol. 303, 19-44 (1999)	99279253	10349636	2	Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Kono, H., Okazaki, Y., Muramatsu, M., and Hayashizaki, Y.
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Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsunura, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y., RIKEN integrated sequence analysis (RISA) system-184-format sequencing pipeline with 384 multicapillary sequencer
Genome Res. 10 (11), 1757-1771 (2000)
20530913
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11076861

4 The RIKEN Genome Exploration Research Group Phase II Team and the PANTOM Consortium

JOURNAL TITLE Functional annotation of a full-length mouse cDNA collection
REFERENCE Nature 409, 685-690 (2001)
AUTHORS 5

JOURNAL TITLE The PANTOM Consortium and the RIKEN Genome Exploration Research Group Phase I & II Team.
REFERENCE Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs
AUTHORS Nature 420, 563-573 (2002)
6 (bases 1 to 2232)
Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Bono, H., Carninci, P., Hayashida, K., Hayatsu, N., Hiramoto, K., Hirooka, T., Hirozane, T., Hori, F., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Kasukawa, T., Katoh, H., Kawai, J., Kojima, Y., Kondo, S., Kono, H., Kouta, M., Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Murata, M., Nakamura, M., Nishii, K., Nomura, K., Numazaki, R., Ohno, M., Ohsato, N., Okazaki, Y., Saito, R., Saitoh, H., Sakai, C., Sakai, K., Sakazume, N., Sano, H., Sasaki, D., Shibata, K., Shinagawa, A., Shiraki, T., Sogabe, Y., Tagami, M., Tagawa, A., Takahashi, F., Takaku-Akahira, S., Takeuchi, Y., Tanaka, T., Tomaru, A., Toya, T., Yasunishi, A., Muramatsu, M. and Hayashizaki, Y.

TITLE Direct Submission

JOURNAL TITLE Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail: genome-res@gs.c.riken.jp, URL: http://genome-gsc.riken.jp/, Tel: 81-45-503-9222, Fax: 81-45-503-9216)

COMMENT CDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of genome exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in Riken. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.

URL: http://genome-gsc.riken.jp/
URL: http://fantom.gsc.riken.jp/
Location/Qualifiers

FEATURES

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ORIGIN

Alignment Scores:
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Score: 735.50 Matches: 147
Percent Similarity: 79.25% Conservative: 25
Best Local Similarity: 67.74% Mismatches: 42
Query Match: 20.85% Indels: 3
DB: 3 Gaps: 2

US-10-006-265-17 (1-662) x AK030512 (1-2232)

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Db 212 CCATTAAAGAGTCTTGAGACCAAGGTTGAGAACATCGCTGAGACCAAGTACCA 271
QY 454 TPlyGluIleProIleSerGluArgIleGlyIleIleCysAspTyrThrIlePheTyr 473
||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
Db 272 TGGAGGAGATTCTTAAGAGTCTTGAAGTGAATGATTTATCAACATTAACCTGATTTTC 331
QY 474 GlnaIaGluGlyIleGlySerIlePheSerIleThrValaIleSerIleIleGlnIleTyrGly 493
||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
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QY 494 LeuGluSerIleuIleArgIleThrSerTyrIleValaIleMetAlaSerThrIleAla 513
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QY 514 GlyIleThrAsnGlyThrSerIleAsnPheIleThrIleSerPheSerValPheGluIle 533
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QY 534 ILeuIleThrSerIleIleGlyIleIleuIleIleuIleIleuIleIleuIleValaIle 553
||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
Db 512 GTCCTTCTTAACATCTCTAATGAGAGAGGCTCTTCTTCTTCTTCTTCTTCTTCTTCTT 571
QY 554 TyrGlyLeuIleuIleProAsnIleuIleThrIleIleuIleuIleuIleuIleuIleuIleu 573
||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
Db 572 TTTGGCTTCAAGCAAGCAAGCGTTGACTCCCTGTGTGTCTGTATGTTCCCAAGCT 631
QY 574 AlaGluSerIleAlaThrIleIleGlyAspAspPheIleAspIleuIleuIleuIleuIleuIleu 593
||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
Db 632 GCGAAGAGTATTTAGCCATGCTCGGAGATGGTTTCAAG--AAGTCAATATGAG 688
QY 594 GluSerAspAspSerValaIleuIleuIleuIleuIleuIleuIleuIleuIleuIleuIleuIleu 613
||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
Db 689 GAGACTGAAAGTCTGCGGACACAGAGACGCTGCTTAAACATATGCTCCGCTCCCGCG 748
QY 614 AspIleuIleuIleuIleuIleuIleuIleuIleuIleuIleuIleuIleuIleuIleuIleu 633
||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
Db 749 GAT-----CTCATTTGACCAAGCTGTGAGAACTTTGAGAAATTTCTGAGAGTATTG 802
QY 634 ThrAspGluAlaArgThrGlyGlnGluAsnIleuIleuIleuIleuIleuIleuIleuIleuIleu 650
||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
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Db 803 ACGAGGAGAGCTGGAAGGCTCAGCGGAGCATTTTGGAGGAGAACCGAAT 853
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RESULT 2
BC071555 5264 bp mRNA linear HTC 02-JUN-2004
LOCUS BC071555
DEFINITION Homo sapiens CDNA clone IMAGE:4374041, containing frame-shift
errors.
ACCESSION BC071555
VERSION BC071555.1 GI:47938807
KEYWORDS HTC.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

REFERENCE
AUTHORS Struhsberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G., Klausner, R.D., Collins, F.S., Wagner, L., Shemen, C.M., Schuler, G.D., Altesh, S.F., Zeeberg, B., Buetow, K.H., Scheffer, C.F., Bat, N.K., Hopkins, R.F., Jordan, H., Moore, T., Wax, S.I., Wang, J., Hsieh, F., Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L., Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L.,

TITLE	JOURNAL PUBLISHED	REFERENCE AUTHORS TITLE	JOURNAL
Scheetz, T.E., Brownstein, M.J., Usdin, T.B., Toshitsuki, S., Grancini, P., Prange, C., Raba, S.C., Loquett, N.A., Peters, G.J., Abramson, R.D., Mullaly, S.J., Bosak, S.A., McEwan, P.J., McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S., Morley, K.C., Hale, S.E., Garcia, A.M., Gay, L.J., Hilly, S.W., Villalón, D.K., Muzny, D.M., Sodergren, E.U., Lu, X., Gibbs, R.A., Fahy, J., Helton, E., Kettelman, M., Madan, A., Rodrigues, S., Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y., Bouteffar, G.G., Blakeley, R.W., Touchman, J.W., Green, E.D., Dickson, M.C., Rodriguez, A.C., Greenwood, J., Schmitt, J., Myers, R.M., Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Smilans, D.E., Schercher, A., Schein, J.E., Jones, S.J. and Marra, M.A.	Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)	Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences	
2 (pages 1 to 5264)	14477932	Strausberg, R.	
Direct Submission			
Submitted (01-JUN-2004)		National Institutes of Health, Mammalian	

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Best Local Similarity:	28.55%
Query Match:	18.74%
DB:	3
	Gaps: 20
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QY	55 TipSerProGlyLysGluThrSerYr--ThrgIntYrThrValLys-----Arg 70
Db	581 TGGGATGCTGTGAAGGGAACACACTTGTGAGACCAACTTCACCTTTAAATCTGAATGGCA 6400

QY	71	ThrTyrAlaPheGlyGlu-----LysHisAsp-----AsnCysThrThra	84
Db	641	ACACCAAGATTGCTGATTGCAGAAAGCAAAAGCTGACACCCCACTCAAGCATGTTGAT	700
QY	85	SerSerThrSerSerGluAsnArgAlaSerCysSerPhePheLeuProArgIleThrIlePro	104
Db	701	TATTTCTACT-----CTGATTTTTTGTCC-----	721
QY	105	AspPentYrThrIleGluValGluAlaGluAsnGlyAspGlyValIleLysSer---His	123
Db	722	---AACATTGAAGCTGGGTGAAGACAGAGAAATCCCTTGGGAAGGTTACATCAGATCAT	778
QY	124	MetThrYrYrTPraPheGluAsnIleAlaLysThrGluPurPolySilePheArgVal	143
Db	779	ATCAATTTTGGATCCTGTATATTAAGTG---AAGCCCAATCCGCAATATTTATATCAGTG	835
QY	144	LysProValleuGlyIleLysArgMetIleGlnIleGluTrpIleLysProGluLeuAla	163
Db	836	ATCAACTCAGAGGAACCTCTAGATATCTTAAATATGACATGACCAACCAAGATTAAG	895
QY	164	ProValSerSerAspLeuLysYrYrThrLeuArgPheArgThrValAsnSerThrSerTrp	183
Db	896	AGTGTTATATA---CTAAATATATACATTCATATATGAGCAAAAGATGCTCAACTGAG	952
QY	184	MetGluValaAsnPheAlaLysAsnArgLysAspLysAsnGlnThrYrAsnLeuThrGly	203
Db	953	AGCCAGAAATTCCT---CCTGAAGACACAGCATCCACCGATCTTCACTCATCTCAAGAC	1009
QY	204	LeuGlnProPheThrGluYrValIleAlaLeuArgCysAlaValLysGluSerLys---	222
Db	1010	CTTAAACCTTTTACGAAATATGTGTTTATGAGATTCGCTGTATGAAAGAAAGATGTAAGGA	1069
QY	223	PheTrpSerAspTrpSerGlnGluLysMetGlyMetThrGluGluAlaProCys---	241
Db	1070	TACGGAAGTACCTGAGATGAAGAAAGCAAGGGAGTACCTATGAAGATAGACCATTA	1129
QY	242	GlyLeuGluLeuTPraPheValLeuLysProAlaGluAlaAspGlyArgProValArg	261
Db	1130	GCACCAAGTTCTGTGTAAATATGATCCATCCATCTCAAGGCTCAGAACTGTCA	1189
QY	262	LeuLeuTrpLysLysAlaArgGlyAlaProValLeuGluLysThrLeuGlyYrAsnIle	281
Db	1190	CTCGTGTGAAGACATGCTCCTCTTTGAAGCCAAAGAAATCTTGATTAAGAAAGTG	1249
QY	282	TrpYrYrProGluSerAsnThrAsnLeuThrGlnThrMetAsnThrTrpAsnGlnGln	301
Db	1250	ACTCTCACAGATGGAATTCACATTTACAAATATACACAGTATATGCCAC-----AAA	1303
QY	302	LeuGluLeuHisLeuGlyGlyGluSerPheTrpValSerMetIleSerYrAsnSerLeu	321
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QY	322	GlyLysSerProValAlaThrLeuArgIleProAlaIleGlnGluLysSerPheGlnCys	341
Db	1364	GGCAAAATCAGATGACGCTGTTTAACTATCCCTGCGCTGATCACTTCAAGCTACACCT	1423
QY	342	IleGluValMetGlnAlaCysValAlaGluAspGlnLeuValValLysTrpGlnSerSer	361
Db	1424	GTAATGATCTTAAAGCATTCGCCCAAGATTAACATGCTTTGGGTGAATGATCACTCCA	1483
QY	362	AlaLeuAspValAsnThrTrpMetIleGluTrpPheProAspValaAspSerGluProThr	381
Db	1484	AGGAATCTGTAAGAATATATATCTTGAAGGGGTGTGTATTCAGATTAAGCAACCTGT	1543
QY	382	ThrLeuSerTrpGluSerValSerGlnAlaThrAsnTrpThrIleGlnGlnAspLysLeu	401
Db	1544	ATCACAGACTGCGCAACAAAGATGTGATCCGTGATCGCATGCACTTATTTAAAGGAATTA	1603
QY	402	LysProPheTrpCysYrTranIleSerValYrProMetLeuHisAspLysValGlyGlu	421
Db	1604	GCAGAGCAAAATGCTATTTGATTAACAGTATCTCCATATATGCTGATGGAACGAGAAC	1663
QY	422	ProYrSerIleGlnAlaYrAlaLysGlyValaProSerGluGlyProGluThrLys	441

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Qy      442 ValGlaAsnIleGlyValIleThrValThleThrTrpIleGluIleProIleSerGlu 461
Db      1724 AC-AAAAAAGTGGAGAAAAAGAAAGCTGCTTCTTGAAGGAGCAACTCTCTGTTGATGTT 1782
Qy      462 ArgIleGlyIleIleCysAsnIleThrIlePheThrGlnIleGluIleGlyIleGlyPhe 481
Db      1783 CAGAATGATTTATTCAGAAATTTATCTATTTTATTAAGAACCATTCATTTGGAATGAAACT 1842
Qy      482 SerIleThrValAsnSerIleLeuGlnIleGlyIleGluIleSerIleuIleuIleuIleu 501
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Qy      522 AsnIleThrIleuIleuIleuIleuIleuIleuIleuIleuIleuIleuIleuIleuIleu 541
Db      1963 ACTTTTACATACCCCAAGTTGCTCAAGAGAAATGGAGCATATGCTGCTGTTGTC 2022
Qy      542 GlyIleGlyIleuIleuIleuIleuIleuIleuIleuIleuIleuIleuIleuIleuIleu 561
Db      2023 TTAGCATTCCTATTGCAACTCTTCTGGAGTCTGTTCTTCTTATTAAGCAGACCTA 2082
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Qy      582 -----TTTCCAGAAAGTTCGAAATCACTGAC----- 2280
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Qy      595 SerAspAspSer-----ValAsnThrGluAspArgIleLeuIleuIleuIleuIleuIleu 608
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Qy      609 CysSerThrProSerAspIleuValIleAspIleuValIleAsnIleGlyAsnVal 628
Db      2254 -----TTTCCAGAAAGTTCGAAATCACTGAC----- 2280
Qy      629 LeuGlnIleuIleuIleuIleuIleuIleuIleuIleuIleuIleuIleuIleuIleuIleu 646
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Qy      647 GlyGluIleuAsnIleuIleuIleuIleuIleuIleuIleuIleuIleuIleuIleuIleuIleu 661
Db      2332 GGG-----TCTTCATGATGATCATCT 2352

RESULT 3
AY310138      3055 bp      mRNA      linear      HTC      07-JUL-2003
DEFINITION    Rattus norvegicus Acl055 mRNA, complete cds.
ACCESSION     AY310138
VERSION       AY310138.1 GI:32264598
KEYWORDS      HTC.
SOURCE        Rattus norvegicus (Norway rat)
ORGANISM      Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.
1 (bases 1 to 3055)
XU,C.S., LI,W.Q., LI,Y.C., HAN,H.P., WANG,G.P., CHAI,L.Q.,
YUAN,J.Y., YANG,K.J., YAN,H.M., CHANG,C.F., ZHAO,L.F., MA,H.,
WANG,L., WANG,S.F., SHI,J.B., RAHMAN,S., WANG,Q.N. and ZHANG,J.B.
Liver regeneration after PH
Unpublished
2 (bases 1 to 3055)
XU,C.S., LI,W.Q., LI,Y.C., HAN,H.P., WANG,G.P., CHAI,L.Q.,
YUAN,J.Y., YANG,K.J., YAN,H.M., CHANG,C.F., ZHAO,L.F., MA,H.,
WANG,L., WANG,S.F., SHI,J.B., RAHMAN,S., WANG,Q.N. and ZHANG,J.B.
```

```
TITLE      Direct Submission
JOURNAL    Submitted (29-MAY-2003) Henan Bioengineering Key Lab, Henan Normal
           University, No. 148 Jianshe Road, Xinxiang City, Henan 453002, P.R.
           China
FEATURES   source
            Location/Qualifiers
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              DRTKGTSSCMWGYPIYFVNI EWVEENMLGNVSESPINFDVDKVPSPHNL
              VTNSELSILKLAWNSGLDILRLKSDIOYRTDASWIOVLEDTVPRTSVQ
              DIKPTVEYVFRISIKENGKYSMSSEASGTTEDRPSKPSFWYKNAHPOEYR
              SARLWKTLPLSEANGKIDIEVTVTQSSVSQTYTNGTELIYVLTNNRYASLAAR
              NVGKSPATVLTIPGSHRKVDLAPKQNLWENTPSPKPVNKTILECVISENSPC
              IPDWQEDGTNVRHLRGLSKCYLITVTFPGGPGVPSMRAVYLKQAPSGPT
              VRTKLVKKEAVLEWMDHLPVDVQNFIRINYSISYTSVGEKVVAVVSDSHTEYLSL
              SSDLTYKVMVAYTEEGKDGPEFTFTLKFGESSCAAGMSIANSWPTADASSFD
              DVOYIKKHIVPVPDPSKSHLOMSPHPPRRNPSKOMVSDANFTDVSVEITANN
              KRPCTDDKSLDLPKKEKISTEGHSSSGIGGSSCMSSRPSISSSENBQSTASTQ
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Qy      74 PheGlyIleuIleHisAspAsnCysThrThrAsnSerSerThrSerGluAsnIleuAlaSer 93
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DB 1112 TCGCAAACTTACACAGATTAAACGGACA---GAGTTGATAGTAAACCTCCCAATTAAC 1165
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QY 330 ArgIleProAlaIleGlnGlnLysSerPheGlnCysIleGluValMetGlnAlaCysVal 349
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QY 350 AlaGluAspGlnLeuValValLysTrpGlnSerSerAlaLeuAspValAsnThrTrpMet 369
DB 1271 AAAGATTAACCTGCTGTGGTGAATGACACCGCATTAACCTGTGAACAAATACATA 1330
QY 370 IleGluTrpPheProAspValAspSerGluProThrThrLeuSerTrpGlnSerValSer 389
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QY 410 SerValTrpPrometLeuHisAspLysValGlyLysProTrpTrpSerIleGlnAlaTrpAla 429
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QY 450 ValThrIleThrTrpLysGluLysLeuProLysSerGluValGlyIleIleCysAsnTrp 469
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QY 490 LeuGlnTrpGlyLeuGlnSerLeuLysArgLysThrSerTrpIleValGlnValMetAla 509
DB 1691 ACAAGATACACACTCTCTTTGAGTAGCAGTACATCTATACATGCTCACATGCGACAGA 1750
QY 510 SerThrSerAlaGlyLysThrAsnGlyThrSerIleAsnPheLysThrLeuSerPheSer 529
DB 1751 TACACAGAAAGAGTGGGAGAGATGGCGGCAATTCATTTTAAACACATAAGTTTGGT 1810

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QY 530 ValPheGluIleIleLeuIleThrSerLeuIleGlyGlyLeuLeuIleLeuIle 549
DB 1811 GAA-----TCTGTCTGTGTGCGGCTCCGGCTTATGAGATGCCCGGA 1852
QY 550 -----LeuThrValAlaIleTrpGlyLysLysPro 559
DB 1853 AACTCTGGCCTACAGACAGCATCATATTGATGACTGTACCAATTAATAAAA--- 1909
QY 560 AsnLysLeuThrHisLeuCysTrpProThrValProAsnProAlaGlnSerIleAla 579
DB 1910 -----CACATC---TGCGCAATGTCCAGATCTTCCAAAGATCATTTTCC 1954
QY 580 ThrTrp-----HisGlyAspAspPheLysAspLysLeu----- 590
DB 1955 CAGTGTCACTCACACACCCCGCCAAAGCAATTTTAACTCCAAAGATCAGATGACTCA 2014
QY 591 AsnLeuLysGlnSerAspAspSer---ValAsnThrGluAspArgIleLeuLysProCys 609
DB 2015 GATGCAATTTCACTGACGTAAAGCGTGTGGAATAGAAAGCAACAAACAAAGCCTTGT 2074
QY 610 SerThrProSerAspLysLeuValIleAspLysLeuValValAsnPheGlyAsnValLeu 629
DB 2075 -----CCAGATGACCTGAAATTCCTTGAC----- 2098
QY 630 GlnGluIlePheThrAspGlu-----AlaArgThrGlyGlnGluAsnAsnLeuGlyGly 647
DB 2099 -----CTGTCAAGAGAGAAATAATAGTACAGAGGGCACAGCAGTGGCATTTGGGGG 2152
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DB 2153 -----TCCCTGTCGATGTCCTCT 2170

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RESULT 4
 BB617934
 LOCUS
 DEFINITION BB617934 RIKEN full-length enriched, adult male pituitary gland Mus
 musculus cDNA clone 5330424C19 5', mRNA sequence.

ACCESSION
 BB617934
 BB617934.1 GI:15396442

VERSION
 BB617934.1

KEYWORDS
 EST.

SOURCE
 Mus musculus (house mouse)

ORGANISM
 Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE

1 (bases 1 to 663)
 Arai, K., Hiramoto, K., Horii, F., Ishii, Y., Ito, M., Kawai, D.,
 Kono, H., Kondo, M., Koya, S., Matsuyama, T., Miyazaki, A., Nomura, K.,
 Ohno, M., Okazaki, Y., Okido, T., Saito, R., Sakai, C., Sakai, K.,
 Sano, H., Sasaki, D., Shibata, K., Shinagawa, A., Shiraki, T.,
 Sogabe, Y., Suzuki, H., Tagami, M., Tagawa, A., Takahashi, F.,
 Takeda, Y., Tanaka, T., Toy, T., Muramatsu, M., and Hayashizaki, Y.
 RIKEN Mouse ESTs (Arai, K., et al. 2001)
 Unpublished (2001)

TITLE

JOURNAL

COMMENT

Contact: Yoshihide Hayashizaki
 Laboratory for Genome Exploration Research Group, RIKEN Genomic
 Sciences Center (GSC), Yokohama Institute
 The Institute of Physical and Chemical Research (RIKEN)
 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
 Tel: 81-45-503-9222
 Fax: 81-45-503-9216
 Email: genome-res@sc.riken.jp, URL: http://genome.gsc.riken.jp/
 Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K.,
 Itoh, M., Kono, H., Okazaki, Y., Muramatsu, M., and Hayashizaki, Y.
 Normalization and subtraction of cap-trapper-selected cDNAs to
 prepare full-length cDNA libraries for rapid discovery of new
 genes. Genome Res. 10 (10), 1617-1630 (2000)
 Wagi, K., Fujiwara, S., Inoue, K., Togawa, Y., Iwawa, M., Ohara, E.,
 Watahiki, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T.,
 Matsunura, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kita, A.,
 and Hayashizaki, Y.
 RIKEN integrated sequence analysis (RISA) system-384-format
 sequencing pipeline with 384 multicapillary sequencer. Genome Res.

Percent Similarity: 61.11% Conservative: 27
 Best Local Similarity: 47.47% Mismatches: 76
 Query Match: 13.42% Indels: 1
 DB: 5 Gaps: 1

US-10-006-265-17 (1-662) x B0455838 (1-653)

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Db 14 TCATGGCGATATATATCAAAATTCACAAAGTGAAGAACTACACAAAAAACTTTAAATTA 73
Oy 404 PheTPCyTYrAsnIleSerValTYrPheMetLeuHisAspLysValGlyGluProTYr 423
Db 74 TTTGATGCTCAACAATGCTAGCTATCTTACTATCTGAAAAATAAGTAGCAGCTCATAT 133
Oy 424 SerIleGlnAlaTYrAlaLysGluGlyValProSerGluGlyProGluThrLysValGlu 443
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Oy 444 AsnIleGlyValLysThrValThrIleThrTrpLysGluIleProLysSerGluArgLys 463
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Oy 464 GlyIleIleCyAsnTYrThrIlePheTYrGlnAlaGluGlyGlyLysGlyPheSerLys 483
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Oy 484 ThrValAsnSerSerIleLeuGlnTYrGlyLeuGlnSerLeuLysArgLysThrSerTYr 503
Db 314 ACAGGAACCTGATGCTCTACAGTACACACTGAAAGTCTTACAGGCTAATACATATAC 373
Oy 504 IleValGlnValMetAlaSerThrSerAlaGlyTYrThrAsnGlyThrSerIleAsnPhe 523
Db 374 ACTGCTATATATACATGAGCAAGCAAGACCTGCTGGAACCAAGGAGAGCAAAACATTC 433
Oy 524 LysThrLeuSerPheSerValPheGluIleIleLeuIleThrSerLeuIleGlyGly 543
Db 434 AAGACTTTGAAATTCATTAAGAAAGACCTTATTTTCATTCGAAATCCAGTTGATTAAGC 493
Oy 544 LeuLeuIleLeuIleIleLeuThrValAlaTYrGlyLeuLysPheAsnLysLeuThr 563
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Oy 564 HisLeuCyTrpProThrValProAsnProAlaGlnSerSerIleAlaThrTYr 581
Db 551 AAGTTTGCTGCTGATGATGCCAATCTCTGACAGAGCGTTGCAGTGCAGTGG 604

RESULT 6
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LOCUS 637 bp mRNA linear EST 25-JUL-2003
DEFINITION B0932D09-5 NIA Mouse Unfertilized Egg cDNA Library (long 1) Mus
ACCESSION musculus cDNA clone NIA:B0932D09 IMAGE:30475340 5', mRNA sequence.
VERSION CE174021
KEYWORDS GI:33283570
SOURCE EST.
ORGANISM Mus musculus (house mouse)
MUS musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 637)
Pao, Y., Ko, N.-T., Lim, M.-K. and Ko, M.-S. H.
Construction of long-transcript enriched cDNA libraries from
submicrogram amounts of total RNAs by a universal PCR amplification
method
Genome Res. 11 (9), 1553-1558 (2001)
JOURNAL MEDLINE
PUBMED
COMMENT
Laboratory of Genetics
National Institute on Aging/National Institutes of Health
333 Cassell Drive, Suite 4000, Baltimore, MD 21224-6820, USA
Email: cdna@nigun-grc.nia.nih.gov
Plate: B0932 row: D column: 09

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Seq primer: M13 Reverse
 High quality sequence stop: 637
 POLYA=NO.

FEATURES
 source Location/Qualifiers

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ORIGIN

Alignment Scores:

Pred. No.: 1,3e-39 Length: 637
 Score: 468.50 Matches: 96
 Percent Similarity: 63.59% Conservative: 21
 Best Local Similarity: 52.17% Mismatches: 54
 Query Match: 13.28% Indels: 13
 DB: 7 Gaps: 4

US-10-006-265-17 (1-662) x CE174021 (1-637)

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Db 119 CCTCGGAGTGTGAACGCTGGAAATATGTGACCTTGACATGTGGCATTCCTTCCTC 178
Oy 27 CysLysPheSerLeuAlaAlaLeuProAlaLysProGluAsnIleSerCyValTYr 46
Db 179 TGCAAAATTCAGCGCGAGTCTCGCCAGCTAAGCAAGAACATTTCTGGCTTTTAC 238
Oy 47 TyrArgLysAsnLeuThrCyThrTrpSerProGlyLysGluThrSerTYrThrGlyTYr 66
Db 239 TTCACAGAAATTCGATTCGATTCGACGACGACGACGACGACGACGACGACGACGAC 298
Oy 67 ThrValLysArgThrTYrAlaPheGlyGluLysHisAspAsnCyThrThrAsnSer 86
Db 299 ATTGTGACTTGAATCTTACTCTATGAAAA-----AGCAAT 334
Oy 87 ThrSerGluAsnArgAlaSerCySerPhePheLeuProArgIleThrIle-----Pro 104
Db 335 TATGTGACAAATGCTACAGAGCTTCATATTTCTTCCGCTTCCTGCAATGCCCCCA 394
Oy 105 AspAsnTYrThrIleGluValAlaGluAlaGluAsnGlyAspGlyValIleLysSerHisMet 124
Db 395 GACATCGACGCTGTGAAGTACAAAGCTCAAAATGAGATGTGTAAGTTAATCTGACATC 454

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Qy 125 ThrTyrTrpArgbGluAsnIleAlaIysThrGluProProlysiIlePheArGValIys 144
 Db 455 ACATATGGCATTTAATCTCCATACGAAAACGAAACCACTTAATTTTAATGTCGAAT 514
 Qy 145 ProValIleuGlyIleIysArgMetIleGlnIleGluTrpIleIysProGluIuAlaPro 164
 Db 515 CCAATT-----TGTAAATGAAGATGTTCCAGATACAAATG---AAACCGCGTGAAGAAAGACT 565
 Qy 165 ValSerSerAspIuIysTyrTrpTrpIuAsArgPheArgThrValAsnSerThrSerpMet 184
 Db 566 CGTGGGTTTCCTTACTAGATGATGATCTTCGTTGCAAGTGTCAACAGTACCACTGACG 625
 Qy 185 GluValAsnPhe 188
 Db 626 GAAGTCATTTT 637

RESULT 7
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 LOCUS
 DEFINITION
 AK089305 2804 bp mRNA linear HTC 03-APR-2004
 full-length enriched library, +ve dendritic cells cDNA, RIKEN
 stimulating factor 3 receptor (granulocyte), full insert sequence.
 AK089305
 VERSION AK089305.1 GI:26105194
 KEYWORDS HTC; CAP trapper.
 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE
 AUTHORS Carninci, P. and Hayashizaki, Y.
 TITLE High-efficiency full-length cDNA cloning
 JOURNAL Meth. Enzymol. 303, 19-44 (1999)
 MEDLINE 99279253
 PUBMED 10349636

REFERENCE
 AUTHORS Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K.,
 Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M., and Hayashizaki, Y.
 TITLE Normalization and subtraction of cap-trapper-selected cDNAs to
 JOURNAL prepare full-length cDNA libraries for rapid discovery of new genes
 MEDLINE 20499374
 PUBMED 11042159

REFERENCE
 AUTHORS Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P.,
 Konno, H., Akiyama, J., Nishi, K., Kitsuai, T., Tashiro, H., Itoh, M.,
 Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishino, T., Harada, A.,
 Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K.,
 Fujiwaka, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watabiki, M.,
 Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsunaga, S., Kawai, J.,
 Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y.
 TITLE RIKEN integrated sequence analysis (RISA) system--384-format
 JOURNAL sequencing pipeline with 384 multicapillary sequencer
 MEDLINE 20530913
 PUBMED 11076861

REFERENCE
 AUTHORS The RIKEN Genome Exploration Research Group Phase II Team and the
 TITLE FANTOM Consortium.
 JOURNAL Functional annotation of a full-length mouse cDNA collection
 REFERENCE Nature 409, 685-690 (2001)

TITLE The FANTOM Consortium and the RIKEN Genome Exploration Research
 JOURNAL Group Phase I & II Team.
 REFERENCE Analysis of the mouse transcriptome based on functional annotation
 AUTHORS Nature 420, 563-573 (2002)

JOURNAL 6 (bases 1 to 2804)
 REFERENCE Adachi, T., Aizawa, K., Akimura, T., Arakawa, T., Bono, H., Carninci, P.,
 Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hashizume, W.,
 Hayashida, K., Hayatsu, N., Hiramoto, K., Hiraoka, T., Hirozane, T.,
 Hori, F., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Kasukawa, T.,

Kato, H., Kawai, J., Kojima, Y., Kondo, S., Konno, H., Kouda, M.,
 Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Murata, M.,
 Nakamura, M., Nishi, K., Nomura, K., Nunazaki, R., Ohno, M., Ohsato, N.,
 Okazaki, Y., Saito, R., Saitoh, H., Sakai, C., Sakai, K., Sakazume, N.,
 Sano, H., Sasaki, D., Shibata, K., Shingawa, A., Shiraki, T.,
 Sogabe, Y., Tagami, M., Tagawa, A., Takahashi, F., Takaku-Akanishi, S.,
 Takeda, Y., Tanaka, T., Tomaru, A., Toyota, T., Yasunishi, A.,
 Muramatsu, M., and Hayashizaki, Y.
 TITLE Direct Submission
 JOURNAL Submitted (16-APR-2002) Yoshihide Hayashizaki, The Institute of
 Physical and Chemical Research (RIKEN), Laboratory for Genome
 Exploration Research Group, RIKEN Genomic Sciences Center (GSC),
 RIKEN Yokohama Institute, 1-7-22 Suenhiro-cho, Tsurumi-ku, Yokohama,
 Kanagawa 230-0045, Japan (E-mail: genome-res@gsr.riken.jp,
 URL: http://genome.gsc.riken.jp/, Tel: 81-45-503-9222,
 Fax: 81-45-503-9216)

COMMENT
 cDNA library was prepared and sequenced in Mouse Genome
 Encyclopedia Project of Genome Exploration Research Group in Riken
 Genomic Sciences Center and Genome Science Laboratory in RIKEN.
 Division of Experimental Animal Research in Riken contributed to
 prepare mouse tissues.
 Tissues were provided by Dr. John Todd (Dept. of Medical Genetics
 Wellcome Trust Centre for Molecular Mechanisms in Disease Wellcome
 Trust/MRC building Addenbrookes Hospital Cambridge) whose
 assistance we gratefully acknowledge.
 Please visit our web site for further details.
 URL: http://genome.gsc.riken.jp/
 URL: http://fantom.gsc.riken.jp/.
 URL: http://location/Qualifiers

FEATURES
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 (MGD:MGI:1339755, GI:NM_007782, evidence: BLASTN, 99%,
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ORIGIN
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 Best Local Similarity: 26.68% Mismatches: 250
 Query Match: 13.19% Indels: 95
 DB: 3 Gaps: 26

US-10-006-265-17 (1-662) x AK089305 (1-2804)
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 Qy 73 AlaPheGlyGluIysIleAspAsnSerThrTrpAsnSerSerThr----- 87
 Db 682 AGCTTGAAGAGCGGCCCGAC---TCTCAGTACCAAGGAGCAACATCCCGATGTGTG 738
 Qy 88 ---SerGluAsnArgIaSerCysSerPhePheLeuProArgIleThrIleProAspAsn 106
 Db 739 GCAAAAGAGGACGAGACCACTGCTCATCCCGGAAAAAACTGTGCTGTACAGCAT 798
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Qy 145 PROVALLEU-----GLYLEYLSARGMETILEGINILEGLITRIPPLEYS 159
Db 919 CCTATGTAAGTCTCTACACAGCTGGCTGGCTGGCTGAGCTGGAAGCCATGGAAGCC 978
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Db 979 AGTAGATCATGGAAGAGAGGTGAACCTTGCTTACAGCCAGCCCAAGGAGCCAA 1038
Qy 180 SerThrSerTrpMetGluValAsnPhenAlaYsbAnArgLYbAspLYbAsnGlnThrTyr 199
Db 1039 -----TGAGCTGTGGTGTCCAGCTGCTCCAGCAAGAGCAAG-----TTT 1080
Qy 200 AsnLeuThrGlyLeuGlnProPheThrGlnTyrValIleAlaLeuArgCysAlaValLys 219
Db 1081 GAGCTTGGGGGCTCCATCAGAGCCCACTGTAACCTTACAGATGAGTGC-----ATTGCG 1137
Qy 220 GluSer-----LYbPheTrpSerAspTrpSerGlnGlnLYbMetGlyMetThrGlnGlu 237
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Db 1198 AAGGCCCCCATCAGACAGCTGAGACAGCTGTGTGAGAAAGAGCAACTGAT---CGAGGG 1254
Qy 257 ArgArgProValArgLeuLeuTrpLYbLYbAlaArgLYbAlaProVALLeuGlu----- 274
Db 1255 ACAAGTAGTGTGAGCTGCTTGTGAAGCA-----ACGCCCTGAGAGAGACAGT 1305
Qy 275 ---LYbThrLeuGlyLYbAsnILE---TrpTYrTrpGlnSerAsnThrAsnLeuThr 292
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Qy 313 ValSerMetIleSerTYrAsnSerLeuGlyLYbSerProVALAlaThrLeuArgILEPro 332
Db 1426 GTGACCTGTGGCTGCTACCAAGAGAGGAGCTTCTTCACTACTACAGTg----- 1476
Qy 333 AlaIleGlnGlnLYbSerPheGlnCysIleGluValMetGlnAlaCysValAlaGluAsp 352
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Qy 353 GlnLeuValLYbLYbSTPGLnSerSeraLeuAspValAsnThrTrpMetILEGluTrp 372
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Qy 392 ThrAsn-----TrpThrILEGln----- 397
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Qy 398 ---GlnAspLYbLYbSProPheTrpCysTYrAsnILESerValTYrPrometLeuHis 416
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Db 1738 GGCATCTGGGAGCTCTGTAAATGTCTACACCTTCGTGAGAGAGAGACTCTCTCTCAT 1797
Qy 437 GLYProGluThrLYbValGluAsnILEGlyValLYbThrValThrIleThrTrpLYbGlu 456
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Qy 475 AlaGluGlyGlyLYbGlyPheSerLYbThrValAsnSerSerILEGlnTYrGlyLeu 494
Db 1912 GATGCTGGGAGCAACCTCTTCTCCGTACCCCTGAACATCTCCCATGACTTGTGCTG 1971
Qy 495 GluSerLeuLYbArgLYbThrSerTYrILEValGlnValMetAlaSerThrSerAlaGly 514
Db 1972 AAGCACTGGAGCCCGGACAGTTGTATCATGCTTACCTCATAGCGCACAGCTGGGAGAGG 2031
Qy 515 GlyThrAsnGlyThrSerILEAsnPhenLYbThrLeuSerPheSerValPheGlnILE 534
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DEFINITION Homo sapiens CSF3R gene, VIRUAL TRANSCRIPT, partial sequence,
genomic survey sequence.
ACCESSION AY412152
VERSION AY412152.1 GI:39768117
KEYWORDS GSS.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 2592)
Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejarival,A.,
Todd,M.A., Tanenbaum,D.M., Civallo,D.R., Lu,F., Murphy,B.,
Ferreira,S., Wang,G., Zheng,X.H., White,T.J., Smutsky,J.J.,
Adams,M.D. and Cargill,M.
Inferring nonneutral evolution from human-chimp-mouse orthologous
gene trios
Science 302 (5652), 1960-1963 (2003)
JOURNAL PUBMED 14671302
REFERENCE 2 (bases 1 to 2592)
Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejarival,A.,
Todd,M.A., Tanenbaum,D.M., Civallo,D.R., Lu,F., Murphy,B.,
Ferreira,S., Wang,G., Zheng,X.H., White,T.J., Smutsky,J.J.,
Adams,M.D. and Cargill,M.
Direct Submission
Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,
Rockville, MD 20850, USA
This sequence was made by sequencing genomic exons and ordering
them based on alignment.
COMMENT
FEATURES
location/Qualifiers
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ORIGIN
Alignment Scores: 5.8e-38 length: 2592
Pred. No.: 462.50 Matches: 165
Score:

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Percent similarity: 39.84% Conservative: 82
 Best Local Similarity: 26.61% Mismatches: 278
 Query Match: 13.11% Indels: 95
 Gaps: 25

US-10-006-265-17 (1-662) x AY412152 (1-2592)

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 DB TGCCTGAAC-----TGGGGCAACAGCCTCGACATCTTGAGACCAAGTT---GAG 348
 QY PheSerLeuAlaAlaLeuProAlaLysProGluAsnLysSerCysValTyTyTyArg 48
 DB CTGCGGCGAGGCTACCTCCAGCCATACCCCAACCTCTCCCTGCTC----- 396
 QY LysAsnLeuThr-----CysThrTrpSerProGlyLysGluThrSerTy 63
 DB ATGAACTCTCAACCAACGACCTCATCTGCGAGGAGCAGAGCCTGAGCCCACTA 456
 QY ---ThGlnTyThrValLysArgThrTyArgAlaPheGlyGluLysHisAspAsnCysThr 82
 DB CCACACGAGCTCACTCTGAAGAGTTTCAAGAGCCGGGGC-----ACTGTCA 504
 QY ThrAsnSerSerThr-----SerGluAsnArgAlaSerCysSerPhe 96
 DB ACCCAAGGGGAGCTCATCTGAGCTGCTGCCAAGAGCGGAGAGCCACTGCTGCATC 564
 QY PheLeuProArgLysThrLeuProAspAsnTyThrLysGluAlaGluAsnGly 116
 DB CCAAGCAACACCTGCTGTTGTACAGAAATATGGGCTCTGGTGAGCGAGGAATGCG 624
 QY AspGlyValLysSerHisMetThrTyTrpArgLeuGluAsnLeuAlaLysThrGlu 136
 DB CTGGGGACCAAGCATGTCCTCCCAACATGTCTTGATCCCATGTGTGGAACTGGAG 684
 QY ProProLysLysPheArgValLysProValLeuGlyLysArgMetLysGlnLysGlu 156
 DB CCCCCATGCTGCGGACCATGAGACCC----- 711
 QY TrpLysProGluLeuAlaProValSerSer----- 167
 DB AGCCCTAAGGGCCCTCCCTCCCAAGGAGGCTGCTCAACGCTGCTGGAGCCA 765
 QY ---AspLeuLysTyThrLeuArgPheArgThrVal---Asn 179
 DB TGGCAGCAGAGGCTGCAATTAATCAGAAATGTGAGCTGGCCACAAGCCGAGCGTGA 825
 QY SerThrSerTrpMetGluValAsnPheAlaLysAsnArgLysAspLysAsnGlnThrTy 199
 DB GAAGCCAGCTGGGCACTGTGTGGC-----CCCTCCCTTGGAGGCCCTTCAGTAT 876
 QY AsnLeuThrGlyLeuGlnProPheThrGluTyValLysLeuAlaLysArgCys---AlaVal 218
 DB GAGCTGCGGGGCTCTCCAGCAGCGGCTTACACCTCGATACGCTGATCCGCTGG 936
 QY LysGluSerLysPheTrpSerAspTrpSerGlnGlyLysMetGlyMetThrGluGlu 238
 DB CCCCTGCTGGCAGCTGAGACGACTGGAGCCCAAGCTGAGAGCTGAGATACCGAAG 996
 QY AlaPro---CysGlyLeuGluLeuTrp-----ArgValLeuLysProAlaGluAla 254
 DB GCCCCCACTGTCAAGCTGACACATGATGTGGCGCAGAGCAGAGCTGGAGCCC----- 1047
 QY AspGlyArgArgProValArgLeuLeuTrpLysLysAlaArgGlyAlaProValLeuGlu 274
 DB AGGACAGTGCAGCTGTCTTGAGAGCCA-----GTGCCCTGGAGAGAA 1089
 QY LysThrLeuGlyTyAsnLysLeuTrpTyTyTyProGluSerAsnThrAsn--- 290
 DB GACAGCGAGAGCATCAAGTTATGTGTCTTGGAGACCTTCAGGCCAGGCTGGGGCC 1149
 QY LeuThrGluThrMetAsnThrThrAsnGlnLeuGluLysGlyLysGlyLysSer 310

DB 1150 ATCTGCCCCCTCTGCAACACCAAGAGCTCAGCTCCACTTCCACTGCTTCAGAAAGCC 1209
 QY PheTrpValSerMetLysSerTyAsnSerLeuGlyLysSerProValAlaThrLeuArg 330
 DB CANNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN 1269
 QY IleProAlaLysGlnGlyLysSerPheGlnCysLysGluValMetGlnAlaCysValAla 350
 DB NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN 1317
 QY GluAsp-----GlnLeuValValLysTrpGlnLysSerSerAlaLeuAspValAsnThrTrp 368
 DB CGAGACCTTCACAGGCTCTGGGTAGAGCTGGAGGCC-----AATCCATGG 1365
 QY ---MetLysGluTrpPhe-----ProAspValAspSerGluProThr 381
 DB CCTCAGGAGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1425
 QY ThrLeuSerTrpGluSerValSerGlnAlaThrAsnTrpThrLysGlnLysAspLysLeu 401
 DB ACTGGAGAGATGGAACAGATGAGAGAGCAGGAGGAGTTTCTGCTGAAGAGAAAC--ATC 1482
 QY LysProPheTrpCysTyAsnLysSerValTyTrpMetLeuHisAspLysValGlyGlu 421
 DB AGGCTTTCAGCTCTATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1542
 QY ProTySerLysGlnAlaTyArgLysGluGlyValProSerGluGlyProGluThrLys 441
 DB TCCACAGATGCTATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1602
 QY ValGluAsnLysGlyValLysThrValThrLysTrpLysGluLysProLysSerGlu 461
 DB CTAAAGCATTGGGCAAGCTGGGAGCAGCTGAGTGGGTGCTGAGGCCCTGAGCTG 1662
 QY ArgLysGlyLysLysCysAsnTyThrLysPheTyArgLysGlnLysGlyLysPhe 481
 DB GGGAGAGGCCCTTACCCACATCACCATCTTGTGGACCAAGCTGAGAAACAGTCTTC 1722
 QY SerLysThrValAsnSerSerLysGlnTyGlyLysGluSerLeuLysArgLysThr 501
 DB TCCGATCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1782
 QY SerTyLysLeuAlaGlnValMetAlaSerThrSerAlaGlyLysThrAsnGlySerLys 521
 DB CTGATACATCATCATCATCATCATCATCATCATCATCATCATCATCATCATCATCAT 1842
 QY AsnPheLysThrLeuSerPheSerValPheGluLysLeuLysLysSerLeuLys 541
 DB ACCCTGATGACCTTGAACCCAGAGGGGTGAGCTACATCATCATCTGGGCTGTGGGC 1902
 QY GlyGlyLeuLeuLysLeuLysLysLeuThrValAlaTyGlyLysLysProAsnLys 561
 DB CTCTGCTGTGCTACCTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGT 1962
 QY LeuThrHisLeuCysTrpProThrValProAsnProAlaGluSerSerLysLeuThrTrp 581
 DB AAGATCCCTC---TGGCAGATGTGCCAGACCAAGCTCAAGAGAGCTGGGCTGCTGG 2019

RESULT 9
 BC040954 2792 bp mRNA linear HTC 19-NOV-2003
 LOCUS Homo sapiens colony stimulating factor 3 receptor (grm1uc0cyf),
 DEFINITION RNA (cDNA clone IMAGE:558879), containing frame-shift errors.
 ACCESSION BC040954
 VERSION BC040954.1 GI:27155071
 KEYWORDS HTC.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 1 (bases 1 to 2792)
 Struhsberg,R.D., Collins,F.S., Wagner,L., Shenmen,C.M., Schuler,G.D.,
 Klausner,R.D.,

Altechul,S.F., Zeeberg,B., Buetow,K.H., Schaefer,C.F., Bhat,N.K., Hopkin,R.F., Jordan,H., Moore,T., Max,S.I., Wang,J., Hsieh,F., Diatchenko,L., Marinova,K., Farmer,A.A., Rubin,G.M., Hong,L., Stetson,M., Soares,M.B., Bonaldo,M.F., Casavant,T.L., Scheer,T.E., Brownstein,M.J., Ueda,T.B., Toshiyuki,S., Carinini,P., Prange,C., Raha,S.S., Loquellano,N.A., Peters,G.J., Abramson,R.D., Mollath,S.J., Bosak,S.A., McEwan,P.J., Mcherson,K.J., Malek,J.A., Gunaratne,P.H., Richards,S., Wortley,K.C., Hale,S., Garcia,A.M., Gay,L.J., Hulyk,S.W., Villalón,D.K., Muzny,D.M., Sodergren,E.J., Lu,X., Gibbs,R.A., Fahey,J., Helton,E., Kettelman,M., Madan,A., Young,A.C., Shevchenko,Y., Sanchez,A., Whiting,M., Madan,A., Young,A.C., Shevchenko,Y., Bonfard,G., Blakesley,R.W., Touchman,J.W., Green,E.D., Dickson,M.C., Rodriguez,A.C., Grimwood,J., Schmitz,J., Myers,R.M., Buterfield,Y.S., Krzywinski,M.I., Skalska,U., Smalun,D.B., Scherch,A., Schein,J.E., Jones,S.J., and Matra,M.A. Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences
Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)

JOURNAL MEDLINE
PUBMED
22388257
12477932
2 (bases 1 to 2792)
Strausberg,R.
Direct Submission
Submitted (06-DEC-2002) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA
NIH-MGC Project URL: <http://mgc.ncl.nih.gov>
Contact: MGC help desk
Email: cgabs-remail.nih.gov
Tissue Procurement: Invitrogen
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Institute for Systems Biology
<http://www.systemsbiology.org>
contact: amadan@systemsbiology.org
Anup Madan, Jessica Fahey, Erin Helton, Mark Kettelman, Anuradha Madan, Stephanie Rodriguez, Amy Sanchez and Michelle Whiting

REMARK
COMMENT

FEATURES
source
1. 2792
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:5588879"
/tissue_type="Ovary, pooled from 3 adults"
/clone_lib="NIH MGC_125"
/lab_host="DH10B"
/note="Vector: pCMV-SPORT6"

ORIGIN

Alignment Scores:
Pred. No.: 5.16e-34 Length: 2792
Score: 426.50 Matches: 162
Percent Similarity: 38.18% Conservative: 85
Best Local Similarity: 25.04% Mismatches: 234
Query Match: 12.09% Indels: 166
DB: 3 Gaps: 25

US-10-006-265-17 (1-662) x BC040954 (1-2792)

Qy 9 CysValaAnLeuGlyMetMetTrpThrTrpAlaLeuTTrpMetLeuProSerLeuGlyAs 28
Db 397 TGCCGGAAC-----TGCGGCAACCTCGACATCTCGACACAGTT---GAG 441
Qy 29 PheSerLeuAlaAlaLeuProAlaLysPrGluAenIleSerCysValTyrTrpTrg 48

Db 442 CTGGCGGACAGGCTACCTCCAGGACATACCCACAAACCTCTCTGCTC----- 489
Qy 49 LysAnLeuThr-----CysThrTrpSerProGlyLysGluThSerTyr 63
Db 490 ATGAACCTCAACAACGACGAGCTCATCTCCAGTGGGAGCCAGACCTGAACTCCCTA 549
Qy 64 ---ThrgInTyrThrValLysArgThrTyrTrpAlaPheGlyGlyLysIleAspAsnCysThr 82
Db 550 CCCACCACTTCACTGTAAGATTCAAGAGCCGGGCGC-----AACTGTAG 597
Qy 83 ThrAnSerSerThr-----SerGluAenArgAlaSerCysSerPhe 96
Db 598 ACCCAAGGAGACTCATCTGAGATCGCTGCCCAAGACGGGACAGGCACTGCTGATC 657
Qy 97 PheLeuProArgIleThrIleProAspAnfTyrThrIleGluValGluAlaGluAnGly 116
Db 658 CCACGCAACACACTGCTGTGTACCAAGATATGGGATCTGGGTCAGGCGAGAAATCG 717
Qy 117 AspGlyValIleLysSerHisMetThrTyrTrpArgLeuGluAenIleAlaLysThrGlu 136
Db 718 CTGGGACCAACATGTCCCAACAACGTGTCTTGAATCCATGATGTGTGAACCTGAG 777
Qy 137 ProProLysIlePheArgValLysProValLeuGlyIleLysArgMetIleGlnIleGlu 156
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Qy 157 TrpIleLysProGluLeuAlaProValSerSer----- 167
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Qy 168 ---AspLeuLysTyrThrIleuAArgPheArgThrVal---Asn 179
Db 859 TGGCAGCCAGGCTGCACATTAATCAGAAAGTGAAGCTGCCCAAGCCGACGTTGA 918
Qy 180 SerThrSerTrpMetGluValAsnPheAlaLysAsnArgLysAspLysAsnGlnThrTyr 199
Db 919 GAAGCCACTGCGGACATGCTGGC-----CCCTCCCTTGGAGAGCCCTTCAGAT 969
Qy 200 AsnLeuThrGlyLeuGlnProPheThrGluTyrValIleAlaLeuArgCysAlaValLys 219
Db 970 GAGCTCGGGGCTCTCCCAAGCCAGGCTTACACCTGAGATACGCTGATCCGCT-- 1027
Qy 219 GluSerLysPheTrpSerAspTrpSerGlnGluLysMetGlyMetThrGluGluGluAl 239
Db 1028 -----GG 1029
Qy 239 AProCysGlyLeuGluLeuTrpArgValLeuLysProAlaGluAlaAspGlyArgArgPr 259
Db 1030 CCCCCTGC----- 1036
Qy 259 OValArgLeuLeuTrpLysLysAlaArgGlyAlaProValLeuGluLysThrLeuGlyTyr 279
Db 1037 ---CTGGCACTGGGGC----- 1051
Qy 279 rAsnIleTrpTyrTyrProGluSerAenThrAsnLeuThrGluThrMetAenThrTrAs 299
Db 1052 ---ATCTGCCCCCTGCACACACACAGA 1077
Qy 299 nGlnGlnLeuGluLeuHisLeuGlyGlyGluSerPheTrpValSerMetIleSerTyrAs 319
Db 1078 GCTCAGCTGACCTTCCACCTGCTTCAAGAGCCAGAGGTGAGCCCTTGAGCTTAA 1137
Qy 319 nSerLeuGlyLysSer-----ProVal-----AlaThrLeuArgIleProAlaIle 334
Db 1138 CTCAGCGGAGACTCTGTCCTCACTCCGAGTGTCTTCAAGAAAGAGAGCCAGCTCT 1197
Qy 334 eGlnGluLysSerPheGlnCysIleGluValMetGlnAlaCysValAlaGluAap----- 352
Db 1198 GACCAAGCTCAT-----GCCATGCGCCGAGACCTCA 1230
Qy 353 -GlnLeuValValLysTrpGlnSerSerAlaLeuAspValAsnThrTrp----- 368

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Db      1231 CAGCCTCTGGGTAGCTGGAGCCCC-----AATCATGCTCGCTGAGGCTA 1278
Qy      369 -MetIleGluTrpPhe-----ProAspValAspSerGluProThrThreUsert 385
Db      1279 TGTGATTGAGTGGGGCTGGGCCCCCAGCGGAGCATATGACAAGACCTGGAGGAT 1338
Qy      385 pGluSerValSerGlnAlaThrAnrPrThrIleGlnAlaAspLysLeuLysProPheTr 405
Db      1339 GGAACAGAAATGAGAGCCACGGGGGTTTCTGTGAAGAGAAC---ATCAGGCCCTTTCA 1395
Qy      405 pCyStrYrAnrIleSerValYrProMetLeuHleAspLysValGlyGluProTySerIl 425
Db      1396 GCTCTAGATGATATGCTGATGCTCTTGTACGACGACACCATCCATCCCTCCAGATGT 1455
Qy      425 eGlnAlaYrAlaLysGluGlyValAlProSerGluGlyProGluThrLysValGluAnrI 445
Db      1456 CTATGCTTACTCTCAAGAAATGGCTCCCTCCATGCCCGAGACTGATCTAAAGACAT 1515
Qy      445 eGlyValLysTrValThrLethrTrpLysGluLleProLysSerGluArgLysGlyI 465
Db      1516 TGGCAGAGACTGGGACAGCTGAGTGGTGCTGAGCCCCCTGAGCTGGGAGAGAGCCC 1575
Qy      465 eIleCyAsnTrYrThrllePheYrGlnAlaGluGlyLysGlyPheSerLysThrVa 485
Db      1576 CTTTACCCACTACACCATCTTGTGACCAACGCTCAGAACCAAGTCTTCCGCCATCTT 1635
Qy      485 IaSerSerIleLeuGlnTrYrGlyLeuGluSerLeuLysArgLysThrSerYrIleVa 505
Db      1636 GAATGCTCTCCCGTGGCTTGTCTTCCATGGCTGGAGCCCGGAGTGTGATACAT 1695
Qy      505 IglValMetAlaSerSerAlaGlyLysThrAnrGlyLysThrSerIleAsnPhelysTh 525
Db      1696 CCACCTCATGCTGCGACGAGCTGGGGCCACCAACAGTACAGTCTCACCCTGATGAC 1755
Qy      525 rLeuSerPheSerValPheGluLleLeuLethrThrSerLeuLleGlyLysLeuLe 545
Db      1756 CTTGAGCCCGACAGGGGTGGAGCTACACATCTCTGGGCTTGTGGCTCTCTGCTT 1815
Qy      545 uIleLeuLleIleLeuThrValAlaYrGlyLeuLysLysProAsnLysLeuThrHle 565
Db      1816 GCTCACCCTGCTCTGTGGAACTGCTGCTGTGTGACGCCCAAGAGAAATCCCT 1875
Qy      565 uCyStrProTrValProAsnProAlaGluSerSerIleAlaThrTrp----- 581
Db      1876 C--TGGCCAAGTGTCCACAGACCAAGCTCAGACAGCTGAGGCTCGGGTGCCACAAT 1932
Qy      582 ----HleGlyAspAspPhelys-----AspLysLeuAs 591
Db      1933 CATGAGAGAGATGCTTCCAGCTGCCGCGCTTGGACGCAACCATCACCAAGCTCAC 1992
Qy      591 nLeuLysGluSerAspAsp 597
Db      1993 AGTGTCTGAGAGAGATGCAA 2011

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RESULT 10
CP915066      651 bp      mRNA      linear      EST 05-NOV-2003
LOCUS      B0973F04-5 NIA Mouse Unfertilized Egg cDNA library (Long 1) Mus
DEFINITION      Musculus cDNA clone NIA:B0973F04 IMAGE:30479295 5', mRNA sequence.
ACCESSION      CP915066
VERSION      CP915066.1 GI:38186268
KEYWORDS      EST.
SOURCE      Mus musculus (house mouse)
ORGANISM      Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE      1 (bases 1 to 651)
AUTHORS      Piao,Y., Ko,N.T., Lim,M.K. and Ko,M.S.H.
TITLE      Construction of long-transcript enriched cDNA libraries from
            submicrogram amounts of total RNAs by a universal PCR amplification
            method
JOURNAL      Genome Res. 11 (9), 1553-1558 (2001)
MEDLINE      21429098

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PUBMED      11544199
COMMENT      Contact: Dawood B. Dudekula
            Laboratory of Genetics
            National Institute on Aging/National Institutes of Health
            333 Cassell Drive, Suite 4000, Baltimore, MD 21224-6820, USA
            Email: cdna@igsun.gic.nia.nih.gov
            Plate: B0973 row: F column: 04
            Seq primer: M13 Reverse
            High quality sequence stop: 651
            POLYA=No.
FEATURES
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            /dev_stage="Unfertilized Egg"
            /lab_host="DH10B"
            /clone_1fb="NIA Mouse Unfertilized Egg cDNA library (Long
            1)"

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/note="Vector: pCMV-SPORT6 (Invitrogen); Site_1: SalI;
Site_2: NotI; Mouse cDNA project by the Laboratory of
Genetics, National Institute on Aging (NIA), Intramural
Research Program, NIH (http://igsun.gic.nia.nih.gov/cDNA).
This is a long-transcript enriched cDNA library (Ref.
Genome Res. 11: 1553-1558 (2001). [PMID: 11544199]). Total
RNAs were extracted from a pool of 1488 unfertilized eggs.
Double-stranded cDNAs were synthesized with an oligo(dT)
primer (Invitrogen):
5'-pGACTAGTTCATGATCGCAGCGCGCCCTTTTCTTTT-3',
treated with T4 DNA polymerase, and ligated by
ethanol-precipitation. The cDNAs were ligated to
Lone-linker Lb-SalI, purified by phenol/chloroform, and
separated from free linkers by Centricon 100. Then, the
cDNAs were amplified by long-range high fidelity PCR using
Ex Tag polymerase (Takara) with a primer SalI-S. The
products were purified by phenol/chloroform and Centricon
100. The cDNAs were digested with SalI and NotI enzymes
and cloned into SalI/NotI site of pCMV-SPORT6 plasmid
vector. The DH10B E. coli host was transformed with the
ligation mixture by the standard chemical method. The
average insert size is about 2.5 kb. The library was
constructed by Yulan Piao."

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ORIGIN

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Alignment Scores:
Pred. No.:      7.39e-32      Length:      651
Score:          397.00      Matches:      79
Percent Similarity: 64.90%      Conservative: 19
Best Local Similarity: 52.32%      Mismatches: 41
Query Match:    11.25%      Indels:      12
DB:              7      Gaps:      3

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US-10-006-265-17 (1-662) x CP915066 (1-651)

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Qy      6 GlnProSerCyValAsnLeuGlyMetTrpThrPrAlaLeuTrpMetLeuProser 25
Db      229 CAGCCTCTGGGTAGCTGGAGCCCCAATGATGAGCTTGGCACTGTGGGCAATCTCTTTC 288
Qy      26 LeuCyLysPheSerLeuAlaLeuProAlaLysProGluLysnIleSerCyValTrp 45
Db      289 CTCTGCAATTCAGCTGSCAATCTCTGCGCACTAAGCAGAAATCTTCCGCGCTTT 348
Qy      46 TrpTrpArgLysAsnLeuThrCyStrTrpSerProGlyLysGluThrSerYrTrgln 65
Db      349 TACTTGACAGAAATCTGACTTGGACAGCAGAGAAAGAAACCAATGATATACAC 408
Qy      66 TrpTrpValLysArgThrTrpAlaPheGlyGluLysHleAspAsnCyStrThrTrp 85
Db      409 TACATTGTGACTTGTGACTTACTGATGAGAAA-----AGC 444

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Accession	Version	Keywords	Source	Organism	Reference Authors Title Journal Remark
Y398					
Db 1382					
QY 409					
Db 1442					
QY 429					
Db 1502					
QY 449					
Db 1562					
QY 467					
Db 1616					
QY 487					
Db 1676					
QY 507					
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Db 1796					
QY 547					
Db 1823					
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Db 1877					
QY 574					
Db 1937					
RESULT 12					
LOCUS					
DEFINITION					
ACCESSION					
VERSION					
KEYWORDS					
SOURCE					
ORGANISM					
REFERENCE					
AUTHORS					
TITLE					
JOURNAL					
REMARK					
REFERENCE					
AUTHORS					
TITLE					
JOURNAL					
COMMENT					

was normalized. Library was constructed by Life Technologies, a division of Invitrogen.

Location/Qualifiers

1..1931

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="CSOD1054YG09"

/issue_type="Placenta Cot 25-normalized"

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ORIGIN

Alignment Scores:

Prod. No.: 1.53e-30 Length: 1931

Score: 392.00 Matches: 130

Percent Similarity: 43.95% Conservative: 66

Best Local Similarity: 29.15% Mismatches: 179

Query Match: 11.11% Indels: 71

DB: 3 Gaps: 19

US-10-006-265-17 (1-662) x CR610771 (1-1931)

QY 199 TYAsnLleuThrgLYleuGlnProPheTherhGlnrYValIlealaleuArgCys---Ala 217

Db 27 TAAGACTCTGGGGGTCTCTCCACACCAGCGGCTTAACCTCGAGATACGCTGATCCGC 86

QY 218 ValLygLuSerLysePheTrSerAspTrpSerGlnGlnuLybMetGlyMetThrGlnu 237

Db 87 TGGCCCCCTGCTGGCCACTGGAGCCACTGGAGCCCCAGCCTGGAGCTGAGAACTACCGAA 146

QY 238 GlnAlaPro---CysGlyYleuGlnLeuTrp-----ArgValLeuLyProAlaGlu 253

Db 147 CGGGCCCCCACTGTCAAGATGGACATGTGGCGGAGAGAGCACTGGACCC----- 200

QY 254 AlaAspGlyArgArgProValaArgLeuLeuTrpLybLybAlaArgGlyAlaProValLeu 273

Db 201 -----AGGACAGTGGAGCTGTCTTGAAAGCA-----GNGCCCTGGAG 239

QY 274 Gln-----LyseThrLeuGlyTyTrasnIleTrpTyTrProGluSerAsnThrAsn 230

Db 240 GAAGACAGCGAGCGAGTCAAGGTTATGTGGTTCTTGGAAGACCTTCAGGCGAGCTGGG 299

QY 291 ---LeuThrGlnThrMetAsnThrThrArgnGlnGlnLeuGlnuLybMetGlyGlu 309

Db 300 GCCATCTGCCCCCTGTGCACACACACAGAGCTCAGCTGCACCTTCCACCTGCTTCAGAA 359

QY 310 SerPheTrpValSerMetLysSerTyTrasnSerLeuGlyLySer-----ProVal 366

Db 360 GCCCAGGAGGTGGCCCTTGCGCCCTTAATCACTCAGCGGAGACTCTGCTCCACCTCGGTG 419

QY 327 ----AlaThrLeuArgGLeProAlaIleGlnGlnuLybSerPheGlnCysIleGluVal 344

Db 420 GTCTTCTCAGAAAGCAGAGGCCACCTCTGACCCAGACTCCAT----- 461

QY 345 MetGlnAlaCysValAlaGluAsp-----GlnLeuValValLySTrGlnInsSerAla 362

Db 462 -----GCCATGGCCCGAGACCTTCACAGCCTCTGGGGTAGGCTGGAGCCCCC--- 509

QY 363 LeuAspValAsnThrTrp-----MetIleGlnTrpPhe-----ProAsp 375

Db 510 -----AATCCATGGCTCAGGCGCTAATGATATAGTGGGCCCTGGCCCCCAGC 566

QY 376 ValAspSerGlnuProThrThrLeuSerTrpGluSerValSerGlnAlaThrAsnTrpThr 395

Db 561 GCGAGCAATATGACMAAGACCTCGAGATGAGACGAATGGAGAGCACCGGGGTTCTG 620

QY 396 IleGlnGlnAspLyLeuLeuProPheTrpCysIlyTrasnIleSerValTyTrPrometLeu 415

Db 621 CTGAAGAGAAAC---ATCAGGCCCTTTAGCTTAATGATAGATACATCGAGACTCCCTTGAC 677

QY 416 HisAspLyValGlyGluProTySerIleGlnAlaTrValAlaGlyGlyValProSer 435

Db 678 CAGGACCACTGGAGACCTCCAGCATGTCTATGTCTTCAAGAAATGGCTCCTCC 737

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QY 436 GUGUGYProGUThrValGluAenilegVallyThrValThrleThrTrpLys 455
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DB 738 CATGCCCCAGAGCTGCATTAAGCATTTGGCAAGAGCTGGGACAGCTGGAGTGGGCG 797
QY 456 GUUleProLysSerGluArgLysGlyleleCyAenTyThrlePheTyGlnAla 475
    |||||
DB 798 CCTGAGCCCTCGAGCTGGGAAAGAGCCCTTACCACTACCATCTTTGGACCAAC 857
QY 476 GUUGlyGlyLysGlyPhe-----SerLys-ThrValAs 486
    |||||
DB 858 GCTCAAGAACAGCTCTTCTGCTATGCTGACCCGTAACCCCTCCAGGCGCATCTGTA 917
QY 486 nSerSerleleuGlnTyGlyleuGluSerleuLysArgLysThrSerTyrlleValAl 506
    |||||
DB 918 TGCCTCTCCCTCGGCTGTGCTTCCTCATGGCTGGAGCCCGGACGCTGTATCACTCA 977
QY 506 nValMetAlaSerThrSerleaglyGlyThraGnglyThrSerleAenPheLysThrle 526
    |||||
DB 978 CCTCATGGCTGCCAGCCAGGCTGGGGCCCAACAGTACAGTCCATCCCTGATGACCTT 1037
QY 526 userPheSerValPheGluileleleuileThrSerleuilegLyGlyGlyleuL 546
    |||||
DB 1038 GACCCCAAGAGGGGTGGAGCTACACATCATCTGGGCGCTTCCGCTCTGCTGTGCT 1097
QY 546 eleuileleleuThrValAlaTyGlyleuLysLysProAenLysleuThrHisleuCy 566
    |||||
DB 1098 CACCTGCTCTGTGGAACTGCTGCTGCTGTTCAGCCCAACAGAGAAATCCCTC-- 1155
QY 566 eTPProThrValProAenProAlaGlyLysSerleleAthrTrp----- 581
    |||||
DB 1156 -TGGCCAAAGTGTCCAGACCCAGCTCACAGCAGCTGCGCTCTGGTGTCCCATCAT 1214
QY 582 -HisGlyAenPheLys-----AapLysleuAenle 592
    |||||
DB 1215 GGAGAGAGATGCTCTTCAGCTGCGGCTTGGACAGCCACCATCACCAAGCTCAGT 1274
QY 592 uLyGlySerAapP 597
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DB 1275 GCTGAGAGAGATGTA 1290

RESULT 13
BC020454 1512 bp mRNA linear HTC 19-NOV-2003
LOCUS Mus musculus interluekin 6 signal transducer, mRNA (cDNA clone
DEFINITION IMAGE:3598166).
ACCESSION BC020454
VERSION BC020454.1 GI:18045025
KEYWORDS HTC.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
REFERENCE
AUTHORS Strausberg,R.L., Feingold,E.A., Grouse,L.H., Derge,J.G.,
Klausner,R.D., Collins,F.S., Wagner,L., Shenmen,C.M., Schuler,G.D.,
Altschul,S.F., Zeeberg,B., Buetow,K.H., Scheer,C.F., Bhat,N.K.,
Hopkins,R.F., Jordan,H., Moore,T., Max,I., Wang,J., Hsieh,F.,
Diatchenko,L., Marusina,K., Farmer,A.A., Rubin,G.M., Hong,L.,
Stapleton,M., Soares,M.B., Bonaldi,T.B., Casavant,T.L.,
Scheetz,T.E., Brownstein,M.J., Umedin,T.B., Toshiyuki,S.,
Carninci,P., Prange,C., Raha,S.S., Loquellano,N.A., Peters,G.J.,
Abramson,R.D., Muhlthay,S.J., Bosak,S.A., McSwan,P.J.,
McEranan,K.J., Malek,J.A., Gunaratne,P.H., Richards,S.,
Wojcik,K.C., Hale,S., Garcia,A.M., Gay,L.J., Hulyk,S.W.,
Villalón,D.K., Muzny,D.M., Sodergren,E.J., Lu,X., Gibbs,R.A.,
Sanchez,A., Whiting,M., Madan,A., Young,A.C., Shcherenko,Y.,
Bouffard,G.G., Blakeley,R.W., Touchman,A.J.C., Green,E.D.,
Dickson,M.C., Rodriguez,A.C., Grimwood,J., Schmutz,J., Myers,R.M.,
Butterfield,Y.S., Krzywinski,M.I., Skalka,U., Smalls,D.E.,
Scherer,A., Schein,J.E., Jones,S.J. and Marra,M.A.
Generation and initial analysis of more than 15,000 full-length

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JOURNAL human and mouse cDNA sequences
MEDLINE Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
PUBMED 22388257
REFERENCE 12477932
AUTHORS 2 (bases 1 to 1512)
TITLE Strausberg,R.
JOURNAL Direct Submission
Submitted (03-JUN-2002) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
USA
REMARK NIH-MGC Project URL: http://mgc.nci.nih.gov
COMMENT Contact: MGC help desk
Email: cgapbs-remail.nih.gov
Tissue Procurement: Jeffrey Green M.D.
cDNA Library Preparation: Life Technologies, Inc.
DNA Sequencing Arrayed by: The I.M.A.G.E. Consortium (ILNL)
Sequencing Center: Baylor College of Medicine Human Genome
Sequencing Center
Center code: BCM-HGSC
Web site: http://www.hgsc.bcm.tmc.edu/cdna/
Contact: amg@bcm.tmc.edu
Gunnar, P.H., Garcia, A.M., Lu, X., Hulyk, S.W., Louised, H.,
Kowis, C.R., Sneed, A.J., Martin, R.G., Muzny, D.M., Nanavati,
A.N., Gibbs, R.A.
Clone distribution: MGC clone distribution information can be found
through the I.M.A.G.E. Consortium/ILNL at: http://image.llnl.gov
Series: IRAC Plate: 16 Row: K Column: 14
This clone was selected for full length sequencing because it
passed the following selection criteria: matched mRNA gi: 6754337
This clone has the following problem: no poly-a-tail.
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location/Qualifiers
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1. organism="Mus musculus"
2. mol_type="mRNA"
3. strain="FVB/N"
4. db_xref="taxon:10090"
5. clone="IMAGE:3598166"
6. tissue_type="mammary tumor. C3(1)-Tag model. Infiltrating
ductal carcinoma. 5 month old virgin mouse."
7. clone_id="NCI CGAP_Mam6"
8. lab_host="DH10B"
9. note="Vector: pCMV-SPORT6"
ORIGIN
Alignment Scores:
Score: 1.03e-26 Length: 1512
Pct: 355.00 Matches: 90
Percent Similarity: 50.33% Conservative: 63
Best Local Similarity: 29.61% Mismatches: 133
Query Match: 10.06% Indels: 18
DB: 3 Gaps: 11
US-10-006-265-17 (1-662) x BC020454 (1-1512)
QY 35 ProAlaLysProGluAenileSerCyValTyTyTyArgLysAenleuThrCyThr 54
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DB 613 CCATATAAAGCTTCAAAATTTGACTTGTGATGAGGAGGAGAAATATGCTGTGCGAG 672
QY 55 TysPheProGlyLysGlyThrSerTy-----ThrGlnTyThrValLysArgThrTyAla 73
    |||||
DB 673 TGGGACCCCGGAGAGGAGACTTACCTTGAAACAAATPACCTTGAATATCAGAGTGGGCA 732
QY 74 PheGlyGlyLysHisAapAenCyThrThrAenSerSerThrSerGluAenArgAlaSer 93
    |||||
DB 733 ---ACAGAGAGAGTTTCTGATGCTGCAATGCAAGATGACACT-----TCA 774
QY 94 CysSerPhe---PheLysProArgGlyleThrleProAenPheTyThrleleGluValGlu 112
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DB 775 TGTATGTGCTGAGCTACATGCGCCACCTATATGTC-----AACATGGAAGTCTGGGTGGA 826
QY 113 AlaGluAenGlyAapGlyValleleLysSerHisThrTyTyTyArgLysleuGluAenle 132

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Db      829 GCAGAGATGCCCCCTGGAGAGCTCTCTCAGAGTCTATCAATTGTGACCCCGTGATAAA 888
Qy      133 AlAlvThrcIuPrpPolysIlePheArgValLysProValLeuGlyIleYsaGmeC 152
Db      889 GTGAAGACCCACCCCAATTAATTAATTCAGTACCACTCAGAGAATTAATCCAGTAA 948
Qy      153 lIeGnlIeGluTrpIleYsaProGluLeuAlaProValSerSerApeLeuYsaYrThr 172
Db      949 TTTAAGGTATCATGGGTCACTTCAGGCGTGGCGCTTT---TTAGATCTAAAGTCTGAC 1005
Qy      173 LeuArgPheArgThrValAsnSerThrSerTyrMetGluValAsnPheAlaYsaAsnArg 192
Db      1006 ATCCATATATGAGCAACAAAGATGCTCAATCTGATCCAGTCCCTCTT---GAAAGTACA 1062
Qy      193 LysApeLysAsnGlnThrTyrAsnLeuThrcIyLeuGlnProPheThrGluYrValIle 212
Db      1063 ATGTCTCTCGAACTTCTCTCACTGTGCAGACCTCAAGCTTTTACGAATATGTGTTT 1122
Qy      213 AlAlvArgCysAlaValLysGluSer-----LysPheTrpSerApeTrpSerGlnGlu 230
Db      1123 AGGATCCGG---TCCATTAAGACAGTGGGAGAGGCTACTGAGTGAAGTGAAGAGAG 1179
Qy      231 LysMetGlyMetThrGluGluAlaProCys---GlyLeuGluLeuTyrPargValLeu 249
Db      1180 GCTAGTGGGACCAATFACGAAGACAGACATCCAAACCAAGTTTCTGTATTAAGACA 1239
Qy      250 LysProAlaGluAlaAspGlyArgArgProValArgLeuLeuTrpLysValaArgGly 269
Db      1240 AATTCATCCCATGAGGAGCAATATAGATCTGTACGGCTCATATGAAAGGACGCTCTT 1299
Qy      270 AlAPrValLeuGluLysThrLeuGlyTyrAsnIleTrpYrProGluSerAsnThr 289
Db      1300 TCTGAAGCCAAATGGGAAATCTTGATTAAGAAGTG-----ATTCTTACGAGTCAAG 1353
Qy      290 AsnLeuThrGluThrMetAsnThrThrAsnGlnLeuGluLeuHisLeuGlyGlu 309
Db      1354 TCAGTCTCAACAAACGTACACAGTCACTGGCAGAGCTGACCGTGAATCTCACCAATGAC 1413
Qy      310 SerPheTrpValSerMetIleSerTyrAsnSerLeuGlyLysSerProValAlaThrLeu 329
Db      1414 CGCTATGTAGCGCTCTCTACGACGACAAACAGAGTGGCAATCAGTCACTGCTCTC 1473
Qy      330 ArgIleProAla 333
Db      1474 ACCATCCCCCAGC 1485

RESULT 14
CAS61173      592 bp      mRNA      linear      EST 19-NOV-2002
LOCUS      K0283D09-5N NIA Mouse Unfertilized Egg cDNA Library (Long) Mus
DEFINITION      musculus cDNA clone NIA:K0283D09 IMAGE:30052652 5', mRNA sequence.
ACCESSION      CA561173
VERSION      CA561173.1 GI:25105828
KEYWORDS      EST.
SOURCE      Mus musculus (house mouse)
ORGANISM      Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (base 1 to 592)
Pao,Y., Kargul,G.J., Dudekula,D.B., Qian,Y., Luo,A., Stagg,C.A.,
Martin,K., Aliba,K., Tanaka,T. and Ko,M.S.H.
Systematic Analyses of NIA Mouse Unfertilized Egg cDNA Library
(Long)
Unpublished (2001)
Other_ESTs: K0283D09-3
Contact: Dawood B. Dudekula
Laboratory of Genetics
National Institute on Aging/National Institutes of Health
333 Caseville Drive, Suite 4000, Baltimore, MD 21224-6820, USA
Email: cdna@igun.grc.nia.nih.gov
Plate: K0283 row: D column: 09
Seq primer: M13 Reverse

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High quality sequence stop: 592
POLYA=NO.

FEATURES
source Location/Qualifiers

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/issue_type="Unfertilized Egg"
/lab_host="DH10B"
/clone_lib="NIA Mouse Unfertilized Egg cDNA Library (Long)"
/note="Vector: pSPORT1 (Invitrogen); Site 1: SalI; Site 2: NotI; Mouse cDNA project by the Laboratory of Genetics, National Institute on Aging (NIA), Intramural Research Program, NIH (http://igun.grc.nia.nih.gov/cDNA). This is a long-transcript enriched cDNA library (Ref. Genome Res. 11: 1553-1558 (2001). [PMID: 11544199]). Total RNAs were extracted from a pool of 1488 unfertilized eggs. Double-stranded cDNAs were synthesized with an Oligo(dT) primer [Invitrogen]: 5'-pGACTAGTCTAGATCGCAGCGCCGCTTTTCTTTT-3', treated with T4 DNA polymerase, and purified by ethanol-precipitation. The cDNAs were ligated to lone-linker Lr-Sal4, purified by phenol/chloroform, and separated from free linkers by Centricon 100. Then, the cDNAs were amplified by long-range high fidelity PCR using Ex Taq polymerase (Takara) with a primer Sal4-S. The products were purified by phenol/chloroform and Centricon 100. The cDNAs were digested with SalI and NotI enzymes and cloned into SalI/NotI site of pSPORT1 plasmid vector. The DH10B E. coli host was transformed with the ligation mixture by the standard chemical method. The average insert size is about 2.5 kb. The library was constructed by Yulan Pao (NIA)."

ORIGIN

Alignment Scores:

Pred. No.: 1,63e-26 Length: 592
Score: 347.00 Matches: 67
Percent Similarity: 65.89% Conservative: 18
Best Local Similarity: 51.94% Mismatches: 34
Query Match: 9.84% Indels: 10
DB: 6 Gaps: 2

US-10-006-265-17 (1-662) x CA561173 (1-592)

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Qy      6 GlnProSerCysValAsnLeuGlyMetMetTrpThrAlaLeuTrpMetLeuProSer 25
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Db      289 CTCTGCAAAATTAAGCTTGGCAGTCTGCGAGTAAAGCCAGAAACATTTCTGCGCTTTC 348
Qy      46 TyrTyrArgLysAsnLeuThrCysThrTyrSerProGlyLysGluThrSerTyrThrGln 65
Db      349 TACTTGGACGAAGATGTGACTTGGCACTTGGACACGAGAAAGAAACATGATATACACG 408
Qy      66 TyrThrValLysArgThrTyrAlaPheGlyLysYsaAsnAsnCysThrThrAsnSer 85
Db      409 TACATTTGATCTTGACTTACCTCATAGAAA-----AGC 444
Qy      86 SerThrSerGluAsnArgAlaSerCysSerPhePheLeuProArgIleThrIle----- 103
Db      445 AATTATATGAGCAATGCTCAGAGGCTTCATTTCTTTTCCCGCTGTCGAATGCCCC 504
Qy      104 ProAspAsnTyrThrIleGluValGluAlaGluAsnGlyArgGlyValIleYsaSerHis 123
Db      505 CCAGACATCTGACGAGTGTGAAGTACAAAGCTCAAAATGAGAGTGAAGTAAATCTGAC 564

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QY 124 MetThrTyrTrpArgLeuGluAsnIle 132
 Db 565 ATCACTATTGGCATTTAATCTCCATA 591

RESULT 15
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 LOCUS K0279C07-SN NIA Mouse Unfertilized Egg cDNA Library (long) Mus
 DEFINITION musculus cDNA clone NIA:K0279C07 IMAGE:30052254 5', mRNA sequence.
 ACCESSION CA560924
 VERSION CA560924.1 GI:25105579
 KEYWORDS EST.
 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 479)
 Piao,Y., Kargul,G.J., Dudekula,D.B., Qian,Y., Luo,A., Stagg,C.A.,
 Martin,P., Alpa,K., Tanaka,T. and Ko,M.S.H.
 Systematic Analyses of NIA Mouse Unfertilized Egg cDNA Library
 (Long)
 Unpublished (2001)
 Other ESTs: K0279C07-3
 Contact: Dawood B. Dudekula
 Laboratory of Genetics
 National Institute on Aging/National Institutes of Health
 333 Cassell Drive, Suite 4000, Baltimore, MD 21224-6820, USA
 Email: cdna@igsun.grc.nia.nih.gov
 Plate: K0279 row: C column: 07
 Seq primer: M13 Reverse
 High quality sequence stop: 479
 POLY=A-No.

FEATURES
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 1. 479
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 /mol_type="mRNA"
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 /clone="NIA:K0279C07 IMAGE:30052254"
 /tissue_type="Unfertilized Egg"
 /lab_host="DH10B"
 /clone_11b="NIA Mouse Unfertilized Egg cDNA Library
 (Long)"
 /note="Vector: pSPORT1 (Invitrogen); Site_1: SalI; Site_2:
 NotI; Mouse cDNA project by the Laboratory of Genetics,
 National Institute on Aging (NIA), Intramural Research
 Program, NIH (http://igsun.grc.nia.nih.gov/cDNA). This is
 a long-transcript enriched cDNA library (Ref. Genome Res.
 11: 1553-1558 (2001). [PMID: 11544191]). Total RNAs were
 extracted from a pool of 1488 unfertilized eggs.
 Double-stranded cDNAs were synthesized with an Oligo (dT)
 primer (Invitrogen):
 5'-GGACTAGTTCTGATCGAGCGCGCCCTTTTCTTTTCTTTT-3',
 treated with T4 DNA polymerase, and purified by
 ethanol-precipitation. The cDNAs were ligated to
 lona-linker L1-SalI4, purified by phenol/chloroform, and
 separated from free linkers by Centricon 100. Then, the
 cDNAs were amplified by long-range high fidelity PCR using
 Ex Tag polymerase (Takara) with a primer SalI4-S. The
 products were purified by phenol/chloroform and Centricon
 100. The cDNAs were digested with SalI and NotI enzymes
 and cloned into SalI/NotI site of pSPORT1 plasmid vector.
 The DH10B E. coli host was transformed with the ligation
 mixture by the standard chemical method. The average
 insert size is about 2.5 kb. The library was constructed
 by Yulan Piao (NIA)."

ORIGIN
 Alignment Scores:
 Pred. No.: 4e-26 Length: 479
 Score: 342.00 Matches: 66
 Percent Similarity: 65.62% Conservative: 18

Best Local Similarity: 51.56%
 Query Match: 9.69%
 Db: 6
 Gaps: 2

US-10-006-265-17 (1-662) x CA560924 (1-479)

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Db	179	TGCAATTCACGCTGGCAGTCTGCCAGCTAAGCAGAGAACTTCTGTGCTTTAC	238
QY	47	TyrArgIysaAnLeuThrCysThrTrpSerProGlyIysGluThrSerTyrThrGlnTyr	66
Db	239	TTGCACAGAAATCTGACCTTGACCTTGAGACAGAGAAAGAAACCAATGATCCAGCAT	298
QY	67	ThrValIysaArgTrpTyrAlaPheGlyGluIysHisAspAncyCysThrThrAsnSerSer	86
Db	299	ATTGTGACTTGTACTTCTCTATGAAAA-----AGCAAT	334
QY	87	ThrSerGluAsnArgAlaSerCysSerPhePheLeuProArgIleThrIle-----Pro	104
Db	335	TATAGTCACATGCTACAGAGCTTCAATCTTTCCCTTCTGCAATGCCCA	394
QY	105	AspAnTyrThrIleGluAlaGluAsnGlyAspGlyValIleIysSerHisMet	124
Db	395	GACATCTGCACTGTGAAGTCAAGCTCAAAATGAGATGTAAAGTTAATCTGACATC	454
QY	125	ThrTyrTrpArgLeuGluAsnIle 132	
Db	455	ACATATTGGCATTTAATCTCCATA 478	

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Indexing Officer: NKIDANE - NIGIST M. KIDANE

Team: OIPEScanning

Dossier: 09757415

Legal Date: 02-14-2005

No.	Doccode	Number of pages
1	SRNT	56

Total number of pages: 56

Remarks:

Order of re-scan issued on

